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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:18:40 ; Search time 157.96 Seconds
(without alignments)
1240.873 Million cell updates/sec

Title: US-08-484-274-17
Perfect score: 1296
Sequence: 1 ATGCGTGAGAACACAGAA.....AAACTGGTCTGTCATCCTAA 1296

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/ptodata/2/ina/5A-COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B-COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5C-COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5D-COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6-COMB.seq.*
6: /cgn2_6/ptodata/2/ina/6CTUS-COMB.seq.*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-17
2	1296	100.0	1296	2	US-08-484-274A-17
3	1288	99.4	1296	1	US-08-391-339-8
4	1288	99.4	1296	2	US-08-484-274A-8
5	1006.4	77.7	1296	1	US-08-391-339-7
6	1006.4	77.7	1296	2	US-08-484-274A-7
7	958.4	74.0	1296	1	US-08-391-339-6
8	958.4	74.0	1296	2	US-08-484-274A-6
9	956.8	73.8	1692	2	US-08-484-274A-3
10	925.6	71.4	1293	1	US-08-391-339-4
11	925.6	71.4	1293	2	US-08-484-274A-4
12	925.6	71.4	1689	1	US-08-391-339-3
13	58.8	4.5	62	1	US-08-391-339-27
14	58.8	4.5	62	2	US-08-484-274A-27
15	58.4	4.5	69	1	US-08-391-339-30
16	58.4	4.5	69	2	US-08-484-274A-30
17	56.2	4.3	69	1	US-08-391-339-33
18	56.2	4.3	69	2	US-08-484-274A-33
19	53.6	4.1	68	1	US-08-391-339-32
20	53.6	4.1	68	2	US-08-484-274A-32
21	53	4.1	61	1	US-08-391-339-31
22	53	4.1	61	2	US-08-484-274A-31
23	52.8	4.1	65	1	US-08-391-339-28
24	52.8	4.1	65	2	US-08-484-274A-28
25	49.8	3.8	7218	1	US-08-232-463-14
26	39.8	3.1	3489	4	US-08-728-323A-1

c

27 39.8 3.1 32207 3 US-08-770-379-20 Sequence 20, Appl
28 34.6 2.7 543 7 5273901-6 Patent No. 5273901
29 34.4 2.7 1291 5 US-08-997-897-1 Sequence 1, Appl
30 34.2 2.6 9551 1 US-08-056-200-93 Sequence 93, Appl
31 34.2 2.6 9551 4 US-08-800-644-93 Sequence 93, Appl
32 34 2.6 1447 2 US-08-403-378B-14 Sequence 14, Appl
33 33.6 2.6 3292 1 US-07-814-964-12 Sequence 12, Appl
34 33.6 2.6 3292 1 US-08-258-442-12 Sequence 12, Appl
35 33.6 2.6 3292 6 PCT-US92-11107-12 Sequence 7, Appl
36 33.6 2.6 3292 2 US-08-471-033-18 Sequence 12, Appl
37 33.4 2.6 2004 3 US-08-471-044-18 Sequence 18, Appl
38 33.4 2.6 2004 3 US-08-463-483A-18 Sequence 18, Appl
39 33.4 2.6 2004 3 US-08-471-046A-18 Sequence 18, Appl
40 33.4 2.6 2004 3 US-08-470-566B-18 Sequence 18, Appl
41 33.4 2.6 2004 4 US-08-469-334-18 Sequence 18, Appl
42 33.4 2.6 2004 5 US-09-300-529-18 Sequence 18, Appl
43 33.4 2.6 2576 2 US-08-471-033-35 Sequence 35, Appl
44 33.4 2.6 2576 2 US-08-471-033-35 Sequence 35, Appl
45 33.4 2.6 2576 5 US-09-300-529-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-391-339-17
; Sequence 17, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B44F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1296
US-08-391-339-17

Query Match 100.0%; Score 1296; DB 1; Length 1296;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	61	GCTTTGATGCTTCAACGCTGCTGATTCGAAGTTACCTTGAATGATCCAAACCCACAGGT	120						
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Qy	181	ATGCCAGCAAACTTACATAGCTTCCAAAGTGGCTTCTTGACCCAAATGGTCCATGTCC	240						
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Qy	301	AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCACTGTG	360						
Db	301	AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCACTGTG	360						
Qy	361	CCTTTGATCAAGTCTTCCGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGT	420						
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Qy	421	CACCTTACCGTGTACCGTGGAGAACAGACTTCGCGACGGACCGTGGAGTTGGGAACIT	480						
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Db	481	CGTGTCTCAACGGTGTGCTGACTCAAAATCCTCAGCGTGATGCATTCGGTGATTTCGAT	540						
Qy	541	CCTAACCTTCTCAGCGCTTTACCAAGGAACTCTTATCGAAGAACGGTCACACCATC	600						
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Qy	1021	GCNCTCGCTCCCTGCCAGTTCCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCCGTC	1080						
Db	1021	GCNCTCGCTCCCTGCCAGTTCCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCCGTC	1080						
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Qy	1141	TTCCGCTCAGGCTCACCTCGGTATGACTTGGTCTCCAAATGACCGCAACCCCTCGTTCTGAG	1200						
Db	1141	TTCCGCTCAGGCTCACCTCGGTATGACTTGGTCTCCAAATGACCGCAACCCCTCGTTCTGAG	1200						
Qy	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATTCGCACCAACCCGTTTCGGT	1260						
Db	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATTCGCACCAACCCGTTTCGGT	1260						
Qy	1261	ATTGGTAAAGTCCAAAGCAAACTGGTCTGCATCTAA	1296						
Db	1261	ATTGGTAAAGTCCAAAGCAAACTGGTCTGCATCTAA	1296						

RESULT 2
US-08-484-274A-17
; Sequence 17, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1296
US-08-484-274A-17

Query Match 100.0%; Score 1296; DB 2; Length 1296;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGAATGATCCAAACCCACCCAGGT 120
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Db 121 GAAGTGCTCTTTTCGGTAAGCGTCTGCTTCAACGGTTCTCGTGTGTTCCAAATGTCC 180
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Qy 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGCTGATTCGAT 540
Db 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGCTGATTCGAT 540
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Db 541 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCTTATCGAAGAAACGGTTCACACCATC 600
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Db 721 ACCAAGGCTGTTCTGCTGTTGATGACAGTGTGTTGACAGTGGTGCACACTCCAAAGTCT 780
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Db 781 CTTGCTAACTCCCTTGGTGATGACATCCCATTCGATACCGAAGCTGGATACCATCGTG 840
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Db 841 ATGCCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAGTTCAATC 900
Qy 901 GCTACTCTTATGGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
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Qy 961 GCTGCTCTTAACCTGGAAGCGTCTCACGCTTCTCTACACTCGCGCTGAAGTTCGTTCCA 1020
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Qy 1021 GCTCTCGCTCTGCGAGTTCTGAAGAACTTACTTCCAAAGTGGTGGTTCGCTCCAAGC 1080
Db 1021 GCTCTCGCTCTGCGAGTTCTGAAGAACTTACTTCCAAAGTGGTGGTTCGCTCCAAGC 1080
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Db 1081 ATCCCGGATTCCTTCCAGTGGTGGTGGTGGTCTACCCGCTACTTCCAGAGCTTATCTACGCT 1140
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Db 1141 TTGGTTCAGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTCTGAG 1200
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Db 1261 ATTGTAAGTCCAAGCAAACTGGTCTCGATCCTAA 1296
RESULT 3
US-08-391-339-8
; Sequence 8, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESS: Monsanto Co. B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-391-339-8
Query Match 99.4%; Score 1288; DB 1; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGGCTGAGAACCACCAAGGTTGCTATCGCTGGAGCTGGAATCGTTGGTCTTTTGCACCT 60
Db 1 ATGGCTGAGAACCACCAAGGTTGCTATCGCTGGAGCTGGATCGTTGGTGTTCGACT 60
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGAATGATCCAAACCCACCCAGGT 120
Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGAATGATCCAAACCCACCCAGGT 120
Qy 121 GAAGTGCTCTTTTCGGTAAGCGTCTGCTTCAACGGTTCTCGTGTGTTCCAAATGTCC 180
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Db 181 ATGCCAGGAAACTTGAATAGGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATGTGCC 240
Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTCTTCTGCTGGA 300
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Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGACGAGCCGTGGAGGTGGGAACCTT 480
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Qy 481 CGTCTCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGCTGATTCGAT 540
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Qy 1081 ATCCCGGATTCCTTCCAGTGGTGGTGGTGGTCTACCCGCTACTTCCAGAGCTTATCTACGCT 1140
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Db 121 GAAGGTGCTTCTTCTCGGTACGGTGGTGTCTCAACGGTTCCTCCGTGTGTTCCTCAATGTCC 180
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Db 481 CGTCTGCTCAACGGGTGCTGCTACTCAATCTCTCAGCGCTGATGCATTTGGTTCGAT 540
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Db 541 CCTAACTTCTCTCACGCCCTTTACCAAGGAATCTTATCGAAGAACCGTTCACACATC 600
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Db 601 AACCCACAAGGTCTCGTGACTCTCTTGTGTTGCTGCTTTCATCGCTAACCGTGGAGATTC 660
QY 661 GTGCTGCTCGTCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
Db 661 GTGCTGCTCGTCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
QY 721 ACCAAGGTGTTCTTCTGCTGTTGATGAGCTGTTGTTGCAAGCTGGTGCACACTCCAACTCT 780
Db 721 ACCAAGGTGTTCTTCTGCTGTTGATGAGCTGTTGTTGCAAGCTGGTGCACACTCCAACTCT 780
QY 781 CTTGCTAACTCCCTGGTGATGACATCCCATTTGGATACCGAACCGTGGATACCAATCTCGT 840
Db 781 CTTGCTAACTCCCTGGTGATGACATCCCATTTGGATACCGAACCGTGGATACCAATCTCGT 840
QY 841 ATCGCAACCCAGAGCTGCTCCACGTATTTCCAACCTACCGATGCTTCTTGAAAGTTTCATC 900
Db 841 ATCGCAACCCAGAGCTGCTCCACGTATTTCCAACCTACCGATGCTTCTTGAAAGTTTCATC 900
QY 901 GCTACTCTCTATGAGATGGGTCTTCTGTTGCTTGGAAACCGTTTTCGCTGCTCTCACT 960
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QY 961 GCTGCTCTTAACCTGGAAGGGTCTCAGCTTCTTACACTCAGCTCGTAAGTTGCTTCCA 1020
Db 961 GCTGCTCTTAACCTGGAAGGGTCTCAGCTTCTTACACTCAGCTCGTAAGTTGCTTCCA 1020
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Db 1021 GCTCTCGCTCTCTGAGATGTTCTCAAGAACCTTACTTCAACCTGGATGGTTCCTGCTCAAGC 1080
QY 1081 ATCCGGGATTCCTCTCCAGTGTGCTGCTGCTTACCCGTTACTCCAGACGTTTATCTACGCT 1140
Db 1081 ATCCGGGATTCCTCTCCAGTGTGCTGCTGCTTACCCGTTACTCCAGACGTTTATCTACGCT 1140
QY 1141 TTCGGTACGGTTCAGCTCGGTATGACTGGTGTCTCAANTACCGCAACCCCTCGTTCTGAG 1200
Db 1141 TTCGGTACGGTTCAGCTCGGTATGACTGGTGTCTCAANTACCGCAACCCCTCGTTCTGAG 1200
QY 1201 CTTCTCGGAGGTGAGAAGACCTCTATCGACATCTCTTCCATTCGCAACACCGTTTCGCT 1260
Db 1201 CTTCTCGGAGGTGAGAAGACCTCTATCGACATCTCTTCCATTCGCAACACCGTTTCGCT 1260

QY 1261 ATTGGTAAGTCCAAGCAAACTGGTCTTCATCCTAA 1296
Db 1261 ATTGGTAAGTCCAAGCAAACTGGTCTTCATCCTAA 1296
RESULT 4
US-08-484-274A-8
; Sequence 8, Application US/08484274A
; Patent No. 5716760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-8

Query Match 99.4%; Score 1288; DB 2; Length 1296;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATCGCTGAGAACCAAGAGGTGGTATCGCTGAGCTGGAATCGTTGGTGTGGACT 60
Db 1 ATCGCTGAGAACCAAGAGGTGGTATCGCTGAGCTGGAATCGTTGGTGTGGACT 60
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Db 61 GCTTTGATGCTTCAACGTCGTTGATTCAGGTTACCTTGTATGATCCAAACCCACCAAGT 120
QY 121 GAAGGTGCTCTTTCGGTAACGTTGGTTCACAGGTTCTCCGTTGTTCCTCAANTGTC 180
Db 121 GAAGGTGCTCTTTCGGTAACGTTGGTTCACAGGTTCTCCGTTGTTCCTCAANTGTC 180
QY 181 ATCCAGGAAACTTGACTAGCGTTCCTCAAGTGGCTTCTTGACCAAAATGGGTCCATTCCTC 240
Db 181 ATCCAGGAAACTTGACTAGCGTTCCTCAAGTGGCTTCTTGACCAAAATGGGTCCATTCCTC 240
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Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACTCATCAAGTCCACTGTG 360

Db 301 AGACCAACAAGGTGAGGAGCAAGCTAAGGCACCTCCGTAACTCATCAAGTCCACTGTG 360
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Qy 421 CACCTTACCGGTGACCGTGGAGAGCACACTTCGCGACGGACCGTGGAGGTGGAACTT 480
Db 421 CACCTTACCGGTGACCGTGGAGAGCACACTTCGCGACGGACCGTGGAGGTGGAACTT 480
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Db 481 CGTCTCTCAACGGGTCTGCTACTCAAAATCCCTACGCGTGTATGCTGCTGATTCGAT 540
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Db 541 CTTAACTTGTCTCAGCCCTTTTACCAAGGGAATCCCTTATCGAAGAGACGGTACACCATC 600
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Db 601 AACCCACAAGGTCTGCTGACTCTCTGTTTTCGTGCTTTTCATCGCTAACGGTGGAGAGTTC 660
Qy 661 GTGCTGCTCGTGTATCGGATTCGAGACTGAAAGTCTGCTCTCAAGGATACACACC 720
Db 661 GTGCTGCTCGTGTATCGGATTCGAGACTGAAAGTCTGCTCTCAAGGATACACACC 720
Qy 721 ACCAAGCGTGTCTTGTCTGTATCGACACTGTTGTTGAGCTGGTGCACACTCAAGTCT 780
Db 721 ACCAAGCGTGTCTTGTCTGTATCGACACTGTTGTTGAGCTGGTGCACACTCAAGTCT 780
Qy 781 CTTCGTAACCTCCCTTGGTGATGACATCCATTTGGATACCGACGTGGATACACATCTGT 840
Db 781 CTTCGTAACCTCCCTTGGTGATGACATCCATTTGGATACCGACGTGGATACACATCTGT 840
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Db 841 ATCCGCAACCCAGAGCTCTCCAGCTATTCACAACTACCGATCTCTCGAAAGTTTCAATC 900
Qy 901 GCTACTCTATGAGAGTGGGTCTTGGTGTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 901 GCTACTCTATGAGAGTGGGTCTTGGTGTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Qy 961 GCTGCTCTAAGTGAAGCGTCTCACCTCTCTACACTCGCGCTCGTAAGTTCCTTCCA 1020
Db 961 GCTGCTCTAAGTGAAGCGTCTCACCTCTCTACACTCGCGCTCGTAAGTTCCTTCCA 1020
Qy 1021 GCTCTCGCTCTCCAGTCTTGAAGAAGCTTACTCCAAGTGGATGGTTCGCTCCAAGC 1080
Db 1021 GCTCTCGCTCTCCAGTCTTGAAGAAGCTTACTCCAAGTGGATGGTTCGCTCCAAGC 1080
Qy 1081 ATCCCGGATTCCTTCCAGTGAAGTGGTGTGCTACCCGTACTCCAGAGCTTTATCTACGCT 1140
Db 1081 ATCCCGGATTCCTTCCAGTGAAGTGGTGTGCTACCCGTACTCCAGAGCTTTATCTACGCT 1140
Qy 1141 TTCGCTCAGGTCACCTCGGTATGACTGGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200
Db 1141 TTCGCTCAGGTCACCTCGGTATGACTGGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200
Qy 1201 CTCTCCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Db 1201 CTCTCCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Qy 1261 ATTGTAAGTCCAAAGCAAACTGGTCTGCATCTTAA 1296
Db 1261 ATTGTAAGTCCAAAGCAAACTGGTCTGCATCTTAA 1296

RESULT 5

US-08-391-339-7

; Sequence 7, Application US/08391339

; Patent No. 5463175

; GENERAL INFORMATION:

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-391-339-7

Query Match 77.7%; Score 1006.4; DB 1; Length 1296;

Best Local Similarity 86.0%; Pred. No. 0;

Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAAGGTTCGTATCGCTGAGCTGGAATCGTTGGTCTTTGCACT 60

Db 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGANTCGTTGGTGTATGCACT 60

Qy 61 GTTTTGTGCTTCAACGCTCGTGGATTCACAGTTACCTTGAATGATCCAAACCCACAGT 120

Db 61 GTTTTGTGCTTCAACGCTCGTGGATTCACAGTTACCTTGAATGATCCAAACCCACAGT 120

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Db 121 GAAGTGTCTCTTTTCGGTAAACGCTGCTTCAACGGTTCCTCGTGTGTTCCAATGTCC 180

Qy 181 ATCCGAGCAAACTTCACTAGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC 240

Db 181 ATCCGAGCAAACTTCACTAGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC 240

Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTGTGTTGTTCTTGGTCTGGA 300

Db 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTGTGTTGTTCTTGGTCTGGA 300

Qy 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360

Db 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360

Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGTAGCCACCTTATCCGTACCAAGGT 420

Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGTAGCCACCTTATCCGTACCAAGGT 420

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QY 421 CACCTTACCCTGTTACCGTGGAGAGACAGACTTCGCCAGGGACCGTGGAGGTTGGAACTT 480
Db 421 CATCTGACCGTATCGTGGAGAGACAGACTTCGCCAGGGACCGGAGGTTGGAACTG 480
QY 481 CGTGTCTCAACGCTGTTCCGTACTCAAACTCTCAGCGCTGATGCATTCGGTGATTTCCAT 540
Db 481 CGGCGTCTCAACGCTGTTCCGACGAGATCTCTCTGCTGATGCTTTCGGTGATTTCCAT 540
QY 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTTCGAGAGAGAACGGTCCACACCATC 600
Db 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTTCGAGAGAGAACGGTCCACACCATC 600
QY 601 AACCCACAAGTCTCCGAGCTCTCTTGTTCCTGCTTTCATCCTTTCATCCTTTCATCCTTTCAT 660
Db 601 AATCCGAAGGCTCTGCTGAGCTCTCTTGTTCCTGCTTTCATCCTTTCATCCTTTCATCCTTTCAT 660
QY 661 GTGCTCTCTGCTGATTCGGAATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACCATC 720
Db 661 GTATCTCGCGCTGCTGAGCTGTTGAGACTGAAGTCTGCTCTCAAGGGTATCACACCATC 720
QY 721 ACCAAGCTGTTCTTGTGTTGATGACGCTGTTGTTGAGCTGTTGTCACACTTCCAAAGTCT 780
Db 721 ACTAAGCTGTTCTGCTGTTGATGACGCTGTTGTTGAGCTGTTGTCACACTTCCAAAGTCT 780
QY 781 CTTCCTAACCTCCCTTGTGATGACATCCCATTCGATACCGAACGTTGATACACATCGTG 840
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QY 841 ATCCGCAACCCAGAGCTGCTCCAGCTATTCACACTACCGATGCTTCTGGAAGTTTCATC 900
Db 841 ATCCGCAACCCAGAGCTGCTCCAGCTATTCACACTACCGATGCTTCTGGAAGTTTCATC 900
QY 901 GCTACTCTATGAGATGGGCTCTGCTGTTGCTGGAACGCTTGTGCTGCTGCTCACT 960
Db 901 GCGACACTATGGAATGGGCTCTGCTGTTGCTGGAACGCTTGTGCTGCTGCTCACT 960
QY 961 GCTGCTCCTTAACCTGGAAGCTGCTGACGCTTCTACACTCCGCTGCTGCTGCTGCTGCTCA 1020
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QY 1081 ATCCCGGATTCCTTCCAGTGATTTGGTGTCTACCCGTACTTCCAGAGCTTATCTACGCT 1140
Db 1081 ATTCCTGATCTCTTCCAGTGATTTGGTGTCTACCCGTACTTCCAGAGCTTATCTACGCT 1140
QY 1141 TTCCGTCACGCTACCTCCGCTGATGACTGCTCCTCAATGACCGCAACCTCTGTTCTCAG 1200
Db 1141 TTTCGTCACGCTACCTCCGCTGATGACTGCTCCTCAATGACCTGCAACTCTGTTCTCAG 1200
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QY 1261 ATTGGTAAGTCAAGCAAACTGCTGCTGCTCACTAA 1296
Db 1261 ATTGGCAATCCAGCAAACTGCTGCTGCTCACTAA 1296
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RESULT 6

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US-08-484-274A-7
: Sequence 7, Application US/08484274A
: Patent No. 576760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
```

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: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOST130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-7
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Query Match 77.7%; Score 1006.4; DB 2; Length 1296;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
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QY 1 ATGGCTGAGAACACACAAAGGTTGGTATCGCTGGAGCTGGAATCGTGTGGTTCGACT 60
Db 1 ATGGCTGAGAACACACAAAGGTTGGTATCGCTGGAGCTGGAATCGTGTGGTTCGACT 60
QY 61 GCTTTGATGCTTCAAGCTGCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
Db 61 GCTTTGATGCTTCAAGCTGCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
QY 121 GAAGTGCCTCTTCGGTAAAGCTGTTGTTCAAGGGTTCCTCCGTTGTTTCAAGTGC 180
Db 121 GAAGTGCCTCTTCGGTAAAGCTGTTGTTCAAGGGTTCCTCCGTTGTTTCAAGTGC 180
QY 181 ATGCCAGGAAGCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGTCCATGCTCC 240
Db 181 ATGCCAGGAAGCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGTCCATGCTCC 240
QY 241 ATCCGTTTCGGCTACTTTCACCAACCATCATGCTTGGTTGATTGCTTTCGTTTGTGGA 300
Db 241 ATCCGTTTCAGCTATTTTCCAAACCATCATGCTTGGTTGATTGCTTTCGTTTGTGGA 300
QY 301 AGACCAAAAGCTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360
Db 301 AGACCAAAAGCTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360
QY 361 CCTTTGATCAAGCTTCTGCTGAGGAGGCTGATGATGAGGCAATTCCTTATCCGTCAGAGGT 420
Db 361 CCTTTGATCAAGCTTCTGCTGAGGAGGCTGATGATGAGGCAATTCCTTATCCGTCAGAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAACAGACTTCGCCAGGGACCGTGGAGGTTGGGAACCTT 480
Db 421 CATCTGACCGTATATCGTGGAGAGAGAGACTTCGCCAGGGACCGTGGAGGTTGGGAACCTG 480
QY 481 CGTGTCTCAACGCTGTTTCGTTACTCAAACTCTCAGCGCTGATGCATTCGGTGTATTCGAT 540
Db 481 CGGCGTCTCAACGCTGTTTCGTTACTCAAACTCTCAGCGCTGATGCATTCGGTGTATTCGAT 540
QY 541 CCGTAAGTCTGCTCAGCGCTTACCAAGGGAATCCTTTCGAGAGAGAACGGTCCACACCATC 600
Db 541 CCTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTTCGAGAGAGAACGGTCCACACCATC 600
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[illegible]

RESULT 7

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US-08-391-339-6
: Sequence 6, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. 884F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391.339

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Db 661 GTATCTCGCGGTGTATCTGGCTTTGAGACGTGAAGGTAGGCGCTTAAAGGCATTACAAACC 720
QY 721 ACCAACGGTGTCTTCTGTTGTATGACAGCTGTCTTGCAGCTGGTGACACACTCCAAGTCT 780
Db 721 ACNACGGCGTCTCGCGGTGTATGACAGCGTGTCTCCAGCGCGCACACTCGAAATCA 780
QY 781 CTGTCTAACTCCCTTGTGTATGATACATCCCATTTGGATACCGAAACGTGGATACCAACATGCTG 840
Db 781 CTGTCTAACTCCCTTGTGTATGATACATCCCGCTCGATACCGAAACGTGGATATCATATATGCTC 840
QY 841 ATCGCCCAACCCAGAACTGCTCCACGTATTTCCAACTACCCGATGCTTCTGGAAGTTTCATC 900
Db 841 ATCGCGAATCCGGAAGCGCTCCACGATTTCCGACGACCGTTCGAGGAAATTCATC 900
QY 901 GCTACTCTATGAGATCGGTCTTCTGTTGCTTGGAAACCGTTGAGTTTCGCTGGTCTCACT 960
Db 901 GCACACCTATAGNAATGGGGTTCGGCTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA 960
QY 961 GCTGCTCCTAACTGGAAAGCGTGTACGTTCTCTACACTCCGCGTCTGTAAGTTGCTTTCCA 1020
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QY 1021 GCTCTCCCTCCCTCCAGTCTGAGAACGTTACTCCAACTGGATGGGTTCCTGCTCCAAAGC 1080
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Db 1201 CTCTCGCAGGTGAGAACCTCTATGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
QY 1261 ATTGGTAAGTCCAAGCAACTGGTCTGCTGATCTTAA 1296
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RESULT 8
US-08-484-274A-6
; Sequence 6, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6

Query Match 74.0%; Score 958.4; DB 2; Length 1296;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 1 ATGCGCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCTGGAATCCCTTGGTGTTCGACT 60
Db 1 ATGCGCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCGCGGATCGCTGGCGGTATGCACG 60
QY 61 GCTTTGATGCTTCAACGTCGTTGATTCGAAGTTACCTTGATTCGAATCCAAACCCACACAGGT 120
Db 61 GCGCTGATGCTTCAAGCGCGCGGATTCGAAGTTACCTTGATTCGAATCCAAACCCACACAGGT 120
QY 121 GAAGGTGCTCTTTTCGGTACGCTGGTGTTCGAAGGTTCCCTCCGTTGTTTCCAAATGTC 180
Db 121 GAAGGTGCTCTTTTCGGTACGCTGGTGTTCGAAGGTTCCCTCCGTTGTTTCCAAATGTC 180
QY 181 ATGCCAGGAACTTGAAGTTCGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCTATGTC 240
Db 181 ATGCCAGGAACTTGAAGTTCGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCTATGTC 240
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Db 241 ATCCGTTTCAGCTATTTTCCAAACCATCATGCTTGGTGTGATTCGTTTCTGTTAGCCGA 300
QY 301 AGACCAACAGGTGAGGAGCAAGCTAAGGCACTCGTACCTTCATCAAGTCCACAGTG 360
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QY 361 CTTTGTATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCAGCAAGGT 420
Db 361 CTTTGTATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCAGCAAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAGCAAGCTTCCGCAAGGAGCGTGGAGGTTGGAACTT 480
Db 421 CATCTGACCGGTATATCTGTTGAGAGAGCAGACTTCCGCAAGGAGCGGAGGTTGGAACTG 480
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QY 541 CCTAATCTGTCTCAGCGCTTTTACCAAGGGAATCTTATCGAAGAGAGAGCGGTACACCAATC 600
Db 541 CCGAATCTGTCTCAGCGCTTTTACCAAGGGAATCTTATCGAAGAGAGAGCGGTACACCAATC 600
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Db 601 AATCCGCAAGGCTGCTGACCCCTCTTGTTCGCGGTTCATCGCGAAGCGTGGCGAATTT 660
QY 661 GTGTCTGCTGTGTATTCGGAATTCGAGACTGAAGGTGCTCTCAAGGGTATCAACACC 720
Db 661 GTATCTCGCGGTGTATTCGCGCTTTGAGACTGAAGGTAGGCGGCTTAAAGGCAATTCACACC 720
QY 721 ACCAAGCGTGTCTGCTGTGTTGATGCAAGCTGCTGCTGAGCTGCTGACACTCCAAAGTCT 780
Db 721 ACGAACCGGTCTTGGCGGTTCGAGCGGTTCGCGAGCGGTTCGCGAGCGCGGCACTCGAAATCA 780
QY 781 CTGTCTAACTCCCTTGTGTATGATGACATCCCATTTGGATACCGAACTGGATACCACTG 840
Db 781 CTGTCTAACTCCCTTGTGTATGATGACATCCCGCTTCGATACCGAACTGGATATCATATGCTC 840
QY 841 ATGCCCAACCCAGAGGTGCTGCTCAAGTATCCCACTACCGGATCTTCTGGAAGTTTCATC 900
Db 841 ATGCCCAACCCAGAGGTGCTGCTCAAGTATCCCACTACCGGATCTTCTGGAAGTTTCATC 900

Db 841 ATCCGAATCCGAAGCCCTCCAGCATTCGACAGCCGATGCGTCAGGAATAATTCATC 900
Qy 901 GCTACTCTATGAGATGGGTCTTCGTGTGCTGGAACGGTTGAGTTCGCTGGTCTCACT 960
Db 901 GCGACACCTATGAAATGGGCTTCGCGTGGGGGTACGGTTGAGTTCGCTGGGCTCACA 960
Qy 961 GCTGCTCTTAAGTGAAGGGTCTCAGTTCTCTACACTCGCGGCTCGTAAGTTGCTTCCA 1020
Db 961 GCGGCTCTTAAGTGAAGGGTCTCAGTTCTCTACACTCGCGGCTCGTAAGTTGCTTCCA 1020
Qy 1021 GCTCTCGCTGCGGAGTCTCAAGAACGTTACTCCAGTGATGGTTTCGGTCCCAAGC 1080
Db 1021 GCGCTCGGCGCTCGAGTTCTCAAGAACGATATTCAAATGATGGGTTCCGGCGGAGC 1080
Qy 1081 ATCCGGGATTCCTTCCTCCAGTGGTGTGCTACCGCTACTCCAGACGTTATCTACGCT 1140
Db 1081 ATCCGGGATTCCTTCCTCCAGTGGTGTGCTACCGGCAACCCGACACCGTATCTATGCT 1140
Qy 1141 TTCGCTCAGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTTCTGAG 1200
Db 1141 TTCGCGCCACGGTCACTCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1200
Qy 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAAAACGTTTCGCT 1260
Db 1201 CVCCTCGGAGGCAAGACCTCAATCGACATTTGCGCCTTCGCAACCAACGCTTTGGT 1260
Qy 1261 ATTGTAAGTCCAAAGCAACTGGTCTGTCATCCTAA 1296
Db 1261 ATTGCAAAATCCAAAGCGGTCCGCAAGTTAA 1296

RESULT 9

US-08-484-274A-3
; Sequence 3, Application US/08484274A
; Patent No. 576760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-274A-3

Query Match

73.8%; Score 956.8; DB 2; Length 1692;

Best Local Similarity 83.6%; Pred. No. 0;
Matches 1084; Conservative 0; Mismatches 212; Indels 0; Gaps 0;
Qy 1 ATGGGCTGAGAACCACAAAGAGTGGTATCGCTGGAGCTGGAATCGTGGTGGTTCGCACT 60
Db 120 ATGCTGAGAACACAAAGAGTGGTATCGCTGGAGCCGGAATCGTGGGCTATGCAGC 179
Qy 61 GCTTGTATGCTTCAACGTCGTGGATTCAAGGTACCTTGTGATTCATCAAAACCCACAGGT 120
Db 180 GCGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGAACCTCCTCGC 239
Qy 121 GAAGGTGCTCTTTCGGTAAACGCTGGTTCGTTCAACGGTTCCTCCGTTGTTCGAATGTCC 180
Db 240 GAAGGTGCTATCGTTTGGGAATCGCGATGCTTCAAGGGCTCATCCGCTCGCTATGTCTCC 299
Qy 181 ATCCGAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGAACCAATGGTGCATTTGTC 240
Db 300 ATCCGCGGAAACTTGACGAGCGTTCGCGAAGTGGCTTTCGACCCGATGGGGCGTTGTCA 359
Qy 241 ATCCGCTTTCGGTACTTTCCAACCATCATCCCTGGTTCGTTGTGATTCGTTTTCGTTGCTGA 300
Db 360 ATCCGCTTTCAGCTATTTTCCAAACCATCATCCCTGGTTCGTTGATTGCTGCTTCTGTAGCCGA 419
Qy 301 AGACCAACAAGGTGAAGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
Db 420 AGACCAACAAGGTGAAGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 479
Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCAGCTTATCCGTCACGAAGCT 420
Db 480 CCTCTCATCAAGTCAATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 539
Qy 421 CACCTTACCGTGTACCGTGGAGAAGCAGACTTTCGCCAGGAGCGCTGGAGCTTTCGGAACCT 480
Db 540 CATCTGACCGTATATCGTGGAGAAGCAGACTTTCGCCAAGGACCGCGAGGTTGGGAACCTG 599
Qy 481 CGTGTCTCAACGGTGTTCGTTACTCAAACTCTCAGGCGCTGATGCTATGCGGTGATTCGAT 540
Db 600 CGGCGTCTCAACGGTGTTCGTCACGCGAGATCCTCAGCGCGGATCGCTTGGGGATTTTCGAT 659
Qy 541 CCTAACTTGTCTCAGCGCTTTTACCAGGGAATCCTTATCGAAGAGAACGCTCACACCATC 600
Db 660 CCGAATCTGTCGATGCGTTTACCAGGCGCATCTTATAGAGAGAACGCTCACAGATT 719
Qy 601 AACCCACAAGGTCTCGTACTCTCTTGTTCGTCGTTTCATCGCTAACCGTGGAGAGTTTC 660
Db 720 AATCCGCAAGGGCTCGTGACCTCTTGTTCGCGCTTTTATCGCGAAGCGGTGGCGAATTC 779
Qy 661 GTGCTGCTGCTGTTTATCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCAACC 720
Db 780 GTATCTCGCGCTGTCTATCGGCTTTTGAGACTGAAGGTAGGGCGCTTAAAGGCGATTACAACC 839
Qy 721 ACCAAGGTGTTTCTGCTGTGATGCACTTCCATTCGATACCGAAGCGTGGATACCAATCT 780
Db 840 ACGAAGGGGTTCTGCGCGCTTATCGAGCGGTTGTGCGAGCGCGGCCACACTCGAATCA 899
Qy 781 CTTGTCTAATCCCTTGGTGTGATGACATCCCATTCGATACCGAAGCGTGGATACCACTCGTG 840
Db 900 CTTGTCTAATTCGTAGGCGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATCGTC 959
Qy 841 ATCCGCAACCCAGAACGCTGCTCCAGCTATTTCCAATACCGATGCTTCTGCGAAGTTTCATC 900
Db 960 ATCCGGAATCCGGAAGCGCTCCAGCATTTCCGACGACCGCATCGCGTCAGAGAAATTCATC 1019
Qy 901 GCTACTCTCTATGAGATGGTCTTCGTGTGCTGGAAACGTTGAGTTCGCTGGTCTCACT 960
Db 1020 GCGACACCTATGGAATGGGCTTCGCTGGCGGCTACGGTTGAGTTCCGCTGGCTCACA 1079
Qy 961 GCTGCTCTTAAGTGAAGCGTGTCTCACGTTCTCTACACTCGGCGCTCGTAAGTTGCTTCCA 1020
Db 1080 GCGGCTCTTAAGTGAAGCGTGGCATGTGCTCTATACCGACGCTCGAANAATCTCTTCCA 1139
Qy 1021 GCTCTGCGTTCCTGCGAGTTCTGAAGAACGTTTACTTCAAGTGGATGGGTTTCGCTGCCAAGC 1080

Db 1140 GCCCTCCGGCTTGGAGTTCTGAAGAAGCAATATTCAAAATGGATGGGGTTCGGCGCCGAGC 1199
QY 1081 ATCCCGGATTCCTCCAGATGATTGGTCGCTACCCGCTACTCCAGACAGTTATCTAGGCT 1140
Db 1200 ATCCCGGATTCCTCCCGTGAATGGCGGCAACCCGACACCCGAGTAATCTATGCT 1259
QY 1141 TTCCGTCACGGTCACCTCGGTATGACTGGTGTCCCAATGACCCGAAACCCCTGCTGTGAG 1200
Db 1260 TTCCGGCATGTCATCTCGGCATGACAGGGGCGCGATGACCGAAGCTCGTCTCAGAG 1319
QY 1201 CTCTCCAGGTGAGAGACCTCTATCGACATCTCTCCATTCCGACCAACACGGTTTCGGT 1260
Db 1320 CTCTCCAGCGGAAAGACCTCAATCGACATTTGGCCCTTCGGACCAACCCGCTTTGGT 1379
QY 1261 ATTTGGTAAGTCCAAAGCAACTGGTCTCGCATCTAA 1296
Db 1380 ATTTGGCAATCCAAGCAACGGGTCCGCAAGTTAA 1415

RESULT 10

US-08-391-339-4
; Sequence 4, Application us/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
US-08-391-339-4

Query Match 71.4%; Score 925.6; DB 1; Length 1293;
Best Local Similarity 83.6%; Pred. No. 1.4e-298;
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;

QY 1 ATGCTGAGAACCAACCAAGAGCTTGGTATCGCTGGAGCTGGAAATCGTTGGTGTTCACAT 60
Db 1 ATGCTGAGAACCAACCAAGAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAGC 60
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATTCCAAAACCCACAGT 120
Db 61 CGCTGTGATGCTTCAAGCGCGCGGATTCAAAGTCAACCTTGAATGACCCGAAACCCCTCTGC 120
QY 121 GAAGGTGCTCTTTCGGTAACGCTTCTCAACGCTTCTCCGTTGTTTCCCAATATGCC 180
Db 121 GAAGGTGCATCGTTTGGGATGCCGATGCTTCAACGCTCATCCGCTGCTCCTATATGCC 180
QY 181 ATGCCGAAACATTCAGTACGCTTCCAAAGTGGCTTTCGACCCAAATGGTCCATTTGCC 240
Db 181 ATGCCGAAACATTCAGTACGCTTCCAAAGTGGCTTTCGACCCGATGGG-CCGTTGTCA 239
QY 241 ATCCGTTTCGGCTACTTTCCAACCATCATGCTTGGTTGATTGATTCGTTCTTGGTCTGGA 300
Db 240 ATCCGTTTCAGCTA-TTTTCCAACCATCATGCC-TGGTTTGAATTCGGCTTCTGTTAGCCGGA 297
QY 301 AGACCAACCAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
Db 298 AGACCAACCAAGGTGAAGGAGCAAGGAGCAAGGAGCAAGCTCCGCAATCTCATCAAGTCCAGGTG 357
QY 361 CTTTGTATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420
Db 358 CCTCTGATCAAGTCTTGGCGGAGGAGCTGATGCGAGGCACTCTGATCCGCCATGAAGT 417
QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGACGGGACCGTGGAGGTTGGAACTT 480
Db 418 CATCTGACCGGTATATCGTGGAGAGCAGACTTCCGCAAGGAGCCGCGAGGTTGGGAACGTG 477
QY 481 CGTCTCTCAACGCTGTTCTGTAACCTCCTCAGCGCTGATGCATTCGCTGATTTCCAT 540
Db 478 CGGCGTCTCAACGCTGTTCCGACGAGATCCTCAGCGCGGATGCGTTCGGGGATTTCCAT 537
QY 541 CCTAACTTGTCTACGCTTTTACCAAGGGAATCTTATCGAAGAGAACGCTCACACCATC 600
Db 538 CGAACTTGTGCGATCGTTTACCAAGGCAATCTTATAGAAGAGAACGCTCACACGAT 597
QY 601 AACCCACAAGTCTCGTGACTCTCTTGTTCGTTTCATCGCTAACGCTGGAGAGTTC 660
Db 598 AATCCGAAGGCTCGTGACCTCTTGTTCGGGCTTATCGCAACGCTGGCAATTC 657
QY 661 GTGCTCTGCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGATATCACCATC 720
Db 658 GTATCTGGCGTGTATCGGCTTTGAGACTGAAGTAGGGCGCTTAAGGCAATACACATC 717
QY 721 ACCAAGGCTGTTCTGCTGTTGATGTCAGCTGTTGTTGAGCTGGTGCACACTTCCAAAGTCT 780
Db 718 ACGAAGCGGCTTCTGGCGGTTGATGTCAGCGGCTTGTGCGAGCGCGCACACTCGAAATCA 777
QY 781 CTTCCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGAAGCTGGATACCATCTGTG 840
Db 778 CTTGCTAATTCGTTAGGCGATGACATCCGCTCGATACCGAAGCTGGATATCATATCTGTC 837
QY 841 ATGCCCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTTCATC 900
Db 838 ATCCGGAATCCGGAAGCGGCTCCACGCAATCCGAGACCGATGCTCAGGAAAATTCATC 897
QY 901 GCTACTCTATGGAGATGGGCTTTCGTTGCTGGAAACCGTTGAGTTCGCTGGTCTCACT 960
Db 898 GCGACACTATGAAATGGGGCTTTCGGCTGGCGGCTACGGTTGAGTTCGCTGGGCTCACA 957
QY 961 GCTGCTCTTAACGAGCGTGTCTACACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 958 GCGCTCTTAACGAGAACGTTGCGCATATACGCGACGCTCGCAAACTTCTTCCA 1017
QY 1021 GCTCTGCTCTGCGAGTTCCTGAAGACGTTACTTCCAAAGTGGGTTTTCGCTCCAAAG 1080
Db 1018 GCGCTCGGCTGCGAGTTCCTGAGAGACGATATTCCAAAATGGATGGGTTTCGCGCGGAGC 1077
QY 1081 ATCCCGGATTCCTTCAGTGAATTTGGTGTGCTACCGGTACTCCAGAGGTTATCTACGCT 1140


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Db 1198 CTCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGGCACCAAAACCGCTTTGGT 1257
Qy 1261 ATTGGTAAGTCCAAGCAAACTGGCTCTGCATCCTAA 1296
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Db 1258 ATTGGCAAAATCCAAGCAAAACGGGTCCGGCAAGTTAA 1293

RESULT 12
US-08-391-339-3
; Sequence 3, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-391-339-3

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	Query Match	71.4%	Score 925.6;	DB 1;	Length 1689;
	Best Local Similarity	83.6%;	Pred. No. 1.7e-298;		
	Matches 1084; Conservative	0;	Mismatches 209;	Indels	Gaps
QY	1	ATGCGCTCAGAACCAACAAGAAGTTTGGTATCCCTCGAGCTGGAATCGTTGGTGTTTGCACT	60		
Db	120	ATGTCTCAGAACCAACAAAAGTAGGCATCCCTCGAGCCGGAATCGTCGGCGTATGCACG	179		
QY	61	CGTTTGTATGCTTCAACGTCGTGGATTCAAAGGTTTACC TTGTATGCCAAACCCACCACGGT	120		
Db	180	CGCGTGATGCTTTCAGCCCGCGGATTCAAAGTCACCTTGATTGATGCCCAACCCCTCTGGC	239		
QY	121	GAAGTGCGCTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCTCCTCGTGTGTTCCAAATGCCC	180		
Db	240	GAAGTGCATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTGCC	299		
QY	181	ATGCCAGAAACTTTGACTTACGCTTCCAAGTGGCTCTTTGACCCCAATGGGTCCATTGTGCC	240		
Db	300	ATGCCGGAAACTTTGACGAGCGTCCGAAATGGCTCTTTGACCCGATGGG--CCGTTGTGCA	358		

Qy	241	ATCCGGTTTCGGCTACTTTCCAAACCATCATGCCCTTGGTTGATTCGTTTCTTGCCTTTCGTGGGA	300
Db	359	ATTCGGGTTTCAGGTA-TTTTCCAAACCATCATGCC-TGGTTTGA-TTCGGCTTTTCGTTTACCGCGGA	416
Qy	301	AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACACTGTG	360
Db	417	AGACCAACAAGGTGAAGGAGCAAGGCGCAANGCACTCCGCANTCTCATCAAGTCCACCGGT	476
Qy	361	CCCTTTGATCAAGTCCCTTGCGTGAAGGAGGCTGATGCCACCCTTATATCCCGTACACGAAGT	420
Db	477	CCCTGATCAAGTCAATTGCGGAGGAGGCTGATGCGAGGCCATCTGATCCGCCATGAAGT	536
Qy	421	CACCTTACCGGTACCGTGGAGNAGCAGACTTCGCCAGAGGACCGTGGAGTTGGGAACCT	480
Db	537	CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAACATG	596
Qy	481	CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCATTTGCGTGATTTCCGAT	540
Db	597	CGCGCTCAACGGTGTTCGCACGCAAGTCTCTCAGCGCCGATCGGTTGCGGGATTTCCGAT	656
Qy	541	CCTAACTGTCTACGCCCTTTTACCAAGGGAATCCCTTATCGAAGAGAACGGTGCACACCATC	600
Db	657	CGGAACCTTCTGCATCGCTTTACCAAGGGCATTTCTTATAGAAGAGAACGGTGCACACGATT	716
Qy	601	NAACCACAAAGTCTCGTGACTCTCTTGTTTGCGTGTTCATCCGCTACGCGTGAGAGTTC	660
Db	717	NAATCGCAAGGGCTCGTGACCCTCTCTTTTTCGGCGTTTTATCCGGAACGGTGGCGAATCT	776
Qy	661	GTGCTGCTCGTGTATATCGGATTTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACACC	720
Db	777	GTATCTGCGCGTGTATCCGGCTTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTTACAACC	836
Qy	721	ACCAAGGGTGTCTTGCTGTTGATGCAGCTGTGTGTTCAGCTGGTGCACACTCCAAGTCT	780
Db	837	AGGAACGGGTTCTGCGCGTTGATGCAGCGGTTGTCTCGACCGCGGCACACTCGAATCA	896
Qy	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATTACCGAAGCTGGATACCAACATCGTG	840
Db	897	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTCTC	956
Qy	841	ATCGCCAAACCCAGAGCTGCTCCAGCTATTTCAACTACCGATGCTCTGGAAGTTCCATC	900
Db	957	ATFCGGAAATCCGGAAGCGCTCCACGATTCGCAACACCGATCGCTCAGGAAATTCATC	1016
Qy	901	GCTACTCTCTATGAGATGGCTCTTCCTGTGTGCTGGAACCGTTTCAGTTTCGGTCTGCATCT	960
Db	1017	CGGACACCTATGGAATGGGGCTTCGCTGCGGGGTACGGTTGAGTTTCGCTGGGCTCACA	1076
Qy	961	GGTGTCTCTAATCGAAGCGTGCTCAAGTGTCTCTACACTCGCGCTCGTAAGTTGCTTCCA	1020
Db	1077	GCGCGTCTCTAATCGAAGCGTGCGCATGTGCTCTATACGCACGCTCGAAGAAATTCATC	1136
Qy	1021	GCTCTCGCTCTCCAGTTCTGAGNAGACGTTACTCCAAGTGGATGGGTTCCCGTCCNAGC	1080
Db	1137	GCCCTCGGGCGTTCGAGTTCTGAAGAAGCATATTCCAAAATGGATGGGTTGGGCGCGAGC	1196
Qy	1081	ATCCCGGATTCCTCTCCAGTGATTTGGTCTGTGCTTACCGCTACTCCAGACGTTATCTACGCT	1140
Db	1197	ATCCCGGATTCGCTCCCGTGATTGGCCGGGCNAACCGGACACCCGACGTAATCTATGCT	1256
Qy	1141	TTCCGTCAGGTCACGTCGGTATGACTGGTGCTTCCAAATGACCGCAACCCCTGTTTCTTGAG	1200
Db	1257	TTTCGGCCATGGTCATCTCGGCATGACAGGGGGCGCGATGACCGCAACGCTTCGCTCTCAGAG	1316
Qy	1201	CTCTCTCGAGGTGGAAGACCTCTATCGACATCTCTTCCATTTCCACCCAAACCGTTTCGGT	1260
Db	1317	CTCCTCGAGGGGAAGACCTCAATCGACATTTCCGCTTTCGCACCAACCCGTTTGGT	1376
Qy	1261	ATTGGTAAGTCCAAAGCAACTGGTCTCTGCATCCTAA	1296
Db	1377	ATTGGCAATCCAAAGCAACGGTTCGGCAAGTTAA	1412

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:16:17 ; Search time 7299.04 Seconds
(without alignments)
775.497 Million cell updates/sec

Title: US-08-484-274-17
Perfect score: 1296
Sequence: 1 ATGCGTGAGACCAAGAA.....AAACTGGTCTGCTCCTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pl3.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: em_fun.*
- 13: em_hum1.*
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- 93: gb_v11.*
- 94: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1296	100.0	1296	5	AR016604	AR016604 Sequence
2	1296	100.0	1296	5	I15337	I15337 Sequence 17
3	1288	99.4	1296	5	AR016595	AR016595 Sequence
4	1288	99.4	1296	5	I15328	I15328 Sequence 8
5	1200.4	92.6	1631	5	A59869	A59869 Sequence 1
6	1006.4	77.7	1296	5	AR016594	AR016594 Sequence 1
7	1006.4	77.7	1296	5	I15327	I15327 Sequence 7
8	958.4	74.0	1296	5	AR016593	AR016593 Sequence
9	958.4	74.0	1296	5	I15326	I15326 Sequence 6
10	956.8	73.8	1692	5	AR016591	AR016591 Sequence
11	925.6	71.4	1293	5	AR016592	AR016592 Sequence
12	925.6	71.4	1293	5	I15325	I15325 Sequence 4

Qy 1261 ATTGGTAAAGTCCAGCAAACTGGTCCATCCCTAA 1296
|||||
Db 1261 ATTGGTAAAGTCCAGCAAACTGGTCCATCCCTAA 1296
|||||

RESULT 2
115337
LOCUS I15337 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 17 from patent US 5463175.
ACCESSION I15337
VERSION I15337.1 GI:1250245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1296)
TITLE Barry.G.F. and Kishore.G.M.
JOURNAL Glyphosate tolerant plants
PATENT: US 5463175-A 17 31-OCT-1995;
FEATURES Location/Qualifiers
source 1..1296
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN

Query Match 100.0%; Score 1296; DB 5; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGCACT 60
|||||
Db 1 ATGGCTGAGAACCAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGCACT 60
|||||

Qy 61 GCTTTGATGCTTCAACGTCGTTCAAGTTACCTTGATGATCCAAACCCACAGGT 120
|||||
Db 61 GCTTTGATGCTTCAACGTCGTTCAAGTTACCTTGATGATCCAAACCCACAGGT 120
|||||

Qy 121 GAAGTGCTCTTTGGGTAAAGCTGGTTGCTTCAACGGTTCCCTCGTTGTTCCCAATGTCC 180
|||||
Db 121 GAAGTGCTCTTTGGGTAAAGCTGGTTGCTTCAACGGTTCCCTCGTTGTTCCCAATGTCC 180
|||||

Qy 181 ATGCCAGAAACTTGACTAGGCTTCCAAAGTGGCTTTTGACCCCAATGGGTCCATGTCC 240
|||||
Db 181 ATGCCAGAAACTTGACTAGGCTTCCAAAGTGGCTTTTGACCCCAATGGGTCCATGTCC 240
|||||

Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTTCTGCTGCTGGA 300
|||||
Db 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTTCTGCTGCTGGA 300
|||||

Qy 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACCTCCCGTAACCTCATCAAGTCCCACTGTG 360
|||||
Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACCTCCCGTAACCTCATCAAGTCCCACTGTG 360
|||||

Qy 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420
|||||
Db 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420
|||||

Qy 421 CACCTTACCGTGTACCGTGGAGAGCACATTCGCCAGGACCGTGGAGTGGGAACCTT 480
|||||
Db 421 CACCTTACCGTGTACCGTGGAGAGCACATTCGCCAGGACCGTGGAGTGGGAACCTT 480
|||||

Qy 481 GGTGCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCTATTCGCTGATTCGAT 540
|||||
Db 481 GGTGCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCTATTCGCTGATTCGAT 540
|||||

Qy 541 CCTAACTTGTCTACGCCCTTTTACCAAGGGAATTCCTTATCGAAGAGAACGGTCCACCAATC 600
|||||
Db 541 CCTAACTTGTCTACGCCCTTTTACCAAGGGAATTCCTTATCGAAGAGAACGGTCCACCAATC 600
|||||

Qy 601 AACCCACAAAGTCTCGTCACTCTCTTGTTCGTTTCATTCGCTTTCATTCGCTTTCGCTTTCGCT 660
|||||

Db 601 AACCCACAAAGTCTCGTCACTCTCTTGTGTTTCGTTTCATTCGCTTTCATTCGCTTTCGCTTTCGCT 660
Qy 661 GTGCTGCTCGTGTATTCGGATTTCGAGACTGAAGGTCTGCTCTCAAGGGTATTCACCACT 720
|||||
Db 661 GTGCTGCTCGTGTATTCGGATTTCGAGACTGAAGGTCTGCTCTCAAGGGTATTCACCACT 720
|||||

Qy 721 ACCAAGGTGTTCTGTTGATTCAGCTGTTGTTGAGCTGTTGTTGAGCTGTTGTTGAGCTGTTGTTGAGCT 780
|||||
Db 721 ACCAAGGTGTTCTGTTGATTCAGCTGTTGTTGAGCTGTTGTTGAGCTGTTGTTGAGCTGTTGTTGAGCT 780
|||||

Qy 781 CTTGCTAACTCCCTTGGTGGATGACATCCATTCGATTCGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCT 840
|||||
Db 781 CTTGCTAACTCCCTTGGTGGATGACATCCATTCGATTCGAGCTGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGCT 840
|||||

Qy 841 ATGCCAAACCCAGAGCTGCTCCAGCTATTCACAACTACCGATGCTTCTGGAAAGTTTCATC 900
|||||
Db 841 ATGCCAAACCCAGAGCTGCTCCAGCTATTCACAACTACCGATGCTTCTGGAAAGTTTCATC 900
|||||

Qy 901 GCTACTCTATGAGAGATGGTCTTCGTTGTTGCTGAAACCGTTGAGTTCGCTGCTCTCACT 960
|||||
Db 901 GCTACTCTATGAGAGATGGTCTTCGTTGTTGCTGAAACCGTTGAGTTCGCTGCTCTCACT 960
|||||

Qy 961 GCTGCTCTTAAGTGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020
|||||
Db 961 GCTGCTCTTAAGTGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020
|||||

Qy 1021 GCTCTCGCTCTGCCAGTTCTGAAGAGCTTACTCTCAAGTGGATGGTTCGCTGCCAAGC 1080
|||||
Db 1021 GCTCTCGCTCTGCCAGTTCTGAAGAGCTTACTCTCAAGTGGATGGTTCGCTGCCAAGC 1080
|||||

Qy 1081 ATCCGGGATTCCTTCCAGTGAATTCGTTGCTTACCCGTTACTTCCAGAGCTTATCTACGCT 1140
|||||
Db 1081 ATCCGGGATTCCTTCCAGTGAATTCGTTGCTTACCCGTTACTTCCAGAGCTTATCTACGCT 1140
|||||

Qy 1141 TTCGCTCACGGTCACTCGGTATGACTGCTGCTCAAGTACCGCAACCTCGCTTCTGAG 1200
|||||
Db 1141 TTCGCTCACGGTCACTCGGTATGACTGCTGCTCAAGTACCGCAACCTCGCTTCTGAG 1200
|||||

Qy 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTCGCAACCAACCGTTTCGGT 1260
|||||
Db 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTCGCAACCAACCGTTTCGGT 1260
|||||

Qy 1261 ATTGTTAAGTCCAAACCAACTGGTCTCGATCTTAA 1296
|||||
Db 1261 ATTGTTAAGTCCAAACCAACTGGTCTCGATCTTAA 1296
|||||

RESULT 3
AR016595 AR016595 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5776760.
ACCESSION AR016595
VERSION AR016595.1 GI:3972872
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1296)
TITLE Barry.G.Francis and Kishore.G.Murthy.
JOURNAL Glyphosate tolerant plants
PATENT: US 5776760-A 8 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..1296
BASE COUNT 271 a 359 c 305 g 361 t
ORIGIN

Query Match 99.4%; Score 1288; DB 5; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTGGTATTCGCTGGAGCTGGAATCGTTGGTGGCACT 60
|||||

Db 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACCT 60
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGGT 120
Db 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGGT 120
QY 121 GAAGTGCCCTTTTCGGTAACGCTGGTTGCTTTCACAGGTTCCCTCCGTTGTTCCAAATGTCC 180
Db 121 GAAGTGCCCTTTTCGGTAACGCTGGTTGCTTTCACAGGTTCCCTCCGTTGTTCCAAATGTCC 180
QY 181 ATGCCAGGAACCTTGACTAGGTTCCAAAGTGGGTTCTTGACCCAAATGGGTCCATTTGTCC 240
Db 181 ATGCCAGGAACCTTGACTAGGTTCCAAAGTGGGTTCTTGACCCAAATGGGTCCATTTGTCC 240
QY 241 ATCCGTTTCGGCTACTTTTCAACCATCATGCTTTGGTTGATTCTGTTTCTGTTGCTTGGGA 300
Db 241 ATCCGTTTCGGCTACTTTTCAACCATCATGCTTTGGTTGATTCTGTTTCTGTTGCTTGGGA 300
QY 301 AGACCAACCAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACATGTG 360
Db 301 AGACCAACCAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACATGTG 360
QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGAGGACCTGAGGTTGGGAACCTT 480
Db 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGAGGACCTGAGGTTGGGAACCTT 480
QY 481 CGTGGTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCAATTCGCTGATTTCCGAT 540
Db 481 CGTGGTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCAATTCGCTGATTTCCGAT 540
QY 541 CCTAACTTGTCTACGCTTTTACCAAGGAATCCTTATCGAAGAGAGCGTCAACCATC 600
Db 541 CCTAACTTGTCTACGCTTTTACCAAGGAATCCTTATCGAAGAGAGCGTCAACCATC 600
QY 601 AACCCACAAGGTCCTGACTCTCTTCTTCTGCTGCTTTCATCGCTTAACGGTGGAGAGTTC 660
Db 601 AACCCACAAGGTCCTGACTCTCTTCTTCTGCTGCTTTCATCGCTTAACGGTGGAGAGTTC 660
QY 661 GTGTCCTCGTGTATCGGATTCGAGACTGAAGGTCGTCCTCAAGGGTATCACCACT 720
Db 661 GTGTCCTCGTGTATCGGATTCGAGACTGAAGGTCGTCCTCAAGGGTATCACCACT 720
QY 721 ACCAAGCGTGTCTTGTGTTGATGACAGCTGTTGTTGACAGCTGGTGACACTCCAACTCT 780
Db 721 ACCAAGCGTGTCTTGTGTTGATGACAGCTGTTGTTGACAGCTGGTGACACTCCAACTCT 780
QY 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCACTCGTG 840
Db 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCACTCGTG 840
QY 841 ATGCCAACCCAGAGCTGCTCAGCTATTTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Db 841 ATGCCAACCCAGAGCTGCTCAGCTATTTCCAACTACCGATGCTTCTGGAAGTTCATC 900
QY 901 GCTACTCTATGAGATGGGCTTCTCGTTGCTGGAGACCGTTGATGCTGCTGGTCTCACT 960
Db 901 GCTACTCTATGAGATGGGCTTCTCGTTGCTGGAGACCGTTGATGCTGCTGGTCTCACT 960
QY 961 GCTGCTCCTAACTCGGAAGCGTGTCTGCTTCTACACTCCGCTCGTAAAGTTCCTTCCA 1020
Db 961 GCTGCTCCTAACTCGGAAGCGTGTCTGCTTCTACACTCACGCTCGTAAAGTTCCTTCCA 1020
QY 1021 GCTCTGCTCCTCGGAGTCTGAAGAACGTTACTCCAAAGTGGATGGGTTTCGCTCCAAAG 1080
Db 1021 GCTCTGCTCCTCGGAGTCTGAAGAACGTTACTCCAAAGTGGATGGGTTTCGCTCCAAAG 1080
QY 1081 ATCCCGGATTCCTTCCAGTGATTTGGTGTGCTTACCGCTACTCCAGAGCTTATCTACGCT 1140

Db 1081 ATCCAGATTCCTTCCAGTGATTGGTGTGCTACCCGCTACTCCAGAGCTTATCTACGCT 1140
QY 1141 TTCCGTCACGGTCACCTCGGTATGACTGGTGTCTCCAATGACGCAACCTCGTTTCTCAG 1200
Db 1141 TTCCGTCACGGTCACCTCGGTATGACTGGTGTCTCCAATGACGCAACCTCGTTTCTCAG 1200
QY 1201 CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAACCCGTTTCGGT 1260
Db 1201 CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAACCCGTTTCGGT 1260
QY 1261 ATTGGTAAGTCCAAAGCAAACTGGTCTCGATCTCTAA 1296
Db 1261 ATTGGTAAGTCCAAAGCAAACTGGTCTCGATCTTAA 1296
RESULT 4
I15328
LOCUS I15328 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 8 from patent US 5463175.
ACCESSION I15328
VERSION I15328.1 GI:1250236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 8 31-0CN-1995;
FEATURES Location/Qualifiers
source 1. 1296
BASE COUNT 271 a 359 c 305 g 361 t
ORIGIN
Query Match 99.4%; Score 1288; DB 5; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACCT 60
Db 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACCT 60
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGGT 120
Db 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACCAAGGT 120
QY 121 GAAGTGCCCTTTTCGGTAACGCTGGTTGCTTTCACAGGTTCCCTCCGTTGTTCCAAATGTCC 180
Db 121 GAAGTGCCCTTTTCGGTAACGCTGGTTGCTTTCACAGGTTCCCTCCGTTGTTCCAAATGTCC 180
QY 181 ATGCCAGGAACCTTGACTAGGTTCCAAAGTGGGTTCTTGACCCAAATGGGTCCATTTGTCC 240
Db 181 ATGCCAGGAACCTTGACTAGGTTCCAAAGTGGGTTCTTGACCCAAATGGGTCCATTTGTCC 240
QY 241 ATCCGTTTCGGCTACTTTTCAACCATCATGCTTTGGTTGATTCTGTTTCTGTTGCTTGGGA 300
Db 241 ATCCGTTTCGGCTACTTTTCAACCATCATGCTTTGGTTGATTCTGTTTCTGTTGCTTGGGA 300
QY 301 AGACCAACCAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACATGTG 360
Db 301 AGACCAACCAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACATGTG 360
QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGAGGACCTGAGGTTGGGAACCTT 480
Db 421 CACCTTACCGTGTACCGTGGAGAGCACTTCCGAGGACCTGAGGTTGGGAACCTT 480
QY 481 CGTGGTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCAATTCGCTGATTTCCGAT 540

Db	481		CGTCGTCACAGGTTGTCGTACTCAAAATCTCACGCGTGATGCAATTCGGTCAATTCGAT	540
Qy	541	CCTAACTTGTCTCAGCGCTTTACCAAGGAATCCTTATTCGAAGGAAGCGGTACACCAATC		600
Db	541	CCTAACTTGTCTCAGCGCTTTACCAAGGAATCCTTATTCGAAGGAAGCGGTACACCAATC		600
Qy	601	AACCCAGAGGTCGTCGTCGTCCTTGTTCGTTTCATCGCTTAACGGTGGAGAGTTTC		660
Db	601	AACCCAGAGGTCGTCGTCGTCCTTGTTCGTTTCATCGCTTAACGGTGGAGAGTTTC		660
Qy	661	GTGCTGCTCGTGTATTCGGATTCGAGACTGAAGGTGCTGCTCAAGGTTATCACCAACC		720
Db	661	GTGCTGCTCGTGTATTCGGATTCGAGACTGAAGGTGCTGCTCAAGGTTATCACCAACC		720
Qy	721	ACCAAGGTTCTTGTGCTGATGCAGCTGTGTGTCAGCTGGTGCACACTCCAAAGTCT		780
Db	721	ACCAAGGTTCTTGTGCTGATGCAGCTGTGTGTCAGCTGGTGCACACTCCAAAGTCT		780
Qy	781	CTTGCTAACTCCCTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCGT		840
Db	781	CTTGCTAACTCCCTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCGT		840
Qy	841	ATCGCCAAACCAGAGCTGCTCCAGTATCCAACTACCGATGCTTCTGGAAGTTCAATC		900
Db	841	ATCGCCAAACCAGAGCTGCTCCAGTATCCAACTACCGATGCTTCTGGAAGTTCAATC		900
Qy	901	GCTACTCCTATGGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT		960
Db	901	GCTACTCCTATGGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT		960
Qy	961	GCTGCTCTAACTGGAAGCGTCTACACCTTCTACACTCGCGCTGCTGCTGCTTCCCA		1020
Db	961	GCTGCTCTAACTGGAAGCGTCTACACCTTCTACACTCGCGCTGCTGCTGCTTCCCA		1020
Qy	1021	GCTCTCGCTCTCGCAGTTCTGAAGACGTTACTCCAACTGATGCGGTTTCCGTCCTCAAGC		1080
Db	1021	GCTCTCGCTCTCGCAGTTCTGAAGACGTTACTCCAACTGATGCGGTTTCCGTCCTCAAGC		1080
Qy	1081	ATCCGGATTCCTTCCAGTGATTTGGTGTGCTACCCGCTACTCCAGAGCTTATCTACGCT		1140
Db	1081	ATCCGGATTCCTTCCAGTGATTTGGTGTGCTACCCGCTACTCCAGAGCTTATCTACGCT		1140
Qy	1141	TTCCGTCACGCTACCTCGGTATGACTGGTGTGCTCAATTCACCGCAACCGCTTCTGAG		1200
Db	1141	TTCCGTCACGCTACCTCGGTATGACTGGTGTGCTCAATTCACCGCAACCGCTTCTGAG		1200
Qy	1201	CTCCTCCGAGTGAGAACCTCTATCCACATCTCTCCATTCGCAACCAACCGTTTCGCT		1260
Db	1201	CTCCTCCGAGTGAGAACCTCTATCCACATCTCTCCATTCGCAACCAACCGTTTCGCT		1260
Qy	1261	ATTGGTAAAGTCCAAAGCAACTGGTCTGCTGCATCCTAA	1296	
Db	1261	ATTGGTAAAGTCCAAAGCAACTGGTCTGCTGCATCCTAA	1296	

RESULT 5
A59869
LOCUS A59869 1631 bp DNA PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9706269.
ACCESSION A59869
VERSION A59869.1 GI:3715060
KEYWORDS
SOURCE Arabidopsis sp.
ORGANISM Arabidopsis sp.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; Capparales; Brassicaceae; Arabidopsis.
Jepson, I.
1 (bases 1 to 1631)
TITLE INDUCIBLE HERBICIDE RESISTANCE
JOURNAL Patent: WO 9706269-A 1 20-FEB-1997;
ZENECA LTD (GB)

FEATURES	source	Location/Qualifiers
BASE COUNT	342 a	454 c 381 g 454 t
ORIGIN		
Query Match 92.6%; Score 1200.4; DB 5; Length 1631; Best Local Similarity 95.1%; Pred. No. 0; Matches 1280; Conservative 0; Mismatches 16; Indels 50; Gaps 2;		
Qy	1	ATGGCTGAGAACCAACAGGTTGCTATCGCTGGAGCTGGAATCGTTGGTGGCACT 60
Db	274	ATGGCTGAGAACCAACAGGTTGCTATCGCTGGAGCTGGAATCGTTGGTGGCACT 333
Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACACAGT 120
Db	334	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACACAGT 393
Qy	121	GAAGTGCTCTTTTCGGTTAAGCTGGTTGCTTCAACGGTTCTCTCGTTGTTTCCAAATGTCC 180
Db	394	GAAGTGCTCTTTTCGGTTAAGCTGGTTGCTTCAACGGTTCTCTCGTTGTTTCCAAATGTCC 453
Qy	181	ATGCCAGAAACTTGAAGTAGGTTCCAAAGTGGCTTTTGACC----- 223
Db	454	ATGCCAGAAACTTGAAGTAGGTTCCAAAGTGGCTTTTGACC----- 513
Qy	224	-----CAATGGTCCATTGTCATCCGTTTCGGTACTTTTCAACCATCATGCCCTTG 275
Db	514	TTACGGATTCATGGGTCCTATGTCATCCGTTTTCAGCTACTTTTCAACCATCATGCCCTTG 573
Qy	276	GTTGATTCGTTTTCGTTGCTGGAAGACCAACAAAGTGAAGGAGCAAGCTTAAGGCACCT 335
Db	574	GTTGATTCGTTTTCGTTGCTGGAAGACCAACAAAGTGAAGGAGCAAGCTTAAGGCACCT 633
Qy	336	CGTAACTCATCAAGTCCACTGTGCTTTGATCAAGTCTTGGTGGAGGAGGTGATGC 395
Db	634	CGTAACTCATCAAGTCCACTGTGCTTTGATCAAGTCTTGGTGGAGGAGGTGATGC 693
Qy	396	TAGCACCTTATCCGTCACGAAGTCACTTACCGTGTACCGTGGAGAGCAAGCTTCGC 455
Db	694	TAGCACCTTATCCGTCACGAAGTCACTTACCGTGTACCGTGGAGAGCAAGCTTCGC 753
Qy	456	CAGGACCGTGGAGGTTGGGAACCTTCGCTCTCAACGGTGTTCGTACTCAAAATCCTCAG 515
Db	754	CAGGACCGTGGAGGTTGGGAACCTTCGCTCTCAACGGTGTTCGTACTCAAAATCCTCAG 813
Qy	516	CGCTGATGCATTCGGTGATTTTCGATCCTTAACCTTGTCTCACGCTTTTACCAAGGAATCCT 575
Db	814	CGCTGATGCATTCGGTGATTTTCGATCCTTAACCTTGTCTCACGCTTTTACCAAGGAATCCT 873
Qy	576	TATCGAAGAGAACGCTCACACATCAACCCACACAGGTCCTGCTGCTTATTCGGATTTCGAGAGG 635
Db	874	TATCGAAGAGAACGCTCACACATCAACCCACACAGGTCCTGCTGCTTATTCGGATTTCGAGAGG 933
Qy	636	TTTCATCGCTAACGGTGGAGAGTTGCTGCTGCTGCTTATTCGGATTTCGAGAGGTAAGG 695
Db	934	TTTCATCGCTAACGGTGGAGAGTTGCTGCTGCTGCTTATTCGGATTTCGAGAGGTAAGG 993
Qy	696	TCGTGCTCTCAAGGTTATCACCACCAACCGGTTCTTCTGCTGTTGATG----- 745
Db	994	TCGTGCTCTCAAGGTTATCACCACCAACCGGTTCTTCTGCTGTTGATGTCGATGCTT 1053
Qy	746	-----CAGCTGTGTTGAGCTGGTGGACACTCCCAAGTCTCTTGGTAACT 790
Db	1054	GTGAATTCAGGCTTATCTGAGCTTGTTCGAGCTGGTGGACACTTCCAAAGTCTCTTGGTAACT 1113
Qy	791	CCCTTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCTGATGCGCAACC 850
Db	1114	CCCTTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCTGATGCGCAACC 1173
Qy	851	CAGAAGCTGCTCCACGTTATCCAACTACCGATGCTTCTTGGAAAGTTATCGCTACTCCTA 910

Db	1174		CAGAAGCTGCTCCACGATATTCCCAACTACCGATGCTTCTGGAAAGTTTCATCGCTACTCCTA	1233
Qy	911		TGGAGATGGGCTCTTCTGTTGGCTGGAAACCGTTGAGTTTCGGTGGTCTCAGTCTGCTCCTA	970
Db	1234		TGGAGATGGGCTCTTCTGTTGGCTGGAAACCGTTGAGTTTCGGTGGTCTCAGTCTGCTCCTA	1293
Qy	971		ACTGGAAAGCGTGTCTACAGTTCTCTACACTCGCGCTCGTAAGTTCGTTCCAGCTCTCGGTC	1030
Db	1294		ACTGGAAAGCGTGTCTACAGTTCTCTACACTCGCGCTCGTAAGTTCGTTCCAGCTCTCGGTC	1353
Qy	1031		CTGCCAGTCTTGAAGAACGTTACTCCAAAGTGGATGGGTTTCCGTTCCAAAGCATCCCGGATT	1090
Db	1354		CTGCCAGTCTTGAAGAACGTTACTCCAAAGTGGATGGGTTTCCGTTCCAAAGCATCCCGGATT	1413
Qy	1091		CCCTTCCAGTGATTTGGTTCGTTACCCGTACTCCAGACGTTATCTACGCTTTCGGTCAAG	1150
Db	1414		CCCTTCCAGTGATTTGGTTCGTTACCCGTACTCCAGACGTTATCTACGCTTTCGGTCAAG	1473
Qy	1151		GTCACTCGGTATGACTGGTGTCTCAATGACCGCAACCGTCTGTTCTGAGCTCCTCGCAG	1210
Db	1474		GTCACTCGGTATGACTGGTGTCTCAATGACCGCAACCGTCTGTTCTGAGCTCCTCGCAG	1533
Qy	1211		GTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAACCGTTTCGGTATTGGTAAGT	1270
Db	1534		GTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAACCGTTTCGGTATTGGTAAGT	1593
Qy	1271		CCAAGCAAACTGGTTCCTGCACTCA 1296	
Db	1594		CCAAGCAAACTGGTTCCTGCACTCA 1619	
RESULT 6				
LOCUS	AR016594			
DEFINITION	Sequence 7 from patent US 5776760.			
ACCESSION	AR016594			
VERSION	AR016594.1 GI:3972871			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1296)			
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.			
TITLE	Glyphosate tolerant plants			
JOURNAL	Patent: US 5776760-A 7 07-JUL-1998;			
FEATURES	Location/Qualifiers			
Source	1..1296			
BASE COUNT	287 a	344 c	332 g	333 t
ORIGIN	/organism="unknown"			
Query Match 77.7%; Score 1006.4; DB 5; Length 1296;				
Best Local Similarity 86.0%; Pred. No. 1e-273;				
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;				
Qy	1	ATGGCTGAGAACACCAAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTCGACT	60	
Db	1	ATGGCTGAGAACACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGGTATGCACT	60	
Qy	61	GCTTTGATGCTTCAACGTCGTGATTAAGGTTACCTTGATGATCCAAACCCACCAGGT	120	
Db	61	GCTTTGATGCTTCAACGTCGTGATTAAGGTTACCTTGATGATCCAAACCCACCCTCCGCGC	120	
Qy	121	GAAGTGGCTTCTTCGGTAAACGCTGGTTCGTTCAACGGTTCCTCGGTTGTTCCAAATGTCC	180	
Db	121	GAAGTGGCATCGTTTGGGAATCGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180	
Qy	181	ATCCAGGAAACTTGACTAGCTGTTCCAAAGTGGCTTCTTGACCCAAATGGGTGCCATTGTCC	240	
Db	181	ATCCCGGAAACTTGACGAGCTGCCGAAGTGGCTCCTTGACCGGATGGGCGGCTTGCTCA	240	

Qy	241	ATCGGTTTCGGCTACTTTTCCAAACCATCATGCCTTGGTGGTGGTTCGTTTCGTTTCGTTGGA	300	
Db	241	ATCGGTTTCAGCTATTTTTTCCAAACCATCATGCCTTGGTGGTGGTTCGTTTCGTTTCGTTGGA	300	
Qy	301	AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACATGTCG	360	
Db	301	AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACATGTCG	360	
Qy	361	CCTTTGTCAAGTCTTTGGCTGAGGAGGCTCATGCTAGCCACCTTATCCGTCAGCAAGGT	420	
Db	361	CCTTGATCAAGTCTTTGGCGGAGGAGCTCATGCGAGCCATCTGATCCGCCATCAAGGT	420	
Qy	421	CACCTTACCCTGACCTGAGGAGCAAGCTTCCGAGGACCGTGGAGGTGGGAACTT	480	
Db	421	CATCTGACCTTATATCTGGGAGGAGCAAGCTTCCGAGGACCGTGGGAACTT	480	
Qy	481	CGTCGCTCAACCGTGTTCGTTACTCAATCTCAGCCCTGATGCATTTCCGTTGATTTCCGAT	540	
Db	481	CGGCGTCTCAACCGTGTTCGCGACGAGATCTCTCTCTGATGCTTTGCGGTGATTTCCGAT	540	
Qy	541	CCTAACTTGTCTCAGCGCTTTTACCAAGGAAATCCTTATCGAAGAGAACGGTCCACCATC	600	
Db	541	CCTAACTTGTCTCAGCTGCTTTTACCAAGGCAATCTTATAGAAGAGAACGGTCCACCATC	600	
Qy	601	AACCCACAAGGTCTGCTGACTCTCTGTTGCTGCTTTCATCGCTAACGGTGGAGAGTTC	660	
Db	601	AATCCGCAAGGCTGCTGACCTCTCTGCGGCTTTTATCGGCAACGGTGGGCAATTT	660	
Qy	661	GTGTCGCTCGTGTATTCGGATTCGACACTGAAGGTGCTGCTCTCAAGGGTATCACACC	720	
Db	661	GTATCTGCGCTGTCTATCGGTTTGGAGACTGAAGGTGCTGCTCTCAAGGGTATCACACC	720	
Qy	721	ACCAACCGGTCTCTGCTGTTGATGCAGCTGTTGCTGAGTGGTGCACACTCCCAAGTCT	780	
Db	721	ACTAAACGGTCTCTGCTGTTGATGCAGCTGTTGCTGAGTGGTGCACACTCTCAATCA	780	
Qy	781	CTTGCTAACTCCCTTGGTGTGATGACATCCCATGGATACCGAACGTGGATACCATCGTG	840	
Db	781	CTTGCTAACTCCCTTGGTGTGATGACATCCCATGGATACCGAACGTGGATATCATATGCTC	840	
Qy	841	ATGCCAACCCAGAAGCTGCTCCAGCTATCCAACTACCGATGCTTCTGGAAAGTTTCATC	900	
Db	841	ATCGCGANTCCGGAAGCCGCTCCAGCATTCGAGACCGATGCTCAGGAAATTCATC	900	
Qy	901	GCTACTCCTATGGAGATGGTCTTCTGTTGCTGGAAACCGTTCAGTTTCGTTGCTTCACT	960	
Db	901	CGCAGACCTATGGAAATGGGCTCTCTGTTGCTGGTACTGTTGAGTTTGGTGGTCTCACA	960	
Qy	961	GCTGCTCCTAACTGGAAAGCGTGTCTACACTCGGCTCGTAAAGTGGTTCCTCA	1020	
Db	961	GCTGCTCCTAACTGGAAAGCGTGTCTATACGACGCTCGGAACTTCTTTTCCA	1020	
Qy	1021	GCTCTCGCTCTGCCAGTCTCTGAAGAACGTTACTCCAAAGTGGATGGGTTTCCGTCCAAGC	1080	
Db	1021	GCCTCTCGGCTCGGAGTCTCTGAAGAACGATATTCGAAATGGATGGGTTTTCGCTCAGC	1080	
Qy	1081	ATCCCGGATTTCCCTTCCAGTGTGCTGCTACCGCTACTCCAGACGCTTATCTACCGCT	1140	
Db	1081	ATTCCTGATTTCTCTCCAGTGTGCTGCTGCAACTCGTACACCCGACGTAATCTATGCT	1140	
Qy	1141	TTCCGCTACCGTCACTCGGTATGACTGGTGGTCTCCAAATGACCGCAACCCCTCGTTTCGAG	1200	
Db	1141	TTTGGTCACGGTCACTTCGGTATGACAGGTCCTCCAATGACTGCAACTCTCGTCTCAGAG	1200	
Qy	1201	CTCCTCGCAGTGGAGACCTCTATCGACATCTCTCCATTCGCAACCAACCCGTTTCGGT	1260	
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Qy	1261	ATTGGTAAAGTCCAAAGCAAACTGGTCTCTGCAATTCGCAACCAACCCGTTTCGGT	1296	
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RESULT 7
LOCUS I15327 115327 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 7 from patent US 5463175.
ACCESSION I15327
VERSION I15327.1 GI:1250235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1296)
AUTHORS Barry G.F. and Kishore, G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 7 31-OCT-1995;
FEATURES
  Location/Qualifiers
    source
      1..1296
      /organism="unknown"
BASE COUNT 287 a 344 c 332 g 333 t
ORIGIN

Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
Best Local Similarity 86.0%; Pred. No. 1e-273;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT 60
Db 1 ATGGCTGAGAACACACAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT 60

Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
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Qy 121 GAAGGTGCTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCTCAATGTCC 180
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Qy 181 ATGCCAGGAACCTTGACTAGGCTTCCAAAGTGGCTTTCTTGACCAAGTGGTCCATTTGTC 240
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Qy 241 ATCCGGGGAACCTTGACGAGGCTGCGGAAGTGGCTCTTGACCGGAGTGGGCGCTGTGCA 240
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Qy 360 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCCACTGTG 360
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Qy 420 CCTTTGATCAAGTCCCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420
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Qy 480 CACTTACCGGTGTAACGTTGAGAGACAGACTTCGCCAGGACCGTGGAGGTGGGAACCTT 480
Db 480 CACTTACCGGTGTAACGTTGAGAGACAGACTTCGCCAGGACCGTGGAGGTGGGAACCTT 480

Qy 540 CGTCTGCTCAACGGTGTTCGTTACTCAATCTCAGCGCTGATGCTATTCGCTGATTTCCGAT 540
Db 540 CGTCTGCTCAACGGTGTTCGTTACTCAATCTCAGCGCTGATGCTATTCGCTGATTTCCGAT 540

Qy 600 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCTTTATCGAAGAGAGACGGTTCACCAATC 600
Db 600 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCTTTATCGAAGAGAGACGGTTCACCAATC 600

Qy 660 AACCCACAAGGTCGTGACCTCTCTTTCGTCGTTCCTCATCGCTTAACGGTGGAGACTTC 660
Db 660 AACCCACAAGGTCGTGACCTCTCTTTCGTCGTTCCTCATCGCTTAACGGTGGAGACTTC 660

Qy 720 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGGTATCACCAACC 720
Db 720 GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGGTATCACCAACC 720
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Qy 721 ACCAACGGTGTTCTTGTGCTGTTGATGCAGCTGTTGTTCGAGCTGGTGCACACTTCCAAAGTCT 780
Db 721 ACTAACGGTGTTCTTGTGCTGTTGATGCAGCTGTTGTTCGAGCTGGTGCACACTTCCAAATCA 780

Qy 840 CTTGCTAACTCCCTTGGTGATGACATCCATTTGGATACCGAACGTTGGATACCACTACCTG 840
Db 840 CTTGCTAACTCCCTTGGTGATGACATCCCTTCCATACCGAACGTTGGATATCATATCTGTC 840

Qy 900 ATGCCCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Db 900 ATCGCGAATCCGAAGCGCTCCAGCATTCGACGACCGATGCGTCAAGGAAATTCATC 900

Qy 960 GCTACTCTTATGGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
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Qy 1020 GCTGCTCCTAACTGGAAGCGTGCACGTTCTTACACTCGCGCTCGCTAAGTTCGCTTCCA 1020
Db 961 CTTGCTCCTAACTGGAACGTCGCGATGCTCTATAGCGACGCTCGGAAACTTCTTCCA 1020

Qy 1080 GCTCTCGCTCCTGCGAGTTCTGAAGACGTTACTCCAAAGTGGTGGTTCGCTCCAAAGC 1080
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Qy 1200 TTGCTGCTACGCTACCTCGGTATGCTGCTCCAAAGTGGTGGTGGTGGTGGTGGTGGTGGT 1200
Db 1141 TTTGGTCAGGTCATCTCGGTATGACAGGTCCTCAATGACTGCAACTCTCGTCTCAGAG 1200

Qy 1260 CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGCT 1260
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Qy 1296 ATTGGTAACTCAAGCAAACTGGTCTCGATCCATCCCTAA 1296
Db 1261 ATTGGCAATCCAAAGCAAGGCTCGCGCAAGTTAA 1296
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RESULT 8

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AR016593
LOCUS AR016593 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5776760.
ACCESSION AR016593
VERSION AR016593.1 GI:3972870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1296)
AUTHORS Barry G.F. Francis and Kishore, G. Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 6 07-JUL-1998;
FEATURES
  Location/Qualifiers
    source
      1..1296
      /organism="unknown"
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 74.0%; Score 958.4; DB 5; Length 1296;
Best Local Similarity 83.7%; Pred. No. 4e-260;
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT 60
Db 1 ATGGCTGAGAACACACAAAGATAGGCATCGCTGGAGCGGAATCGTGGGCTATGTCACG 60

Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
Db 61 GCGCTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
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QY 121 GAAGTGCCCTCTTTTCGGTAAGCGTGTGCTTCAACGGTTTCCCTCCGTTGTGTTTCAAAATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
QY 181 ATGCCAGAACTTGACTACGCTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTTGTCC 240
Db 181 ATCCCGGAAACTTGAAGAGCGTGGCGAAGTGGCTTCTTGACCGATGGGGCCGTTGTCA 240
QY 241 ATCGGTTTCGGCTACTTTCACACCATCATGCTTGGTTGATTCGTTTCTTGTGCTGTGGA 300
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Db 301 AGACCAAAAGGTGAAGGAGCAGGCGAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
QY 361 CCTTTGATCAACTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT 420
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QY 421 CACTTACCGGTGACCGTGAGAGAGCACTTCGCCAGGACCGTGGAGCTTGGGAACCTT 480
Db 421 CATCTGACCGTATATCGTGGAGAGCACTTCGCCAAGCAGGCGGAGGTTGGGAACCTG 480
QY 481 CGTCTCTCAACGGTGTCTGCTACTCAAACTCTCAGCCCTGATGCATTCGCTGATTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTCTGCACGCGAGATCCTCAGCGCCGATCGTTTGGCGGATTTTCGAT 540
QY 541 CCTAACTGTCTCACGCCCTTTACCAAGGGAATCCTTATCAAGAGAACGGTTCACACCATC 600
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QY 961 GCTGCTCCTAACTGGAAGCGTCTCAGCTTCTTACACTCGCGCTCGTAAAGTTGCTTCCA 1020
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L15326
LOCUS L15326 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5463175.
ACCESSION L15326
VERSION L15326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;
FEATURES Location/Qualifiers
 1..1296
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN
Query Match 74.0%; Score 958.4; DB 5; Length 1296;
Best Local Similarity 83.7%; Pred. No. 4e-260;
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACACACAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGGTCACT 60
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Db 61 GCCTGATGCTTCAGCGCCGCGGATTCAAAAGTCACCTTGATTGACCCGAAACCCCTCTGGC 120
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QY 361 CTTTGTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT 420
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QY 421 CACTTACCGGTGACCGTGAGAGAGCACTTCGCCAGGACCGTGGAGGTTGGGAACCTT 480
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Qy	601	AA	CC	CA	AG	GT	CT	CG	T	A	CT	CT	T	T	T	CG	T	CT	T	T	T	CA	T	CG	CT	CA	CG	T	GA	AG	T	TC	660
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Qy	661	GT	GT	CG	CT	CG	T	T	AT	CG	GA	TT	CG	AG	CT	GA	AG	GT	CG	CT	CT	CA	AG	GG	T	AT	CA	CC	CA	CC	720		
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RESULT 10																																	
AR016591																																	
LOCUS	AR016591	1692	bp	DNA																						PAT		05-DEC-1998					
DEFINITION	Sequence 3 from patent US 5776760.																																
ACCESSION	AR016591																																
VERSION	AR016591.1	GI:3972868																															
KEYWORDS	.																																
SOURCE	Unknown.																																
ORGANISM	Unknown.																																
REFERENCE	Unclassified.																																
AUTHORS	1 (bases 1 to 1692)																																
TITLE	Barry, G. Francis and Kishore, G. Murthy.																																
JOURNAL	Glyphosate tolerant plants																																
FEATURES	Patent: US 5776760-A 3 07-JUL-1998;																																
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	1..1692																																
BASE COUNT	381	a	480	c	469	g	361	t	1																		others						
ORIGIN	/organism="unknown"																																
Query Match 73.8%; Score 956.8; DB 5; Length 1692;																																	
Best Local Similarity 83.6%; Pred. No. 1.1e-259;																																	

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Best Local Similarity	83.6%;	Pred. No. 7.6e-251;	
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1 Ddb	1	ATCTCTGACAACCAACAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG	60
61 QY	61	GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATGATGCCAAACCCACCAAGT	120
61 Ddb	61	GGCCTGATGCTTTCAGCGCCGCGGATTCAAAGTCACTTGATTGACCCGAACCCCTCCTGGC	120
121 QY	121	GAAGGTGCTCTTTTCGGTAACGCTGCTTCTTCAACGGTTCCCTCGGTGTTTCCAAATGTCC	180
121 Ddb	121	GAAGGTGCTATCGTTTCGGGAATCGCGGATGCTTCAACGGCTCATCCGCTCGTCCCTATGTCC	180
181 QY	181	ATGCCAGGAAACTTGAAGCTTCCAAAGTGGCTTCTTGACCAATGGGTGCCATTGTCC	240
181 Ddb	181	ATGCCGGGAAACTTGACGAGCGTGCAGAGTGGCTCTTGACCCGATGGG-CCGTTGTCA	239
241 QY	241	ATCCGTTTCGGGTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTTCTTCTGTCTGGA	300
240 Ddb	240	ATCCGTTTCAGCTA-TTTTCCAAACCATCATGCC-TGGTTGATTTCGTTCTGTTAGCCGA	297
301 QY	301	AGACCAACAAGGTGAAGGACCAAGCTTAAGGCACTTCGTAACCTTCATCAAGTCCACGTG	360
298 Ddb	298	AGACCAACAAGGTGAAGGACGAGCGAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357
361 QY	361	CTTTTGATCAAGTCTTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAAGGT	420
358 Ddb	358	CTCTGTATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	417
421 QY	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGACCGCTGGAGGTTGGGAACATT	480
418 Ddb	418	CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGCACCGCGAGGTTGGGAACATG	477
481 QY	481	CGTGTCTCAACGGTGTTCGTACTCAATCTCAGCGCTGATGATTCGTTGGTGTTCGAT	540
478 Ddb	478	CGCGGTCTCAACGGTGTTCGCACGCAGATCTCTCAGCGCGGATGGCTTGGCGGATTTCCGAT	537
541 QY	541	CTTAAGTCTCTCACGCTTTTACCAAGGGAATCTTATCCAGAGAACCGGTCACACCATC	600
538 Ddb	538	CCGAATCTCGGATCGGTTTACCAAGGGAATCTTATAGAAGAGAACCGGTCACACCAT	597
601 QY	601	AACCCACAAGGCTCGTGACTCTCTTGTTCGCTGTTTATCGCTAACCGTGGAGAGTTC	660
598 Ddb	598	AATCCGAAGGCTCGTGACCTCTTTGTTTCGCGCTTTTATCGGAACCGTGGCGAATTC	657
661 QY	661	GTGTCGTGCTGTATTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACCACT	720
658 Ddb	658	GTATCTGCGGTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTAACAAC	717
721 QY	721	ACCAACGGTCTTCTGCTGTGATGACGCTGTTGTTTGCAGCTGGTGCACACTCCAAGTCT	780
718 Ddb	718	ACGAACGGGCTTCTGGCCGTTGATGAGGGTTTGTGCGAGCCGGCGCACACTCGGAATCA	777
781 QY	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACCATCGTG	840
778 Ddb	778	CTTGCTAACTCCCTAGGCCATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	837
841 QY	841	ATCGCCAAACCCAGAGCTGCTCCACGTAATTCAACTACCGATGCTTCTTGGAAAGTTTCATC	900
838 Ddb	838	ATCGGGAATCCGGAAGCCGCTCCACGCATTCGACGACCCGATGCGTCAGGAAATTCATC	897
901 QY	901	GCTACTCCTATCGAGATGGGTCTTCTGTTGCTGGAACCGTTTCAGTTCGCTGGTCTCACT	960

898	CGCACACCTATCGAAATCGGGCTTCGGCTGGCGGGTACGGCTTGAGTTTCGCTGGGCTCACA	957
961	GCTGCTCTTAAGTGAAGCGGTGCTACGTTCTCTACACTCGCGTCTGTAAGTTGCTTTCCA	1020
958	GCCTGCTCTTAAGTGAAGCGGTGCTACGTTCTCTACACTCGCGTCTGTAAGTTGCTTTCCA	1017
1021	GCTCTCGCTTCCTGCGGATTCCTGGAAGACGTTACTTCCAAGTGGATGGTTCGGTCCAAGC	1080
1018	GCCTGCGGCTTCGGATTCCTGGAAGACGTTACTTCCAATGGATGGGTTCGGGCGGAGC	1077
1081	ATCCCGGATTCCTCTCCAGTATTGGTGTCTACCGCTACTTCCAGAGCTTATCTAGGCT	1140
1078	ATCCCGGATTCGCTCCCGTGAATGGCGGGCAACCCGACACCGAGCTAATCTATGCT	1137
1141	TTCCGCTACAGCTACCTCGGTATGACTGGTGTCTCAATGACCGCAACCTCGTTTCTGAG	1200
1138	TTCCGCTATGCTCATCTCGGATGACAGGGCGCGGATGACCGCAACGCTGCTCTCAGAG	1197
1201	CTCCTCGCAGGTGACAGACCTCTATCCACATCTCTCAATTCGCAACCAACCGTTTCGGT	1260
1198	CTCCTCGCAGGCAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCGCTTTGGT	1257
1261	ATTGCTAAGTCCAAGCAAACTGGTCTGCATCTCTAA	1296
1258	ATTGCAAAATCAAGCAAAACGGTCCGCAAGTTAA	1293
RESULT 13		
LOCUS	I15324 1689 bp DNA	PAT 02-APR-1996
DEFINITION	Sequence 3 from patent US 5463175.	
ACCESSION	I15324	
VERSION	I15324.1 GI:1250232	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 1689)	
AUTHORS	Barry,G.F. and Kishore,G.M.	
TITLE	Glyphosate tolerant plants	
JOURNAL	Patent: US 5463175-A 3 31-Oct-1995;	
FEATURES	Location/Qualifiers	
source	1..1689	
BASE COUNT	381 a 479 c 468 g 360 t	1 others
ORIGIN	/organism="unknown"	
Query Match 71.4%; Score 925.6; DB 5; Length 1689;		
Best Local Similarity 83.6%; Pred. No. 7.6e-251;		
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;		
Qy	1	ATGGCTGAGAACCAACAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTGGCACT 60
Db	120	ATGCTGAGAACCAACAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 179
Qy	61	GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTCCTCAAAACCCACCACT 120
Db	180	CGCTGTATGCTTCAAGCGCGCGGATTCAAAGTCACTTGTGATTCACCCGACCCCTCTG 239
Qy	121	GAAGTGGCTCTTTTCGGTAAACGCTGGTTGCTTCAACGGTTCCTCGTTGTTCCAAATGTC 180
Db	240	GAAGTGGCTCTTTTCGGTAAACGCTGGTTGCTTCAACGGTTCCTCGTTGTTCCAAATGTC 299
Qy	181	ATGCCAGGAACTTGAAGCTTGGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCTATGTC 240
Db	300	ATGCCAGGAACTTGAAGCTTGGCTTCCAAAGTGGCTTCTTGACCAATGGGTCCTATGTC 358
Qy	241	ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTCGTTCTTCTGCTGTGA 300
Db	359	ATCCGTTTCAGCTA-TTTTCCAAACCATCATGCTTGGTTGATTCGTTCTTCTGTTAGCCGA 416
Qy	301	AGACCAACAAGGTGAAGGACCAAGCTTAAGGCACTTCGCTAAGTCCACGTGTG 360

Db	417		AGACAAACAGGTGAAGGACGAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	476
Qy	361		CTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT	420
Db	477		CTTCTGATCAAGTCATTTGGCGAGGAGGCTGATGCCAGCCATCTGATCCCCATGAAGGT	536
Qy	421		CACCTTACCGTGTACCGTGTGAGAGAGAGACTTCCGCCAGGACCGTGGAGTTCGGAAC	480
Db	537		CATCTGACCGTATATCTGTGAGAGAGAGACTTCCGCCAAGGACCGCGAGGTTCGGAAC	596
Qy	481		CGTCTGCTCAACGGTGTTCGTACTCAATCTCAGCGCTGATCCATTCGGTGTATTCGAT	540
Db	597		CGCGCTCTCAACGGTGTTCGCACGAGATCTCTCAGGCGCGATCGTTCGGGGATTCGAT	656
Qy	541		CTTAACCTTGTCTCACGCCCTTTACCAAGGGAATCTTATCGAAGAGAACGGTTCACACATC	600
Db	657		CCGAACCTTGTCCGATCGCTTTACCAAGGCAATCTTATAGAAGAACGGTTCACAGATT	716
Qy	601		AACCCACAAGGTCGTGACCTCTCTTTTTCGTTCATCGCTAACCGTGGAGAGTTC	660
Db	717		NATCCGAAGGGCTCGTGACCTCTTGTTCGGCGTTTTATCCGAACGGTGGCGAATTC	776
Qy	661		GTCTCTGCTCGTGTATTCGGATTCGAGACTGAAGTTCGCTCTCAAGGGTATCACACC	720
Db	777		GTATCTCCGCGTGTCTATCGGCTTTTGAGACTGAAGGTAGGCGGCTTAAAGGCATTACAAC	836
Qy	721		ACCAACGGTGTCTCTGCTGTGATGAGCTGTGTTCGAGCTGGTGCACACTCCAAAGTCT	780
Db	837		ACGAACGGCTTCTGCGCTGTGATGACGGTGTTCGACCGCGCGCACTCGCAATCA	896
Qy	781		CTTGTCAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATACCAATCGTG	840
Db	897		CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	956
Qy	841		ATCGCCCAACCCAGAAAGCTGCTCCACGTATTCGAACCTACCGATGCTTCTGGAAAGTTCATC	900
Db	957		ATCGGAATCCGGAAGCGCTCCACGCATTTCCGACACCGCATCGTCAGGAAATTCATC	1016
Qy	901		GTACTCTCTATGAGATGGCTTCTGCTGTGCTGGAACCGCTTGAGTTCGCTGCTCACT	960
Db	1017		GCACACCTATGGAATGGGCTTCCGCTGGCGGTACGGTTGAGTTGCTGGGCTCAC	1076
Qy	961		CTGCTCTCAACTGGAAGCGTCTACGTTCTCTACACTCGCGCTCGTAAGTTGCTTTCCA	1020
Db	1077		CGCGCTCAACTGGAAGCGTGGCATGTGCTATACGCAACGCTCGAAGAACTTCTTCCA	1136
Qy	1021		GCCTCGCTCTCCAGTCTGGAAGACGTTACTCCAAGTGGATGGTTCCTGCCAAGC	1080
Db	1137		GCCTCGCGCTTCGAGTTCTGAAGAACGATATTCCAATGGAATGGGTTCCGGCGGAGC	1196
Qy	1081		ATCCCGGATTCCTTCCAGTGATTTGGTTCGCTACCCGTACTCCAGACGTTATCTACGCT	1140
Db	1197		ATCCCGGATTCGCTCCCGTGATTTGCCGGCAACCCGGACACCCGACGTAATCTATGCT	1256
Qy	1141		TTGGGTACAGGTCACCTCGGTATGATGTGCTTCCAAATGACCCCAACCCCTGTTCTGAG	1200
Db	1257		TTCCGCGATGTTCTATCGCATGACAGGGGCGCGCATGACCCGAACGCTCGTCTCAGAG	1316
Qy	1201		CTCTCCGAGGTGAGAAAGCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260
Db	1317		CTCTCCGAGGGAAGAAAGCTCAATCGACATTTCCGCCCTTCGCAACCAACCCGCTTGGT	1376
Qy	1261		ATTGGTAAAGTCCAAAGAACTGCTCTGCATCCCTAA	1296
Db	1377		ATTGGCAATCCAAAGCAACGGTCCGGCAAGTTAA	1412

RESULT 14
PSEAKSD PSEAKSD 3430 bp DNA BCT 26-APR-1993
LOCUS Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
DEFINITION gene, complete cds.

ACCESSION	M69158	
VERSION	M69158.1	GI:150981
KEYWORDS	ketoglutarate semialdehyde dehydrogenase.	
SOURCE	Pseudomonas putida DNA.	
ORGANISM	Pseudomonas putida	
	Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.	
REFERENCE	1 (bases 1 to 3430)	
AUTHORS	Nurlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.	
TITLE	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas putida	
JOURNAL	Unpublished (1991)	
FEATURES	Location/Qualifiers	
source	1..3430	
gene	/organism="Pseudomonas putida"	
	/db_xref="taxon:303"	
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CDS	/gene="ketoglutarate semialdehyde dehydrogenase"	
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	/codon_start=1	
	/transl_table=11	
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	/protein_id="AA25698.1"	
	/db_xref="GI:150982"	
	/translation="MTLTGYMLIGQTPVTGSRRAIRADPATGQLEPAYLGCTGEHV	
	AOCALAWAFDGYRETTLEORAOFLTIATOIEALGDALIDRAVAESGLPKARIOGE	
	RRTCTQLRTFARVVRAGELDVRVNDNAQPERQPLRADLRQVALGPVAVFGASNF	
	PLAFSVAGDITASALAAAGCPVVKHSAHPGTSGLVQAQAVKICGLPAGVFSLLY	
	GSGREVGIALVSDPRIKAVFTGSRSGGICALCOATQARPEIPVYAEKMSINPVFLPE	
	AALQRAEALAGFVASLTQGAQGFCTNPGLVIAQGPALQRFIDAAESBHVQAAQT	
	MLTGPISAYQAGVGLAGNANAQAAGAGQGNQCAQLFVTOAEAPLADPALQA	
	EYFGAASLVACASDQVHQAHPLEGQLTATLDLDDADIDRALLPTLERKAGRIL	
	VNGWPTGVEVCDAMVHGPPATSDARTTSVGTAAILRLRPLRVCYQDFNALLPQALQ	
	HGNPLQLRLLEDGKREG"	
BASE COUNT	562 a	1140 c 1157 g 571 t
ORIGIN		

Query Match	5.0%;	Score	64.6;	DB	2;	Length	3430;
Best Local Similarity	47.4%;	Pred. No.	3.1e-07;				
Matches	193;	Conservative	0;	Mismatches	214;	Indels	0;
Gaps	0;						
Qy	29	TCGCTGAGCTGGAATCGTTGGTGTGTTGCACCTGTTTGATGCTTCAACGCTGCTGGATTCA	88				
Db	2214	TGTTGGGCGCGGGATTGTTCGGCGTTGCCTGTGCCCTGCAACTGGCCCGCAGGCGCTCC	2273				
Qy	89	AGGTTACCTTGATTGATCCAAACCCACCGAGTGGAAGTGCGCTCTTTTCGGTAACGCTGGTT	148				
Db	2274	GGGTGCTATTGTTCGCGACCGCCAGCACCGCGCATGCGGGGCTCTATGGCAACCGCGGC	2333				
Qy	149	GCYTCAACGGTTCCTCGGTTGTTCCCAATGTCATGCCAGGAACTTCACTAGCGTTCCAA	208				
Db	2334	ACCTGGCCACCGACGAGGTGTTCGGATTGCCGACCTGTTCGATCCTCAAGCGCTTGC	2393				
Qy	209	AGTGGCTTCTTGACCCCAATGGGTCCATTGTCCATCCCTTTCGGCTACTTTCCAAACCATCA	268				
Db	2394	GCATGCTGCTGGACCCGATGGCCCACTGCGCCTGGACTGGAAGTACTCTCCACAGGCCA	2453				
Qy	269	TGCTTGGTTGATTGCTGTTTCTTTCGCTGGAAGACCAACAAAGTGAAGAGAGCAAGCTA	328				
Db	2454	TGCGCTGTTTACGCGCGCTGCTGCTCAACCTGCGCGCGCGCGCTTCCAGCGCATGTGG	2513				
Qy	329	AGGCACTCCGTAACCTCATCAAGTCCACTGTGCTTTTGATCAAGTCTCTTGGCTGAGAGG	388				
Db	2514	CCGGCATCCGCAACCTTGAAACGAGGAGCGCTGGTGCATGGCAGCGCTCTCTGGGCTCGA	2573				
Qy	389	CTGATGCTAGCCACCTTATCCGTCACCAAGGTCACTTACCTTACCGTGTAC	435				
Db	2574	TCGGGCGCAGCGACCTGTTCCAGGAGGATGTTGCTTGGTGGTTC	2620				

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RESULT 15
AR016613
LOCUS AR016613 62 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 27 from patent US 5776760.
ACCESSION AR016613
VERSION AR016613.1 GI:3972890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 62)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 27 07-JUL-1998;
FEATURES
    source
        1..62
            /organism="unknown"
BASE COUNT 12 a 12 c 19 g 19 t
ORIGIN

Query Match 4.5%; Score 58.8; DB 5; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.4e-05;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 CGCTGGAGCTGGAAATCGTTGGTGTTCACCTGCTTTCACGCTCGTGGATTCAA 89
Db 1 CGCTGGAGCTGGAAATCGTTGGTGTTCACCTGCTTTCACGCTCGTGGATTCAA 60

QY 90 GG 91
Db 61 AG 62
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: us-08-484-274-17
Perfect score: 1296
Sequence: 1 ATGCTGAGAACACAGAA.....AACTGCTCTGCATCTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	99.4	1296	13	Q20835 Synthetic glyphosa
2	1288	99.4	8418	20	X57309 Sugar beet T-DNA c
3	1200.4	92.6	1631	18	T85664 CPT1-GOX gene fusi
4	1004.8	77.5	1321	13	Q20834 Modified glyphosat
5	956.8	73.8	1321	13	Q20833 Manipulated glypho
6	953.6	73.6	1692	13	Q22705 Glyphosate oxidore
7	922.4	71.2	1689	13	Q20832 Glyphosate oxidore
8	892.2	68.8	8012	20	X57305 Sugar beet T-DNA c
9	892.2	68.8	8798	20	X57308 Sugar beet T-DNA c
10	39.8	3.1	32207	20	V73805 KSHV LUR DNA (nucl
11	39.8	3.1	137507	19	V19941 KSHV long unique c
12	37.4	2.9	397	20	X89891 Spinocherebellar at

C 13	35.6	2.7	6558	21	245602	cDNA sequence of a
C 14	35.2	2.7	6794	21	245597	cDNA sequence of h
C 15	35	2.7	10266	17	T33007	Mouse SRV-related
C 16	34.6	2.7	543	13	Q23092	Antigen tc-7a gene
C 17	34.4	2.7	1291	20	X87940	Mycobacterium tube
C 18	34.4	2.7	2852	19	V64558	M. tuberculosis im
C 19	34.4	2.7	2852	19	V44449	Mycobacterium tube
C 20	34.4	2.7	2852	20	Z19359	M. tuberculosis an
C 21	34.4	2.7	2852	20	Z19147	M. tuberculosis re
C 22	34.4	2.7	4888	20	X13244	Enterococcus faeca
C 23	34.2	2.6	5059	20	X84332	Stealth virus nucl
C 24	34.2	2.6	9551	20	Z22301	cDNA encoding a hu
C 25	34.2	2.6	54548	21	Z45596	cDNA sequence of th
C 26	34.2	2.6	138169	21	A34791	Human adenosine re
C 27	34.2	2.6	141589	21	A35005	Human adenosine re
C 28	34.2	2.6	141589	21	A35030	Human adenosine re
C 29	34	2.6	1001	16	O80734	Phosphatidylethano
C 30	34	2.6	1447	13	Q30002	HCNP precursor gen
C 31	34	2.6	1447	15	O58686	Human hippocampal
C 32	33.8	2.6	567	21	A29550	HIV codon altered
C 33	33.6	2.6	3292	14	Q46544	Yeast SSRP DNA seq
C 34	33.6	2.6	3292	19	V09525	S. cerevisiae SSRP
C 35	33.4	2.6	2004	17	T13952	Maize-optimized VI
C 36	33.4	2.6	2004	18	T73997	Maize optimised-B.
C 37	33.4	2.6	2004	19	V16170	DNA encoding an 80
C 38	33.4	2.6	2010	15	Q74683	Bacillus cereus ve
C 39	33.4	2.6	2576	17	T13945	Maize-Optimized VI
C 40	33.4	2.6	2576	18	T74006	Maize optimised-B.
C 41	33.4	2.6	2576	19	V16181	Maize optimised DN
C 42	33.4	2.6	2655	15	Q74682	Bacillus cereus ve
C 43	33.4	2.6	2655	17	T13951	Maize-Optimized VI
C 44	33.4	2.6	2655	17	T13954	Maize-Optimized VI
C 45	33.4	2.6	2655	18	T73996	Maize optimised-B.

ALIGNMENTS

RESULT 1	
Q20835	
ID	Q20835 standard; DNA; 1296 BP.
AC	Q20835;
DT	01-MAY-1992 (first entry)
DE	Synthetic glyphosate oxidoeductase gene.
KW	Recombinant; GOR; resistance; ss.
OS	Synthetic.
FT	Key Location/Qualifiers
FT	CDS 1..1296
FT	/*tag= a
XX	
PN	W09200377-A.
XX	
PD	09-JAN-1992.
XX	
PF	24-JUN-1991; 91WO-US04514.
XX	
PR	24-JUN-1991; 91US-0717370.
XX	
PR	25-JUN-1990; 90US-0543236.
XX	
PA	(MONS) MONSANTO CO.
PI	Kishore GM, Barry GF;
XX	
DR	WPI; 1992-041559/05.
DR	P-PSDB; R20642.
XX	
PT	Gene encoding glyphosate oxido-reductase enzyme - used to

PT transform plants to produce plants tolerant to glyphosate
PT herbicide

Claim 1; Page 1032; 142pp; English.

The sequence is that of the gene encoding a glyophosphate oxidoreductase (GOR) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more: A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyophosphate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops. See also 020832-020841 and 022705.

Sequence 1296 BP: 271 A: 359 C: 305 G: 361 T: 0 other: 0

Query Match	99.4%	Score 1288;	DB 13;	Length 1296;
Best Local Similarity	99.6%	Pred. No. 0;		
Matches 1291; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy	1	ATGGCTGAGAACACAAAGGTTGGTATCGCTGGAGCTGGAAATCGTTGGTGTTTGCGACT	60
Db	1	atggctgagaaccacaaagaggttggtatctcgctggagctggaatcgttggtgtttgacct	60
Qy	61	GCTTTGATGCTTCAACGTCGTGTGATTCAAAGGTTACCTTGTATTTGATCCAAACCCACCAAGT	120
Db	61	gctttgatgttcaaagtcgtggattcaaaggttacctctgattgatccaaacccacaaggt	120
Qy	121	GAAGGTGCCCTCTTTCGGTAAACGCTGGTGTGCTTCAACGGTTCCTCCGTTGTTTCCAATGTCC	180
Db	121	gaaggtgctctcttcggttaacgcgtgtgcttccaaagttctctcogttgttccaatgtcc	180
Qy	181	ATGCCAGGAACCTTGACTAGCGTTTCCAAAGTGGCTTCTTTACCCCAATGGTCCATGTGCC	240
Db	181	atgccaggaaccttgactagcgttccaaagtggtctcttgacccaatgggtccatctgtccc	240
Qy	241	ATCCGTTTCGGCTACTTTCOAACCATCATGCCCTGGTGTGATTTCGTTTCTGCTTCTGCTGGA	300
Db	241	atccgtttcagctactttccaaacctatgctccttggttgattcgcttctctgcttgcgtgga	300
Qy	301	AGACCAAAACGCTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCCACTGTG	360
Db	301	agaccaaaacaggttgaaggagcaagctaaaggcaactcgttaacctacatcaagtcacactgtg	360
Qy	361	CTTTTGATCAAGTCTCTTGGCTGAGGAGGCTGATGCTTAGCCACCTTATCCGTCACCAAGGT	420
Db	361	cttttgatcaagtccttggtctgaaggagctgattgctlagccacctatccgtcacgaaggt	420
Qy	421	CACCTTACCGTGTACCGTGGAGAACGAGACTTCGCCAGGAGCGTGGAGGTTTGGGAATT	480
Db	421	caacctaccgtgtaccctgfgagaagcagactctgcgaaggaacgttgagaggttgggaacct	480
Qy	481	CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGGCTGATTGCATTCGGTTCATTTCCGAT	540
Db	481	cgtcgtctcaacgggttctcgtactcaaaaacctcaagcgtctgattgcttggtattctcgat	540
Qy	541	CCTAATCTTGCTCACGCCCTTTACCAAGGAAATCCTTTATCGAAGAGAACGGTCCACCACTC	600
Db	541	ccTaaactgtctcaagcctttaccaaagggaatccttatacgaaagagaacgggtcacaccalc	600
Qy	601	AACCCACAAGGTCCTGTGACTCTCTTGTTCGTCTGTTTCTATCGCTAACGGTGGAGAGTTC	660
Db	601	aaccccaaaggtctcgtgactcctctgcttcgttcgttctcatcgcgtcaacgggtggagagttcc	660
Qy	661	GTGTCTGCTCGTGTATTCGGATTTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCCAC	720

DR	WPI: 1999-313347/26.	
XX		
PT	Glyphosate resistant transgenic sugar beet plants	
XX		
PS	Claim 15: Page 36-41; 55pp; English.	
XX		
CC	This invention describes a novel sugar beet plant, including its	
CC	descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase	
CC	(cp4/epsps) enzyme activity which is obtainable by Agrobacterium	
CC	mediated transformation with a gene allowing expression of cp4/epsps	
CC	in plants, where the plant lacks both right and left T-DNA border	
CC	sequences. The transgenic sugar beet plants of the invention are capable	
CC	of tolerating herbicide treatment with glyphosate (also known as	
CC	N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.	
XX		
SQ	Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;	
Query Match 99.4%; Score 1288; DB 20; Length 8418;		
Best Local Similarity 99.6%; Pred. No. 0;		
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
Qy	1 ATGGCTGAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGCACT 60	
Db		
7095	atggctgagaaacacagaagttggatcgtgagctggaatcgttgggtttgcaact 7154	
Qy	61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATGATFCAAAACCCACCAAGGT 120	
Db		
7155	gctttgatgtctcaacgtcgtggattcaaggttaacttgattgattccaaaacccacaggt 7214	
Qy	121 GAAGGTGCTCTCTTTCGGTAAACGCTGGTGTCTCAACGGCTTCCGTTGTTGCCAATGTC 180	
Db		
7215	gaaggtgctctcttcggaacgcggttgcctcaacgggttccctcgttgttccaatgtcc 7274	
Qy	181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTGTCC 240	
Db		
7275	atgccagaaacttgactagcgttccaaagtggcttcttgacccaatgggtccattgtccc 7334	
Qy	241 ATCCGTTTCGGCTACTTTCCAACCATCATGCTTGGTGTGATTCGTTCTTGGCTGCTGGA 300	
Db		
7335	atccggttcagactcttcccaaccatcatgcttgggttgattgcttcttcttgctgtga 7394	
Qy	301 AGACCAACAAGTGAAGGACCAAGCTAAGGCACTCCGTAACCTCACTCAAGTCCACATGTG 360	
Db		
7395	agaccaacaagggtgaaggagcaagctaaaggcactccgttaacctcatcaagtcacactgtg 7454	
Qy	361 CTTTGATCAAGTCTTGGCTGAGAGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420	
Db		
7455	cctttgatcaagtccttggctgagaggctgatgctagccaccttatccgtcacagaaggt 7514	
Qy	421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGGACCGTGGAGTTGGGAAGTT 480	
Db		
7515	caccttacggtgtaccgtggagaagcagacttcgccaaaggaccgttggaggttgggaactt 7574	
Qy	481 CGTGTCTCAACGGTGTTCGTACTCAATCTCAGCGCTGATGCATTCGCGTATTCGAT 540	
Db		
7575	cgctgtccaaaggtgttcgacccaatcctcagcgtgatgcatgctgcatcttcgat 7634	
Qy	541 CCTAAGTTGTCTACGCCCTTTACCAAGGGAATCCTTATFCGAAGAGAGACGGTCAACCATC 600	
Db		
7635	cctaagttgtctcagcctttaccaaggaatccttatcgaagaagaacggttcaaccatc 7694	
Qy	601 AACCACAGGTCGCTGACTCTCTTGTTCGTGCTTTCATCGCTAAGCGTGGAGAGTTC 660	
Db		
7695	aaccacaaggtctcgtgactctcttcttcgttcgtttccatcgctaaacggttggagagttc 7754	
Qy	661 GTGCTGCTCTGCTTATCCGGATTTCGAGACTGAAGGTGCTGCTCTCAACGGTATCACCACC 720	
Db		
7755	gtgtctgctgtgttatccggattcagactgaaggtcgtgctctcaaggggtatcaccacc 7814	
Qy	721 ACCAAGGCTGCTTGTGCTGTGTGATGCAGCTGTTGTGAGCTGTGTCACACTCCCAAGTCT 780	
Db		
7815	accaacggtctcttctgtgttgatgcagctgttcttgcagctggtgcacactccaagctct 7874	

Qy	781 CTTGCTAACTCCCTTGGTGTGATCAGATCCCAITTTGGATACCGAAGCTGGATACCACTCGTG 840	
Db		
7875	cttgcctaactcccttgggtgagacatcccatlggalacccaagcgggataccacacatcgtg 7934	
Qy	841 ATCGCCACCAACAGAGCTGCTCCACGCTATTCCAACTACCGATGCTTTCGGAAGTTCAATC 900	
Db		
7935	atcgccaaccagaagctgctccacgtattccaactacatgctctctggaaagttcatc 7994	
Qy	901 GCTACTCTTATGGAGATGGGTCTTCGTGTGTGCTGGAACGTTGAGTTGCTGCTCTCACT 960	
Db		
7995	gctaactctatggagatgggttctcgttctgtctggaacacgttgcgtcgttctccact 8054	
Qy	961 GCTGCTCTTAAGTGGAGCGTCTCACGTTCTCTACATCGCGCTCGTAAGTTGCTTCCA 1020	
Db		
8055	gctgctcttaactggaagcgtgctcaegtctctctacactcaacgtcgttaagtgtcttcca 8114	
Qy	1021 GCTCTCGCTCTCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCGGTCCAAGC 1080	
Db		
8115	gctctcgctcctgcccagttctgaagaaagcttactccaagtggaatgggtttccggtccaagc 8174	
Qy	1081 ATCCCGGATTCCTTCCAGTATTGGTGTGCTACCCGCTACTCCAGAGCTTATCTACGCT 1140	
Db		
8175	atccagatctccctccagtgatggtcgtctacccgtactccagaagttatctacgct 8234	
Qy	1141 TTCGGTACGGTACCTCGGTATGACTGTGTGCTTCCAATGACCGCAACCCCTCGTTTCTGAG 1200	
Db		
8235	ttcgggtcacggttcacctcgttatgactggttgctccaaLgaccgcaacccctcgtttctgag 8294	
Qy	1201 CTCCTCGGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260	
Db		
8295	ctctcgcaggtggaagacacctctatcgactctctccattctccattcgcaccaaacccgttcggt 8354	
Qy	1261 ATTGTAAGTCCAAGCAAACTGGTCTGCTGCATCCTAA 1296	
Db		
8355	attggttaagtccaagcaaacgtggtcctgcataccttaa 8390	
RESULT 3		
ID	T85664 standard; DNA; 1631 BP.	
XX	T85664;	
AC		
XX		
DT	21-NOV-1997 (first entry)	
XX		
DE	CPt1-GOX gene fusion.	
XX		
KW	expression cassette; inducible promoter; alcA; alcR; aldA; regulator;	
KW	alcohol dehydrogenase; herbicide resistance gene; glyphosate;	
KW	N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EPSs;	
KW	5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1;	
KW	Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.	
XX		
OS	Chimeric Arabidopsis.	
OS	Synthetic.	
XX		
PN	WO9706269-A1.	
XX		
PD	20-FEB-1997.	
XX		
PF	02-AUG-1996; 96WO-GB01883.	
XX		
PR	03-AUG-1995; 95GB-0015941.	
XX		
PA	(ZENE) ZENECA LTD.	
XX		
P1	Jepson I;	
XX		
DR	WPI: 1997-154273/14.	
XX		
PT	Chemically Inducible cassette for expressing herbicide resistance	
PT	gene in plants - and derived plants, partic. for resistance to	

PT glyphosate, avoids constitutive expression and minimises development
of herbicide tolerant weeds

Example 3: Fig 7; 59pp: English.

CC A chemically inducible plant gene expression cassette which comprises an
CC inducible promoter linked to a gene (I) that confers resistance to a
CC herbicide, is claimed. (I) imparts resistance to N-phosphonemethyl-
CC glycine (glyphosate) or its salts, but may also be a gene for resistance
CC to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolinones,
CC etc. The inducible promoter (e.g. alcA, alcR, alda or other alcR-induced
CC gene promoter) is operatively linked to an alcR regulator sequence.
CC Induced expression of (I) avoids the risk that constitutive expression
CC may interfere with plant development; allows volunteer plants to be
CC controlled by herbicide applied without inducer and minimises the chance
CC that herbicide-resistant strains of weeds will arise. The expression
CC cassette is strictly controlled and suitable for general use in plants
CC (both mono- and dicotyledons). The alcA/alcR gene switch was exemplified
CC with genes conferring resistance to glyphosate. The switch was used to
CC drive inducible expression of glyphosate oxidase (GOX) in plants.
CC Switchable GOX was expressed alone or in conjunction with constitutive
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs
CC were optimised for expression in mono- and dicotyledonous crop species.
CC The present sequence comprises a fusion of the GOX gene fused to the
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPR1). This
CC sequence was ligated into pMUB1 (see T85666) and used in construction of
CC dicot vectors.

XX Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match 92.6%; Score 1200.4; DB 18; Length 1631;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 16; Indels 50; Gaps 2;

QY 1 ATGCGTGAGAACCAAGAGGTTGGTATCGCTGGAGTGGAAATCGTTGGTTCACCT 60
DB 274 atggctgagaaccacaagaggttggatcgctggagctggaatcggttggcttgcact 333
QY 61 GCTTTGATGCTTCAACGTCGCGGATTCGAAGTTACCTTGATTGATCCAAACCCACGAGT 120
DB 334 gctttgatgcttcaacgctcggtgattcaaggttaccttgattgatccaaacccaccaggt 393
QY 121 GAAGTGCTCTTTTCGGTAAACGCTGGTTCCTTCAACGGTTCCTCGGTTCCTCAATGTC 180
DB 394 gaagtgctcttcttcggttaacgctgggttgcttcaacggttctctcgttggttccaatgtcc 453
QY 181 ATGCCAGGAATTCGACTAGCGTTCCTCAAGTGGCTTCCTTGACC----- 223
DB 454 atgccaggaaacttgcactagcgttccaaagtggctctcgtggtatcctgttgaattcaagc 513
QY 224 -----CAATGGGTCCATTGTCCATCGCTTTCGGCTTACTTTTCAACCATCATCGCTTG 275
DB 514 ttaaggatccaagtgggtccatgtccatcgtttcagctacttccaaacccatcgtcgtg 573
QY 276 GTTGATTCGGTTCCTTTCGTTGGTGAAGACCAACAAAGGTGAAGGACGAGCTTAAGGCAC 335
DB 574 gttgattcgttcttctgtctggtgaagaccacaagaagtgaagagcaagctaaaggcact 633
QY 336 CCGTAACCTCATCAAGTCCACTGTGCCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGC 395
DB 634 ccgttaacctcatcaagtcacactgtgcctttgtatcaagtccttggctgaggaggtgtatgc 693
QY 396 TAGCCACTTATCCGTCACGAAGTCACTTACCGTGTACCGTGGAGAACGAGACTTCGCG 455
DB 694 tagccacttatccgtcacgaagtcaacttaccgtgtacgttggaagacagacttcgc 753
QY 456 CAGGACCGCTGGAGCTTGGGAACCTTCGTCGTCACCGGTTCCTACTCAATCCTCAG 515
DB 754 caaggacgctggagggttgggaacttcgtcgtcaacggttctcgtactcaaatcctcag 813
QY 516 CGCTGATGCATTCGGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 575

DB 814 cgcgtgatgcattgctgtagatttcctaaacttgctcagccttttaccagggaactct 873
QY 576 TATCGAAGAGAACGGTCACACCATCAACCCACAAAGGCTCGTGACTCTCTTGTTCGTCG 635
DB 874 tatcgaagagaaacggttcacaccatcaaccacaaggtctcgtgactctcttcttctcgcg 933
QY 636 TTTTCATCGCTAACGGTGGAGAGTTCGTTGCTGCTGCTGTTTATCGGATTCGAGACTGAAG 695
DB 934 ttctcatcgctaaacggtggagagttcgtgctcgtcgttctatcggtatcgagactgaagg 993
QY 696 TCGTGTCTCAACGGGTATCACACCAACCAACGGGTGTTCTTGTGCTGTTGATG----- 745
DB 994 tegtgtctcaagggttatccaccaccacaacggtgttcttctgctgtgtagctgcaggttt 1053
QY 746 -----CAGCTGTTGTTGTCAGCTGCTGTCACACTCCCAAGTCTCTTCTTAAC 790
DB 1054 gtgaattcaagcttactgcagttgttgcagctggtgcacactccaagctcttctgctaa 1113
QY 791 CCGTTGCTGATGATCCATCCCATTTGGATACCGAAGCTGGATACCAACATCGTATCCCAAC 850
DB 1114 ccccttggtgatgacatcccatggtataccgaagctggataccacatcgatgcgcaacc 1173
QY 851 CAGAACTGCTCCACGATTTCCCAACTACCGATGCTTCTGGAAGTTTCATCGCTACTCCTA 910
DB 1174 cagaagctgctccacgtattcccaactaccgagtcttctggaagttcctcgtactactcta 1233
QY 911 TGGAGATGGCTCTTCGTTGCTGGAACCGTTGAGTTGCTGCTGCTGCTGCTGCTGCTGCT 970
DB 1234 tggagatggggtcttctgctgctggaacccgttgagttcgtcgtcgtcgtcgtcgtcgtc 1293
QY 971 ACTGGAAGCGTGTCTACAGTTCTTACATCCGCTTCCTAAGTTGCTTCCAGCTCTCGCTC 1030
DB 1294 actgggaagcgtgctcactgctctctacactcgtgctcgttaagttgcttccagctcgcctc 1353
QY 1031 CTGCCAGTTCTGAAGAAGCTTACTCCAAAGTGGATGGGTTTCCGTCCTCAAGCATCCCGGAT 1090
DB 1354 ctgccagttctgaagaacgttactccaagtggatgggtttccgtccaagcatccagatt 1413
QY 1091 CCGTTCCAGTGATGGTGGCTGCTACCGTACTCCAGACGTTATCTACGCTTTCGGTCCACG 1150
DB 1414 ccccttcagtgattggtcgtgctacccgttactccagacgttatctacgcttctcgttcacg 1473
QY 1151 GTCACCTCCGGTATGACTGGTGTCTCCAAATGACCGCAACCCCTCGTTTCTGAGCTCTCGCAG 1210
DB 1474 gtcacctcgttgaactgggtgctccaatgaccgcaacccctcgttctcgtcgtcgtcag 1533
QY 1211 GTGAGAGACCTCTATCGACATCTCTCCATTCCCAACCAACCGTTTCGGTATTCGTAAGT 1270
DB 1534 gtgagaagacctctatcgacatctctccatctcgacacaaaccgtttcgtgattggttaagt 1593
QY 1271 CCAAGCAAACTGGTCTCGCATCTAA 1296
DB 1594 ccaagcaaaactggtcctcgtcaltctaa 1619

RESULT 4

Q20834
ID Q20834 standard; DNA; 1321 BP.
XX Q20834;
AC Q20834;
XX Q20834;
DT 01-MAY-1992 (first entry)
XX Modified glyphosate oxidoreductase gene.
DE Recombinant; GOR; resistance; ss.
KW Bacterial isolate LBAA.
OS Key
FH Location/Qualifiers
CDS 9..1304
FT /*tag= a
FT /note= "encodes wild type glyphosate oxidoreductase"

XX W09200377-A.
XX 09-JAN-1992.
XX 24-JUN-1991; 91WO-US04514.
XX 24-JUN-1991; 91US-0717370.
XX 25-JUN-1990; 90US-0543236.
XX (MONS) MONSANTO CO.
XX Kishore GM, Barry GF;
XX P-PSDB; R20642.
XX
XX Gene encoding glyphosate oxido-reductase enzyme - used to
XX transform plants to produce plants tolerant to glyphosate
XX herbicide
XX
XX Claim 1; Page 102; 142pp; English.
XX
XX The sequence is that of the gene encoding a glyphosate oxidoreductase
XX (GOR) enzyme which has been modified using mutagenic primers. The
XX gene sequence was redesigned to eliminate as much as possible the
XX following sequences or sequence features (while avoiding the
XX introduction of unnecessary restriction sites), stretches of G's
XX and C's of 5 or more; A + T rich regions (predominantly) that could
XX function as polyadenylation sites or potential RNA destabilisation
XX regions, and codons not frequently found in plant genes. The G + C%
XX of the GOR gene was reduced from 56% in the manipulated version
XX (Q20833) to 52% in the modified version. However it still encodes
XX the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA.
XX It is used to transform plants such that they express the enzyme
XX sufficiently to enhance the glyphosate tolerance of the plant.
XX Transformed plants resistant to glyphosate can be obtd. so that
XX weeds can be selectively controlled in fields contg. crops.
XX See also Q20832-Q20841 and Q22705.
XX
XX Sequence 1321 BP; 293 A; 349 C; 339 G; 340 T; 0 other;

Query Match 77.5%; Score 1004.8; DB 13; Length 1321;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1114; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACCAAGANGTTGGTATCGCTGGAGCTGGNATCGTTGGTGGTCACT 60
DB 9 atggctgagaaacccaaagtagagcctgctgagctggaatcgttgggtatgcact 68
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTTGATTCCAAACCCACAGGT 120
DB 69 gctttgatgcttcaacgctcgtggattcaagtcacacttgattgaccgaacccctcctg 128
QY 121 GAAGTGCTCCTTTCCGGTAAGCTGGTGGTTCACAGGTTCTCGTGGTGGTTCGAATGCC 180
DB 129 gaagtgctcgttttgggaatgcgggaatgcttcaacggtcctatcgttccctatgtcc 188
QY 181 ATGCAGGAAATTCAGTACGCTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTGCC 240
DB 189 atgcgggaaacttgacgagcgtgcggaagtggcctctgaccgatgggcccgtttgca 248
QY 241 ATCCCTTTTGGCTACTTCCAAACCATCATGCTTGGTTCGTTTCTTGGTTCGTGGA 300
DB 249 atccggttcagctattttcccaaccaatcagccctggttgattcgtcttctgttagccgga 308
QY 301 AGACCAACAAGGTGAAGAGCAAGCTAAGGCACCTCCGCTAAACCTCATCAAGTCCACTGTG 360
DB 309 agaccaacaagggtgaaggagcggcgaagcactccgcaactcatcatcaagcccaggtg 368
QY 361 CTTTGTATCAAGTCTTGGCTGAGAGGCTGATTCGCCACCTTATTCGGTCACCAAGGT 420
DB 361 ctttgtatcaagtcttggctgagaggctgatttcgccaccttatttcggtcaccaaggt 420

DB 369 cctctgatcaagltcaltggcggaggaggtgatgagccactctgatccgcocatgaaggt 428
QY 421 CACCTTACCCTTACCGTCGAGAACAGACTTTCGCCAGGACCGTGGAGTTCGGAACCTT 480
DB 429 catctgacggtatatactcgtggagaagcagactcttcgcaagagaccgaggttggcaactg 488
QY 481 GGTGCTCTCAACGGTGTTCGTACTCAAAATCTCAGCGGTGATGCAATTCGGTGATTTCCGAT 540
DB 489 cggcgtctcaacgggtgttcgcacgcagatcctctctgtgactgtcttgcgtgatttcgat 548
QY 541 CCTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGAAACGGTCCACACCATC 600
DB 549 cctaaacttgcgcatactcttaccagaagcattctctcagaagagaaacgggtccacacgalt 608
QY 601 AACCCCAAGGTCGTCTGCTGACTCTTTCGTCTGCTTTCATCGCTTAACGGTGGAGAGTTC 660
DB 609 aatccgcgaaggcgtcgtgacccctctgttttcggcgcttttatcgcgaacgggtggcgaatt 668
QY 661 GTGCTGCTCGTGTATTCGGATTTCGAGACTGAAGTTCGTCTCTCAAGGGTATCACACCTC 720
DB 669 gtatctgcgctgtcatcggttttgagactgaagtcgtctcctcaaaaggcattacaacc 728
QY 721 ACCAACGGTGTCTTTCCTTTCGCTGATGCAGCTGTTCGTTCAGCTGGTGCACACTCCAAGTCT 780
DB 729 actaacgggttcttgcgtgttgatgcagcgtctgttgcagctggcgcacactcttaataca 788
QY 781 CTTGCTAACTCCCTTGGTTCATGACATCCCATTTGGATACCGAAGCTGGATACACATCGTGG 840
DB 789 cttgctaattcgtcgtgagcgtgacatccgcctcgcataccgaacggtgatatcatatcgtc 848
QY 841 ATGCCAACCCAGAACGTCGCTCCACGTATTCCAACTACCGATGCTTTCGGAAGTTCATC 900
DB 849 atcgcgaataccggaagcgcctccacgcattccgcagccgaatgcgtcaggaataatctc 908
QY 901 GCTACTCTATTCGAGATGGTCTTCGTTCGTTCGTAACGGTTCAGTTCGCTGCTCTCACT 960
DB 909 gcgacacctaaggaaatgggtcttcgtgttcgtgtactgttgagtttgcgtggtctcaca 968
QY 961 GCTGCTCTCTAACTGGAAGCGTCTCACGCTTCTCTACACTCGCGCTCGTAAGTTCGTTCCA 1020
DB 969 gctgctcctaactggaacgtgcgcattgctctatagcagcgtcgaataactcttcca 1028
QY 1021 GCTCTGCTCTCTGCCAGTTCCTCAAGAACGTTACTCCAGTGGATGGTTCGTCCTCAAGC 1080
DB 1029 gccctcgcgctcgcaggttcttgaagaacgatatcccaaatggatgggttttcgctcagc 1088
QY 1081 ATCCCGGATTCCTTCCAGTGTTCGTTCGTTCGCTACCGTACTCCAGACGTTATCTACGCT 1140
DB 1089 atctcctgatctctctccagtgattggctgcgtgcaactcgtacacccgcagtaactatgct 1148
QY 1141 TTTCGCTCACGGTTCACCTCGGTATGACTGTGCTTCCAAATGACCGCAACCCCTCGTTCTGAG 1200
DB 1149 ttgtgcaggtcactcctcgttatgacaggtgtctccaaagtacactcgtctcagag 1208
QY 1201 CTCCTCGGAGGTGAGAAGACCTCTATTCGACATCTCTCCATTCGACCAACCGTTCGGT 1260
DB 1209 ctctcgcagggcgaagaagacccctcaatcgacatttgccttcctgcaccacaacgcgttgg 1268
QY 1261 ATTGTGTAAGTCCAAACCAACTGGTCTTCATCTTAA 1296
DB 1269 attggcaaatcccaagcaaacgggttcggcgaagttaa 1304
RESULT 5
Q20833
ID Q20833 standard; DNA; 1321 BP.
XX
AC Q20833;
XX
DT 01-MAY-1992 (first entry)
XX
DE Manipulated glyphosate oxidoreductase gene.
XX

KW Recombinant; GOR; resistance; ss.
XX Bacterial isolate LBAA.
XX Key Location/Qualifiers
XX CDS 9..1304
FT /*tag= a
FT /note= "encodes wild type glyphosate oxidoreductase"
XX WO9200377-A.
XX
XX PN
XX PD
XX PF
XX PR 24-JUN-1991; 91WO-US04514.
XX PR 25-JUN-1991; 91US-0717370.
XX PR 25-JUN-1990; 90US-0543236.
XX (MONS) MONSANTO CO.
XX PA
XX PI Kishore GM, Barry GF;
XX PR MPI; 1992-041559/05.
XX DR P-PSDB; R20642.
XX
XX PT Gene encoding glyphosate oxido-reductase enzyme - used to
XX transform plants to produce plants tolerant to glyphosate
XX herbicide
XX PS Claim 1; Fig 3; 142pp; English.
XX
XX CC The sequence is that of the gene encoding a glyphosate oxidoreductase
XX (GOR) enzyme which has been manipulated such that it is suitable for
XX introduction into and expression in plant transformation vectors, but
XX it still encodes the wild type GOR enzyme. It was obtd. from bacterial
XX isolate LBAA. It is used to transform plants such that they express
XX the enzyme sufficiently to enhance the glyphosate tolerance of the
XX plant. Transformed plants resistant to glyphosate can be obtd. so
XX that weeds can be selectively controlled in fields contg. crops.
XX See also Q20832-Q20841 and Q22705.
XX
XX SQ Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;

Query Match 73.8%; Score 956.8; DB 13; Length 1321;
Best Local Similarity 83.6%; Pred. No. 2.1e-289;
Matches 1084; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACACACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTCACT 60
Db 9 atggctgagaaacacacaaagtaggcatcgctggagccggaatcgctggcgatgcacg 68

QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
Db 69 gcctgagcttcagccgcggagattcaagctcacctgattgacccgaacccctccctggc 128

QY 121 GAAGTGCCCTCTTTTCGGTAACGCTGGTGGTTCACCGGTTCCCTCGTTGTTCCAAATGCC 180
Db 129 gaagtgcatcgcttgggaaatgccgagatgcttcaacggctcatcgctcgccctatgtcc 188

QY 181 ATGCCAGAAACTTGACTACGTTCCAAAGTGGTCTTTCACCCAAATGGGTGCCATTGTGCC 240
Db 189 atgccggaacacttgacgagctgcgcgaagtggctccttgaccogalggggcgctgtgca 248

QY 241 ATCCGTTTCGGCTACTTTCACCAACCATCATGCTTGGTGGTGGTTCGTTTCTGCTTGGTGA 300
Db 249 atccggcttcagctatttttccaaccatcatgccctcggctgattcgctcttcgttagccgga 308

QY 301 AGACCAACCAAGGTGAAGGACAGCTTAAGGCACTCCGCTAACCTCATCAAGTCCACCTGTG 360
Db 309 agaccaacaagaagtgaaggagcaggcgaaagcactccgcaatctcalcaagtcacagctg 368

QY 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420

Db 369 ccgctgatacaagtcattggcggaggagctgatgcgagccactctgatccgcatagaaggt 428
QY 421 CACCTTACCGTGTACCGTGGAGAACGACAGACTTCCAGGAGGACCGTGGAGGTGGGAACATT 480
Db 429 catctgaccgtatatactcgtggagaagcagactctcccaaggaccgcggagggtgggaactg 488
QY 481 CGTCTCTCAACCGGTGTTGCTGACTCAAAATCCTCAGCCGCTGATGCTATGCTGATTTCCGAT 540
Db 489 cggcgtctcaacagtggttgcacgcagatctcgaagccgcatgcgttgcggagattctgat 548
QY 541 CCTAACTTGTCTACGCGCTTTTACCAAGGAATCCTTATCGAAGAACGCGTCAACACCATC 600
Db 549 ccgaacttgcgcgtgcggtttaccgaaggcattcttataagaagagaaacggctcacacgatt 608
QY 601 AACCACAAAGGTCTCGTCACTCTCTTGTTCGTGCTTCATCGCTAACGGTGGAGAGTTTC 660
Db 609 aatccgcaagggtcgctgagacctcttcttcggcggttttatacgcgaacgggtggcgaaatt 668
QY 661 GTGTCTGCTCGTGTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGTTATCACCAACC 720
Db 669 gtatctgcgcgtgtcatcgctcttgagactgaaggtagggcgcttaaaaggcatlacaaacc 728
QY 721 ACCAAAGGTGTTTGTGTTGATGCGAGCTGTTGTTGACGCTGTGTCACACTCAAGTCT 780
Db 729 acgaacggcgttctggccgttgatgcagcgttgctgcgagccgcgcacactcgaaatca 788
QY 781 CTTGCTAACTCCCTTGGTGTGATGACATCCATTGGATACCGAAGCTGGATACCATCGTGTG 840
Db 789 ctgtctaattcgtcagcgaatgacatccgcgctcgtatccgaacgtgggatacatatgctc 848
QY 841 ATCCCAACCCAGAGCTGCTCCACAGTATTCACACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 849 atcgcgaatccggaagccgcctccacgcattccgacgaccgatgcgtcaggaataatctcatc 908
QY 901 GCTACTCTATGGAGATGGGCTCTTCGTGTTGCTGGAACCGTTGAGTTTCGCTGGTCTCACT 960
Db 909 gcgaacctatggaaatggggcttcgcggtggcggttgcggttgcgtgggtgcacaca 968
QY 961 GCTGCTCTAACTGGAAGCGTGTACGTTCTCTACACTCGCGCTCGTAACTGCTTCTCCA 1020
Db 969 gccgtctcctaactggaaacgtgcgcatagtcctctatacgcgacgtccgaaaactctctcca 1028
QY 1021 GCTCTCGCTCCTGCCAGTCTTGAAGACGTTTACTCCAAAGTGGATGGGTTTCCGTCCAAAGC 1080
Db 1029 gccctcgcgcctgcgagttctcgaagaacgatattccaaatggatggggttcgcggcagcgc 1088
QY 1081 ATCCCGGAATCCCTTCCAGTGATTTGGTGGTGTCTACCCGTTACTCCAGAGCTTATCTACCGCT 1140
Db 1089 atcccggtattcgtcccccgtgattggccgggcaaccccggaacccgcagctaatctatgct 1148
QY 1141 TTGCGTCAAGGTCACCTCGGTTATGCTGCTCCAATGACCGAACCTCTGTTTCTGAG 1200
Db 1149 ttcggccacggctcctcttcggcatgacagggggcgcgatgacccgcaacgctcgtctcagag 1208
QY 1201 CTCTCGCAGGTGAGAAGACCTCTATGCACATCTCTCCATTTCCGACCAACCGTTTTCGGT 1260
Db 1209 ctctcgcaggcgaaagacacctcaatgcacatttcgccccttcgcaccaaacccgcttgggt 1268
QY 1261 ATTGGTGAAGTCCCAAGCAAACTGGTCTCTGCAATCCCTAA 1296
Db 1269 atgggcaatcccaagcaaacgggtcccggaagttaa 1304

RESULT 6
Q22705
ID Q22705 standard; DNA; 1692 BP.
XX
AC Q22705;
XX
DT 01-MAY-1992 (first entry)
XX
DE Glyphosate oxidoreductase gene.

Db 1380 attgccaatcccaagcaaacagggtcccggaagttaa 1415

RESULT 7

Q20832

ID Q20832 standard; DNA; 1689 BP.

XX

AC Q20832;

XX

DT 01-MAY-1992 (first entry)

XX

DE Glyphosate oxidoreductase gene.

XX

KW Recombinant; GOR; resistance; ss.

XX

OS Bacterial isolate LBMA.

XX

FH Key Location/Qualifiers

FT CDS 120..1412

FT /*tag= a

FT /note= "glyphosate oxidoreductase coding region"

FT misc_feature 349..350

FT /*tag= b

FT /note= "in the alternative sequence G is present here"

FT misc_feature 375..376

FT /*tag= c

FT /note= "in the alternative sequence T is present here"

FT misc_feature 389..390

FT /*tag= d

FT /note= "in the alternative sequence C is present here"

XX

PN W09200377-A.

XX

XX

PD 09-JAN-1992.

XX

PF 24-JUN-1991; 91WO-US04514.

XX

XX

PR 24-JUN-1991; 91US-0717370.

PR 25-JUN-1990; 90US-0543236.

XX

XX (MONS) MONSANTO CO.

XX

XX Kishore GM, Barry GF;

PI

XX

DR WPI; 1992-041559/05.

DR P-PSDB; R20642.

XX

PT Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide

PT

XX

PS Claim 1; Page 93; 142pp; English.

XX

CC The sequence is that of a gene encoding a glyphosate oxidoreductase (GOR) enzyme. It was obtd. from bacterial isolate LBMA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields coneg. crops. This sequence (SEQ ID No.3 in the specification) contains apparent discrepancies (see feature table) with a supposedly identical sequence (fig 2), since it is unclear from the specification which of these is correct, both sequences have been indexed. See also Q20833-Q20841 and Q22705 - the alternative sequence for the GOR gene.

XX

XX

XX Sequence 1689 BP; 381 A; 477 C; 470 G; 360 T; 1 other;

XX

Query Match 71.2%; Score 922.4; DB 13; Length 1689;

Best Local Similarity 83.5%; Pred. No. 1.4e-278;

Matches 1082; Conservative 0; Mismatches 211; Indels 3; Gaps 3;

QY 1 ATGGCTGAGAACCAAGAGGTTGGTATCCCTGGAGCTGGAATCGTTGGTTCACACT 60

Db 120 atgtctgagaaccacaacaaagtaggcatacgtcgcggaacatcgctcggtatgcacy 179

QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTTACCTTGTATGATCCAAACCCACACAGGT 120

Db 180 gcgctgatactcagcgccgaggttcaaaagtcacactctgattgaccccggaagccctccgcgc 239

QY 121 GAAGGTGCTCTTTCCGGTAACGCTGCTTCTCAACGGTTCCCTCCGTTGTTTCCAATGTCC 180

Db 240 gaagtgcatcgcttgggaatgcggatgcttcaacggctcatccgctcgctccctatgtcc 299

QY 181 ATGCCAGGAACTTACCTAGCGTTCCAAAGTGGCTTCTTTCACCAATGGGTCCATTTGTCCTC 240

Db 300 atgcgggaaacttgacgagcgtgcgaagtgtcctcttgaccgcggtggg-cggtgtca 358

QY 241 ATCCGTTTCGGCTACTTTTCCAAACATCATGCTTGGTTGGTTGATTCTTCTTGTGCTTGGGA 300

Db 359 atccggttcagcta-tttccaaccatacgcc-tggttgattcgcgttcttcgttagccgga 416

QY 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACTCATCATCAAGTCCACTGTG 360

Db 417 agaccaacaaggtagaaggcaggcgaaagcaactccgcaatctcatcaagtccacggtg 476

QY 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTTCAGGAAGGT 420

Db 477 cctctgatcaagtcatcttgcgaggaggtgatcgagccatctgatccgccatgaaggt 536

QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGACCGTGGAGGTTGGGAACCTT 480

Db 537 catctgaccggtatactgttggaagcagactctcgcaaggaccgcgagggtcttggaactg 596

QY 481 CGTCGTCACAACGGTGTCTGCTACTCAATCTCTCAGCGCTGATGCAITTCGCTGATTTTCGAT 540

Db 597 cggcgtctcaacggtgttcgcagcgagatccctcagcgcgatcggttgaggatcttcgat 656

QY 541 CTTAACTTGTCTCACGCCCTTTACCAAGGGAATCCTTTATCGAAAGAGAACGGTTCACACATC 600

Db 657 ccgaactgtcgcatcgctttaccaagggtctctatagaagagaaacgggtccacgatt 716

QY 601 AACCCACAGGTCCTGCTGACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660

Db 717 aatccgcaagggtcgtcgacctctgtttcggcggttttatcgcgcaacggcgcgaaattc 776

QY 661 GTGCTGCTGCTGCTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACACACC 720

Db 777 gtatctgcgctgcatcgctttgagactgaaggtaggcgcttaaaaggcattacaacc 836

QY 721 ACCAACGGTGTTCCTGCTGCTGATGATGAGCTGTTGTTGGAGCTGGTGCACACTCCAAAGTCT 780

Db 837 acgaacggcggttctggtcggttgatgcagcggttgctgcgagcgcgccacactcgaaatca 896

QY 781 CTTGCTAACTCCCTTGGTGATGCATCCCATTCGATACCGAACGTCGATACCATCGTCGTG 840

Db 897 ctgttaattcgtctaggcgatgacatcccgctcgatcaccgaaactggtatcatatcgtc 956

QY 841 ATCGCAACCCAGAGAGCTGCTCCACGATTTTCCAACTACCGATACGCTTCTGGAAGTTTCATC 900

Db 957 atcggaatccggaagcgctccacgcatccgagacgcatgctcagggaaaaattcatg 1016

QY 901 GCTACTTCCTATGAGATGGGTCTTCGTGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960

Db 1017 ggcacacatggaatggggtcttcgctggtggcggttcaggttgatgctcgctgggctcaca 1076

QY 961 GCTGCTCTCTAACTGGGAAGCGTCTCAGCTTCTCTACACTCGCGCTCGTGTAGTTGCTTCCA 1020

Db 1077 gccgctcctaactggaacgctgcgcatgctctatacgcacgctcgaaacactcttccca 1136

QY 1021 GCTCTCGCTCTCCAGGTTCTGAAGAACGTTTACTCCAAGTGGATGGGTTTTCGCTTCCAAGC 1080

Db 1137 gccctcgccctgcaggttctgaagaacgatatattcccaatggatgggttcccgccgagc 1196

QY 1081 ATCCCGGATTCCTTCCACTGATTTGCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTC 1140

Db 1197 atccgggattcgctccccggtgattgcccgggcaaccccgagaccccgacgctaattctatgct 1256
Qy 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTCTCCAAATGACCGCAACCTCGTTTCTGAG 1200
Db 1257 ttcggccatggctcatctcggcatgacagggcgccgatgaccgcaacgctcgctcagag 1316
Qy 1201 CTCCTCGCAGGTGAGAACACCTCTATCGACATCTCTCCATTTCGCACCAACCGTTTCGGT 1260
Db 1317 ctcctcgagcgcaaaagacctcaatcgacatttcgccttcgcacccaaacgctttggt 1376
Qy 1261 ATTGCTAAGTCCAAAGCAAACTGGTCTCATCTCAATCCCTAA 1296
Db 1377 attggcaaatccaaagcaaacgggtccggcaagttaa 1412

RESULT 8
X57305
ID X57305 standard; DNA; 8012 BP.
XX
AC X57305;
XX
DT 26-JUL-1999 (first entry)
XX
DE Sugar beet T-DNA containing cp4/epsps fragment.
XX
KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
XX
OS Beta vulgaris.
XX
PN WO9923232-A1.
XX
PD 14-MAY-1999.
XX
PF 29-OCT-1998; 98WO-EP06859.
XX
PR 31-OCT-1997; 97US-0112003.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Mannerloef M, Steen P, Tenning PP;
XX
DR WPI; 1999-313347/26.
XX
PT Glyphosate resistant transgenic sugar beet plants
XX
PS Claim 8; Page 24-29; 55pp; English.
XX
CC This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
CC mediated transformation with a gene allowing expression of cp4/epsps
CC in plants, where the plant lacks both right and left T-DNA border
CC sequences. The transgenic sugar beet plants of the invention are capable
CC of tolerating herbicide treatment with glyphosate (also known as
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
SQ Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;

Query Match 68.8%; Score 892.2; DB 20; Length 8012;
Best Local Similarity 99.7%; Pred. No. 9.2e-269;
Matches 894; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCGCTGAGAACCAAGCTTGGTATCCCTCGAGCTGCAATCGTTGCTTGGCACT 60
Db 7116 atggctgagaaccacaagaaggttggtatcgctgagctggaatcgttggtgttgact 7175
Qy 61 GCTTTGATGCTTCAACGCTGCTGGATTCAAGGTTACCTTGATTCACCAACCCACGAGGT 120
Db 7176 gctttgatgcttcaacgctcgtggattcaaggtttaccttgattgatcccaacccacaggt 7235

Qy 121 GAAGTGGCTCTCTTCGGTAAACGCATGGTTCCTTCAACGGTTCTTCCGTTCTTCCAAATGTC 180
Db 7236 gaagtgctctcttcggtaaacgctggttgcctcaacggttctctcgttgcctcaatgccc 7295
Qy 181 ATGCCAGCAAACTTCACATAGCGTTCCAAAGTCGCTTCTTGACCCCAATGGTTCATTCGCC 240
Db 7296 atgcaggaacttgactagcgttccaaagtgcctcttgacccaaatgggtccattgtcc 7355
Qy 241 ATCCGTTTCGGCTACTTTTCCAAACCATCATGCTTGGTTGATTTCGTTTCTTGGCTTCTGA 300
Db 7356 atcggtttcagctactttccaaacatcatgcttggttgattcgttctctgcttgcctgga 7415
Qy 301 AGACCAAAACAGGTGAAGGAGCAACCTAAGGCATTCCTTAACCTCATCAAGTCCACTGTG 360
Db 7416 agaccaaaacagg tgaaggagcaagcctaagcactccgtaacctcatcaagtcacatgtg 7475
Qy 361 CCTTTGATCAAGTCCCTTGGCTCAGGAGGCTGATGCTAGCCACCTTATCCGTCACCAAGGT 420
Db 7476 cctttgataaagtctctgctgagagctgatgtacccaccttctccgtcacgaagt 7535
Qy 421 CACCTTACCGTGTACCGTGGAGAACGAGACTTCGCCAGGAGCCGTGGAGGTTGGGAACCT 480
Db 7536 cacttacggtgtaccgtggagaagcagacttcgcaaggaccgtggagggttgggaactt 7595
Qy 481 CGTCTCTCAACGGTGTTCGTACTCAATTCCTACCGCTGATGCAATTCGCTGATTCGAT 540
Db 7596 cgtcgtctcaacggtgttgcgtactcaaatcctcagcgtcgtgcatcggtgatttgcgt 7655
Qy 541 CCTAATCTCTCAGCGCTTTACCAAGGGAATCCCTATTCGAAGAACGCTCACACCATC 600
Db 7656 cctaaactgtctcagcctttaccagaagggaatccttatacgaagaacggttcacaccatc 7715
Qy 601 AACCCACAAGGTCTCGTACTCTCTTGTTCGTCGTTTTCATCGCTAACGGTGGAGGTTTC 660
Db 7716 aaccacaaggctcgtgactctctgttctcgtcttcacgtctaaacggttgaggagttc 7775
Qy 661 GTGCTGCTCGTGTTCGGATTTCGAGACTGAAGTTCGCTGCTCTCAAGGGTATCACACACC 720
Db 7776 gtgtcgtcgtgttatcggaatcgagactgaaggtcgtgctcctcaagggtatccaccac 7835
Qy 721 ACCAACGGTGTCTTCGCTGTGATCGAGCTGTTCGTCGCTGCTGCTCAAGGGTATCACACACC 780
Db 7836 accaaacggtgtctctgctgtgatgcagctgtgtctgcaagctggtgcacactcccaagtc 7895
Qy 781 CTGTCTAATCTCCCTTGGTGTGATGACATCCCATTCGATACCGAGTGGATACCATCGTG 840
Db 7896 ctgtctaactcccttggtgatgacatcccatgtgataccgaacggtggataccacatcgtg 7955
Qy 841 ATCGCCCAACCCAGAGCTGCTCCACGTTATTCCAACTACCGATGCTTCTTGGAAAGTTC 897
Db 7956 atcgccaacccagaagctgctccacgtattcccaactaccgatgcttctcgaaagttc 8012

RESULT 9

X57308

ID X57308 standard; DNA; 8798 BP.

XX

AC X57308;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX

PN WO9923232-A1.

XX

PD 14-MAY-1999.

XX 29-OCT-1998; 98WO-EP06859.
XX 31-OCT-1997; 97US-0112003.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Mannerloef M, Steen P, Tenning PP;
XX WPI; 1999-313347/26.
XX
XX Glyphosate resistant transgenic sugar beet plants
XX
XX Claim 11; Page 31-36; 55pp; English.
XX
XX This invention describes a novel sugar beet plant, including its
XX descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
XX (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
XX mediated transformation with a gene allowing expression of cp4/epsps
XX in plants, where the plant lacks both right and left T-DNA border
XX sequences. The transgenic sugar beet plants of the invention are capable
XX of tolerating herbicide treatment with glyphosate (also known as
XX N-phosphonomethyl-L-glycine) as the active ingredient, e.g. Roundup.
XX
SQ Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;

Query Match 68.8%; Score 892.2; DB 20; Length 8798;
Best Local Similarity 99.7%; Pred. No. 9.6e-269;
Matches 894; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCGGTGAGAACACCAAGAGTTGGTATCGGTGGAGTGGATCGTGTGGTTCACCT 60
DB 7205 atggctgagaaacacacagaggttggtatcgctggagctggaatcgtgtgttcac 7264

QY 61 GCTTTGATGCTTCAACGTCGTCGGATTCAAGATTACCTTGATTGATCCAAACCCACCAAGT 120
DB 7265 gctttgatgcttcaacgctcgtgattcaaggattaccttgattgatccaaacccaccaggt 7324

QY 121 GAAGGTGCGCTCTTCGGTAACGCTGGTTCCTTCAACGGTTCCTCCGTTGTTCCAAATGTC 180
DB 7325 gaaggTgctctctcggtaacgctgggtcttcaacggtctctcccgcttcttccaaTgtcc 7384

QY 181 ATCCGAGGAAACTTGACTACGCTTCCAAAGTGGCTTCTTACCCCAATGGTCCATTGTGTC 240
DB 7385 atgcccaggaacttgactagctgtccaaagtggcttcttgaccacatgggtccattgtcc 7444

QY 241 ATCCGTTTCGGGTACTTCCACACCATCATGCTTGGTTGATTGCTGTTCTGCTGTGGA 300
DB 7445 atccggtttcagctactttccaaacatcatgcttggtgattgctgttcttctgtgtgga 7504

QY 301 ACACCAAAACAGTCAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
DB 7505 agaccaaaacaaaggtgaaaggagcaagctaaaggcactccgtaacctcaacagtcactgtg 7564

QY 361 CTTTTCATCAAGTCCCTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
DB 7565 ccttgatcaagtctcttgctgagggctgatgctgacacattatccgtccacgaagt 7624

QY 421 CACCTTACCGTGTACGTCGGAAGCAGACTTCGCCAGGACCGTGGAGGTGGGAACATT 480
DB 7625 caacctacggtgaactgtgagaagcagacttcgcaaggacgctggaggttgggaactt 7684

QY 481 COTCGTCTCAACCGTGTTCGTACTCAAAATCCCTCAGGCGTGATGCAATTGCGTGAATTTCGAT 540
DB 7685 cgtcgctctcaacaggTgttcgtactcaaaTccctcagcgctgagTgcgtgtgatttcgcat 7744

QY 541 CCTAATCTGTCACGCCCTTTACCAAGGGAATCTTTATCGAAGAGAACCGGTCCACCATTC 600
DB 7745 cctaactgtctcagccctttaccaagggaatcccttatcgaaagacaggttcacaccatc 7804

QY 601 AACCACACAGGTCTCGTGACTCTCTTGTTCGTCTTTCATCGCTAACGGTGGAGAGTTC 660

DB 7805 aaccacaaggctcgtgactctctgttttcgctcgttcatcgtaacggtggagagttc 7864
QY 661 GTGCTCGTCTGTTATTCGGATTTCGACACTGAAGTGTGCTCTCAAGGGTATCACCACC 720
DB 7865 gtgtctgctcgtgttatacgagattcgagactgaagggtcgtctcctcaagggttatcaccacc 7924
QY 721 ACCAAGCGGTGTTCTTGTCTGTGATGCAGCTGTTGTTTCAGCTGTGCACACTCCCAAGTCT 780
DB 7925 accaagcgtgttctctgctgttgatgcagctgtgtgtcagctggtgcacactccaagtct 7984
QY 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGGATTACCGAACGTGGATACCATCGTG 840
DB 7985 ctgtctaactcccttggtgatgacatcccatgtgataccgaacgtggataccacatcgtg 8044
QY 841 ATCGCCAAACCCAGAAGCTGCTCCACACTATTTCCAACTACCGATGCTTCTGGAAAGTTC 897
DB 8045 atcgccaacccaagaagctgctccacgtattccaactaccgatgcttctgaaaagttc 8101

RESULT 10
V73805
ID V73805 standard; DNA; 32207 BP.
AC V73805;
XX
XX 25-FEB-1999 (first entry)
XX
XX KSHV LUR DNA (nucleotides 105,301-137,507).
XX
XX Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
XX dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;
XX diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;
XX glycoprotein; Kaposin; cyclin D; immediate early protein; IEP; OX-2;
XX v-adj; G-protein coupled receptor; FGARAT; ds.
XX
XX Kaposi's sarcoma-associated herpesvirus.
XX
XX US5849564-A.
XX
XX 15-DEC-1998.
XX
XX 29-NOV-1996; 96US-0770379.
XX
XX 29-NOV-1996; 96US-0770379.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX WPI; 1999-069741/06.
XX
XX Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
XX dihydrofolate reductase and is useful for treatment, prophylaxis
XX or diagnosis of Kaposi's sarcoma
XX
XX Disclosure; Column 155-182; 109pp; English.
XX
XX This sequence is a fragment of the Kaposi's sarcoma-associated
XX herpesvirus (KSHV) LUR (long unique region). This fragment contains
XX coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67
XX which encodes tegument protein IV, ORF68 which encodes a glycoprotein,
XX ORF69, K12 which encodes Kaposin, K13, ORF72 which encodes cyclin D,
XX ORF73 which encodes immediate early protein (IEP), K14 which encodes
XX OX-2 (v-adj), ORF74 which encodes G-protein coupled receptor, ORF75
XX which encodes tegument protein/FGARAT, K15. KSHV is a new human
XX Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the
XX most common form of neoplasm occurring in persons with acquired immune
XX deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,
XX prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma
XX and for detecting expression of a DNA virus associated with Kaposi's
XX sarcoma in a cell.
XX

Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other:

[illegible]

CC gene. The human OPA gene is derived from the PCTG4 region of chromosome
CC Xq13. Polymorphisms in this region are associated with mental
CC retardation, autism, depression, bipolar affective disorder or
CC hypothyroidism. One 12 bp insertion polymorphism occurs within the
CC coding region of the human OPA gene, and introduces a 4 amino acid
CC insertion in a putative OPA domain. This domain has been shown to be
CC involved in tissue specific expression. Another polymorphism consists
CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp
CC polymorphism. Another polymorphism consists of a dinucleotide repeat
CC approximately 4.5 kb downstream of the 12 bp polymorphism. The
CC specification describes a method for screening for polymorphisms in a
CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related
CC sequences within the q13 region of the X chromosome have polymorphisms
CC associated with neuropsychiatric disorders. The methods can be used
CC to screen for the presence of a heritably linked form of mental
CC retardation, autism, depression, bipolar affective disorder or
CC hypothyroidism.
XX
SQ Sequence 6558 BP; 1637 A; 1801 C; 1644 G; 1475 T; 1 other;

Query Match 2.7%; Score 35.6; DB 21; Length 6558;
Best Local Similarity 45.2%; Pred. No. 1;
Matches 131; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 665 CTGCTGCTGTTATCGGATCGAGACTGAAGTGTGCTCTCAAGGGTATCACCACCACA 724
DB 6396 CTGGCGCTGGAACTGGGACTGGGCTGGGGTTGGGGAGGCTGCTGCTGCTG 6337

QY 725 ACGGTGTTCTTGTCTGATGCAGCTGTTGTCAGCTGGTGCACACTCCAAAGTCTCTTG 784
DB 6336 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6277

QY 785 CTAACCTCCCTTGGTGATGACATCCCATTTGGATACCGAACGTTGATACCATCG 844
DB 6276 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6217

QY 845 CCACCCAGAGCTGCTCCAGATATCCAACTACCGATGCTTCTGGAAGTTTCATCGTA 904
DB 6216 CTGTCGGATATGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6157

QY 905 CTCTATCGAGATGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
DB 6156 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6107

RESULT 14
245597/C
ID 245597 standard; cDNA; 6794 BP.
XX 245597;
AC
XX
XX
DT 06-APR-2000 (first entry)
XX
DE cDNA sequence of human OPA gene.
XX
KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
KW mental retardation; autism; depression; bipolar affective disorder;
KW hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
XX
OS Homo sapiens.
XX
PN WO955915-A2.
XX
PD 04-NOV-1999.
XX
PE 29-APR-1999; 99WO-US09365.
XX
PR 29-APR-1998; 98US-0083465.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (IOWA) UNIV IOWA RES FOUND.
XX

PI Philibert RA, Glans EI;
XX
DR WPI; 2000-126357/11.
XX
PT Identification of polymorphisms in the PCTG4 region of Xq13 for
PT diagnosing mental retardation or autism -
XX
PS Example 7; Page 68-71; 100pp; English.
XX
CC The present sequence represents the cDNA sequence of the human OPA
CC gene, which is derived from the human PCTG4 region of chromosome Xq13.
CC Polymorphisms in this region are associated with mental retardation,
CC autism, depression, bipolar affective disorder or hypothyroidism.
CC One 12 bp insertion polymorphism occurs within the coding region of
CC the human OPA gene, and introduces a 4 amino acid insertion in a
CC putative OPA domain. This domain has been shown to be involved in tissue
CC specific expression. Another polymorphism consists of a pentanucleotide
CC repeat approximately 7 kb upstream of the 12 bp polymorphism. Another
CC polymorphism consists of a dinucleotide repeat approximately 4.5 kb
CC downstream of the 12 bp polymorphism. The specification describes a
CC method for screening for polymorphisms in a PCTG4 nucleic acid sequence
CC obtained from a subject. The PCTG4 related sequences within the q13
CC region of the X chromosome have polymorphisms associated with
CC neuropsychiatric disorders. The methods can be used to screen for the
CC presence of a heritably linked form of mental retardation, autism,
CC depression, bipolar affective disorder or hypothyroidism.
XX
SQ Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;

Query Match 2.7%; Score 35.2; DB 21; Length 6794;
Best Local Similarity 54.7%; Pred. No. 1.4;
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 643 GCTAACGGTGGAGAGCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
DB 6289 GCTGCTGCCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6230

QY 703 CTCAAGGGTATCACCACCACCAACCGTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 762
DB 6229 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6170

QY 763 GGTGCACA 770
DB 6169 GCTGCTCA 6162

RESULT 15
T33007/C
ID T33007 standard; DNA; 10266 BP.
XX
AC T33007;
XX
DT 23-OCT-1996 (first entry)
XX
DE Mouse SRV-related gene.
XX
KW Mouse; SRV; primer; PCR; polymerase chain reaction; amplification; probe;
KW HMG box; human; bovine; sex; animal; birth; ds.
XX
OS Mus musculus.
XX
FH key Location/Qualifiers
FT CDS 7148..8335
FT /*tag=a
FT /product= SRV-related protein
XX
PN JP08154685-A.
XX
PD 18-JUN-1996.
XX
PE 30-NOV-1994; 94JP-0319525.
XX

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:13:01 ; Search time 3327.86 Seconds
(without alignments)
2407.829 Million cell updates/sec

Title: US-08-484-274-17
Perfect score: 1296
Sequence: 1 ATGGCTGAGAACCAAGAA.....AAACTGGTCTGCATCCTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
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112: gb_gss13:*
113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:*


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PR0013713      FRO013713      619 bp      DNA      GSS      18-SEP-1997
LOCUS          F.rubripes GSS sequence, clone 133B16db11, genomic survey sequence.
DEFINITION     AL004959
ACCESSION      AL004959.1 GI:2450529
VERSION        GSS; genome survey sequence.
KEYWORDS       Fugu rubripes.
SOURCE         Fugu rubripes.
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
                Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
                Tetraodontiformes; Tetraodontidae; Fugu.
REFERENCE      1 (bases 1 to 619)
AUTHORS        Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
                Williams,G. and Brenner,S.
TITLE          Direct Submission
JOURNAL        Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
COMMENT        Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
                Vector: pBluescript II KS
                V_type: phagemid
                PRIMER: KS
                One pass dye-terminator sequencing of cosmid cloned genomic
                sequence.
FEATURES       source      Location/Qualifiers
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                /organism="Fugu rubripes"
                /db_xref="taxon:31033"
                /clone_lib="cosmid 133B16"
                /clone="133B16db11"
BASE COUNT     83 a 163 c 139 g 180 t 54 others
ORIGIN
Query Match    3.1%; Score 40.6; DB 124; Length 619;
Best Local Similarity 43.3%; Pred. No. 0.39;
Matches 139; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

Oy 722 CCACGGTGTCTTCTGCTGTTGATGACGCTGTTGTCAGCTGGTGCACACTCCCAAGTCTC 781
    |||||
Db 26 CTACTGTTNATGACGNCGTTACTGCTGCTGCTACTGCTGCTACTACTACTACTACTGCTG 85

Oy 782 TTGCTTAACCTCCCTGGTCATCAGATCCCACTTGGATACCGAAGCTGGATACCACTCGTA 841
    |||||
Db 86 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 145

Oy 842 TCGCAACCCAGAAAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGAAAGTTTCATCG 901
    |||||
Db 146 CTGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205

Oy 902 CTACTCTCTATGAGATGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
    |||||
Db 206 CTGCTACTGCTGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265

Oy 962 CTGCTCTTAACCTGGAAGCTGCTCAGCTTCCTACACATCGCGCTGCTGAAGTTGCTTCAG 1021
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Db 266 CTGCTGCTGCGNGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325

Oy 1022 CTCTGCTCTCTGCCAGTTCTG 1042
    |||||
Db 326 CTGCTGCTGCTGCTACTGTTG 346

RESULT 7
CNS04QUZ      CNS04QUZ      1003 bp      DNA      GSS      24-MAY-2000
LOCUS          Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION     130A16 of library G from Tetraodon nigroviridis, genomic survey
                sequence.
ACCESSION      AL303092
VERSION        AL303092.1 GI:8184772
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis.
ORGANISM       Tetraodon nigroviridis.
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE      1 (bases 1 to 1003)
AUTHORS        Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
                Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                Weissenbach,J.
TITLE          Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 1003)
AUTHORS        Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE          Human gene number estimate provided by genome wide analysis using
                Tetraodon nigroviridis DNA sequence
JOURNAL        Unpublished
REFERENCE      3 (bases 1 to 1003)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT        This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES       source      Location/Qualifiers
                1..1003
                /organism="Tetraodon nigroviridis"
                /db_xref="taxon:99883"
                /clone="130A16"
                /clone_lib="G"
                /note="Genoscope sequence ID : COBGL30BA08LP1-end : T7"
BASE COUNT     187 a 296 c 282 g 234 t 4 others
ORIGIN
Query Match    3.1%; Score 40.4; DB 123; Length 1003;
Best Local Similarity 47.3%; Pred. No. 0.52;
Matches 122; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Oy 712 ATCACCACCACCAACGGTTCCTTGCCTGTTGATGCAGCTGTTGTCAGCTGCTGCACAC 771
    |||||
Db 726 ACCAACAGTAGGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785

Oy 772 TCCAAGTCTCTTGTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCTGGATAC 831
    |||||
Db 786 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845

Oy 832 CACATCGTGATGCGCAACCCAGAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGA 891
    |||||
Db 846 GCTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905

Oy 892 AAGTTTACGCTACTCCCTATGCAGATGGTCTTCGCTGTTGCTGGAACCGTTACGTTCCGT 951
    |||||
Db 906 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965

Oy 952 GGTCTCACTGCTGCTCCT 969
    |||||
Db 966 GCTGCTGCTGCTGCTGCT 983

RESULT 8
AA940845/c    AA940845      752 bp      mRNA      EST      25-NOV-1998
LOCUS          LD23113.5prine LD Drosophila melanogaster embryo pot2 Drosophila
DEFINITION     melanogaster cDNA clone LD23113 5prime similar to M23221: fs(1)h
                FBgn0004656 PID:g157453 SWISS-PROT:P13709, mRNA sequence.
ACCESSION      AA940845
VERSION        AA940845.1 GI:3100758
KEYWORDS       EST.
SOURCE         fruit fly.
```


Fax: 864 656 4293
Email: rdeane@clmson.edu
Seq primer: T3 primer (AATTAAACCTCTACTAAAGG)
High quality sequence stop: 403.

FEATURES
source
1. .946
Location/Qualifiers
/organism="Pyricularia grisea"
/strain="70-15"
/db_xref="taxon:89476"
/clone="mgae0006cc09f"
/clone_lib="MagnaPort the grisea Appressorium Stage cDNA Library"
/dev_stage="Germinated conidia on appressorium-inductive surface"
/note="Vector: pBluescriptII SK(+) Vector; Site_1: EcoRI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library has an average insert size of 1.5 kbp."

BASE COUNT 304 a 270 c 246 g 123 t 3 others
ORIGIN

Query Match 3.1%; Score 39.8; DB 8; Length 946;
Best Local Similarity 47.7%; Pred. No. 0.77; Mismatches 0; Gaps 0;
Matches 116; Conservative 0; Indels 127; Indels 0; Gaps 0;

Qy 727 GGTGCTCTTGTGTTGATGCGACGTGTTTTCAGCTGTCACATCCCAAGTCTCTTCT 786
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 GTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 787 AACTCCCTTGTGATGACATCCCATGATACCGACGTGGATACCATCGTGTATCGCC 846
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Db 199 CTTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 847 AACCAGAGCTGCTCCACGATTCACACTACCGATGCTCTCGAAAGTTTCATCGCTACT 906
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Db 139 GTTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 907 CCTATGGAGATGGCTTCTGTTGCTGGAACCGTTGAGTTGCTGCTGCTGCTGCTGCT 966
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 GCTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20
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Qy 967 CCT 969
||
Db 19 GCT 17

RESULT 11
CNS016U2 1101 bp DNA GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN16L20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL107204
VERSION AL107204.1 GI:5626158
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES
source
1. .1101
Location/Qualifiers
/organism="Drosophila melanogaster"
/plasmid="pBelOBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16L20"
/note="end : SP6"

BASE COUNT 179 a 71 c 171 g 226 t 454 others
ORIGIN

Query Match 3.0%; Score 39.4; DB 121; Length 1101;
Best Local Similarity 22.0%; Pred. No. 1.1; Mismatches 94; Conservative 134; Mismatches 199; Indels 0; Gaps 0;

Qy 362 CTTTGATCAAGTCTTGCTGAGGAGGCTGATGCTAGCACCTTATCCGTCCAGAGTTC 421
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1017 STSTKTTTSTTBKCYTCKGCBTSCKCGYSYCTYSSTTYTBYTYCTTKKYTGC 958
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Qy 422 ACCTTACCGTGTACGCGGAGAGCAGACTTCGCCAGGACCGTGAGGTTGGGAATTC 481
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Db 957 KGTSTCKTTTCKSVCKBCKSGYKKBCTKSGYCYCKBTTKSKGTSTYKCTCTKBTKC 898
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Qy 482 GTCGCTCTCAACGGTCTTCTGCTACTCAAAATCCCTCAGCGTGATGCTGCTGATTTCCGATC 541
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Db 897 GTCIKYCTTTYSBYTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838
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Qy 542 CTAACTTCTCAGCGCTTTTACCAAGGAATCCCTTATCGAAGAGAACGGTCACACCATCA 601
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Db 837 GTBCYTYVYVYBTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 778
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Qy 602 ACCACAGGCTCTCGTGACTCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
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Db 777 KCGYKKSCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCTBCT 718
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Qy 662 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
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Db 717 CKYKBTCTTCT 658
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Qy 722 CCAAGGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
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Db 657 TSTCBTKTYBTCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 598
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Qy 782 TTGCTAA 788
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Db 597 BRANNA 591

RESULT 12
AV182303 300 bp mRNA EST 21-JUL-1999
LOCUS AV182303 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk635h6 3', mRNA sequence.
DEFINITION AV182303
ACCESSION AV182303.1 GI:5562204
VERSION EST.
KEYWORDS Caenorhabditis elegans.
SOURCE Caenorhabditis elegans
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsukawa,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Gene Library Lab


```
QY 641 TCGCTAACGGTGGAGATTGCTGCTGCTGCTGTTATCGGATTCGAGACTGAAGTCTGTG 700
Db 438 TTGCTGCTGTTGGAGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
QY 701 CTCTCAAGGGTATCACCAACCAACGGTGTCTTCTGCTGTTGATCAGCTGTTGTTGCAG 760
Db 438 CTGGGTTAGTTGCTGCTGCTGCTGCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 379
QY 761 CTGGTGGCACTCCAAAGTCTCTGTTGCTAACTCCCTGGTGGTGGTGGTGGTGGTGGTGG 818
Db 378 CTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321

RESULT 15
CNS05HXN 1076 bp DNA GSS 26-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T3 end of clone
DEFINITION 014F03 of library A from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL338180
VERSION AL338180.1 GI:8231938
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 1076)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 1076)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1076)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1..1076
Location/Qualifiers
/organism="Tetraodon nigroviridis"
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/clone="014F03"
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BASE COUNT 160 a 260 c 309 g 333 t 14 others
ORIGIN

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Best Local Similarity 47.2%; Pred. No. 1.6;
Matches 118; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Db 743 CGCTACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 802
QY 780 TCTTTCCTAACTCCCTTGGTGGATGACATCCCATTCGATACCGAACGTCATACCACATCGT 839
Db 803 TGTGCTGCTGCTACTGTTGCTGCTACTGTTGCTGCTACTGTTGCTGCTACTGTTGCTGCTG 862
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QY 840 GATGCCCAACCCAGAGCTGCTCCACGATATTCACAACTACCGATGCTTCTGGAAAGTTTCAT 899
Db 863 TGTCCGTACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
QY 900 CGCTACTCCTATGGAGATGGGTCTTCGGTGTTCGCTGGAACCGTTGAGTTCGCTGGTCTCAC 959
Db 923 TACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 982
QY 960 TGCTGCTGCT 969
Db 983 TACTGTTGCT 992
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Search completed: January 1, 2001, 01:13:07
Job time: 25806 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 19:08:36 ; Search time 7299.04 Seconds
(without alignments)
773.702 Million cell updates/sec

Title: US-08-484-274-4
Perfect score: 1293
Sequence: 1 ATGCTGAGAACCAACAAAA.....AAACGGGTCGGCAAGTTAA 1293

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1293	100.0	1293	5	I15325		I15325 Sequence 4
3	1293	100.0	1689	5	I15324		I15324 Sequence 3
4	1260	97.4	1692	5	AR016591		AR016591 Sequence
5	1255.2	97.1	1296	5	AR016593		AR016593 Sequence
6	1255.2	97.1	1296	5	I15326		I15326 Sequence 6
7	1160.8	89.8	1296	5	AR016594		AR016594 Sequence
8	1160.8	89.8	1296	5	I15327		I15327 Sequence 7
9	928.8	71.8	1296	5	AR016595		AR016595 Sequence
10	928.8	71.8	1296	5	I15328		I15328 Sequence 8
11	925.6	71.6	1296	5	AR016604		AR016604 Sequence
12	925.6	71.6	1296	5	I15337		I15337 Sequence 17

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VERSION	AR016592.1							
KEYWORDS								
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 1293)							
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.							
TITLE	Glyphosate tolerant plants							
JOURNAL	Patent: US 5776760-A 4 07-JUL-1998;							
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DEFINITION Sequence 4 from patent US 5463175.
ACCESSION I15325
VERSION I15325.1 GI:1250233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1293)
TITLE Barry, G.F. and Kishore, G.M.
JOURNAL Glyphosate tolerant plants
FEATURES Patent: US 5463175-A 4 31-OCT-1995;
source Location/Qualifiers
BASE COUNT 286 a 367 c 359 g 281 t
ORIGIN

Query Match 100.0%; Score 1293; DB 5; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION I15324
VERSION I15324.1 GI:1250232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1689)
TITLE Barry, G.F. and Kishore, G.M.
JOURNAL Glyphosate tolerant plants
FEATURES Patent: US 5463175-A 3 31-OCT-1995;
source Location/Qualifiers
BASE COUNT 381 a 479 c 468 g 360 t 1 others
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QY 241 TCCGGTTTACGCTATTTTCCAAACCATCATGCTGCTGTGATTGCTTCTTGTAGCCGGAAGA 300
Db 360 TCCGGTTTACGCTATTTCCAAACCATCATGCTGCTGTGATTGCTTCTTGTAGCCGGAAGA 419
QY 301 CCAAAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCT 360
Db 420 CCAAAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCT 479
QY 361 CTGATCAAGTCATTTGCCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGTCAAT 420
Db 480 CTGATCAAGTCATTTGCCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGTCAAT 539
QY 421 CTGACCCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGAGGTGGGAAGTCCGG 480
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DEFINITION Sequence 3 from patent US 5776760.
ACCESSION AR016591
VERSION AR016591.1 GI:3972868
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1692)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5776760-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
source 1.1692
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SOURCE	Unknown.			
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REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1296)			
TITLE	Barry.G.Francis and Kishore,G.Murthy.			
JOURNAL	Glyphosate tolerant plants			
FEATURES	Patent: US 5776760-A 6 07-JUL-1998;			
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	/organism="unknown"			

BASE COUNT	286 a	368 c	361 g	281 t
ORIGIN				
Query Match	97.1%; Score 1255.2; DB 5; Length 1296;			
Best Local Similarity	99.5%; Pred. No. 0;			
Matches 1290: Conservative	0; Mismatches 3; Indels 3; Gaps 3;			
Qy	1	ATGCTGAGAACCCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG	60	
Db	1	ATGGCTGAGAACCCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG	60	
Qy	61	GCGCTGATGCTTACAGCGCGGGATTCAAAGTCACTTGTATGACCCGAAACCCCTCTGGC	120	
Db	61	GCGCTGATGCTTACAGCGCGGGATTCAAAGTCACTTGTATGACCCGAAACCCCTCTGGC	120	
Qy	121	GAAAGTGTCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCCTCATGTCC	180	
Db	121	GAAAGTGTCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCCTCATGTCC	180	
Qy	181	ATGCCCGGAAACTTTCAGCAGGCTGCCGAAGTGGCTTCCTTGCACCCGAT-GGGCGGTTGTCA	239	
Db	181	ATGCCCGGAAACTTTCAGCAGGCTGCCGAAGTGGCTTCCTTGCACCCGATGGGGCGTTGTCA	240	
Qy	240	ATCCGGTTCAGCTA-TTTTCCAAACCATCATG-CCTGGTTGATTCGGCTTTCTGTAGCCGGA	297	
Db	241	ATCCGGTTCAGCTA-TTTTCCAAACCATCATGCTGCTTGTGATTCGGCTTTCTGTAGCCGGA	300	
Qy	298	AGACCAACAAAGGTGAAGCAGCGAGCAACGACATCCGCAATCTCATCAAGTCCACGGTG	357	
Db	301	AGACCAACAAAGGTGAAGCAGCGAGCAACGACATCCGCAATCTCATCAAGTCCACGGTG	360	
Qy	358	CCTCTGATCAAGTCAATTTGGCGGAGGAGCTCATTCGGAGCCCATCTGATCCGCCATGAAGT	417	
Db	361	CCTCTGATCAAGTCAATTTGGCGGAGGAGCTCATTCGGAGCCCATCTGATCCGCCATGAAGT	420	
Qy	418	CATCTGACCGTATATCTGTTGGAGACAGACATTCGCCAAGGACCGCGGAGGTTGGGAATG	477	
Db	421	CATCTGACCGTATATCTGTTGGAGACAGACATTCGCCAAGGACCGCGGAGGTTGGGAATG	480	
Qy	478	CGGCGCTCAACGGTGTTCGGACGCAGATCCCTACGCGCGATGCGTTCGGGATTTTCGAT	537	
Db	481	CGGCGCTCAACGGTGTTCGGACGCAGATCCCTACGCGCGATGCGTTCGGGATTTTCGAT	540	
Qy	538	CCGAACCTTCTCGCATCGCTTTACCAAGGCGATTCTTATAGAAGAGACGCTCACACGATT	597	
Db	541	CCGAACCTTCTCGCATCGCTTTACCAAGGCGATTCTTATAGAAGAGACGCTCACACGATT	600	
Qy	598	AATCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATCGCGAAGCGGTGGCGAATTC	657	
Db	601	AATCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATCGCGAAGCGGTGGCGAATTC	660	
Qy	658	GTATCTGCGCGTGTTCATCGGCTTTTCAGACTGAAGGTAGGGCGCTTTAAAGGCATTTACAACC	717	
Db	661	GTATCTGCGCGTGTTCATCGGCTTTTCAGACTGAAGGTAGGGCGCTTTAAAGGCATTTACAACC	720	
Qy	718	ACGAACCGGCTTCTGCCGCTTGATGCAGCGGTTGTTCGACGCGCGCGCACACTCGAAATCA	777	
Db	721	ACGAACCGGCTTCTGCCGCTTGATGCAGCGGTTGTTCGACGCGCGCGCACACTCGAAATCA	780	
Qy	778	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	837	
Db	781	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840	
Qy	838	ATCGGGAATCCGGAAGCGGCTCCACGCATTCGAGACCGGATGCGTCAGGAAATTCATC	897	
Db	841	ATCGGGAATCCGGAAGCGGCTCCACGCATTCGAGACCGGATGCGTCAGGAAATTCATC	900	
Qy	898	GCGACACCTATTCGAAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA	957	
Db	901	GCGACACCTATTCGAAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGCTCACA	960	
Qy	958	GCGGCTCTTAACTTGAACAGTGCAGCATGTGCTCTATACGACGCTCGAANAATCTTCTCCA	1017	

Db 961 GCGCTCCTAACTGGAACGTGGCATGTGCTCTATACGACGCTCGAAGTCTCTTCCA 1020
QY 1018 GCGCTCGCGCTCGGAGTCTCTGAAGAACGATATTTCCAAATGGATGGGTTCCGGCCGAGC 1077
Db 1021 GCGCTCGCGCTCGGAGTCTCTGAAGAACGATATTTCCAAATGGATGGGTTCCGGCCGAGC 1080
QY 1078 ATCCCGGATTGCTTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1137
Db 1081 ATCCCGGATTGCTTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1140
QY 1138 TTCCGCCATGCTCATCTCGGCATGACAGGGGCGCGGATGACCGAAGCTGCTCTCAGAG 1197
Db 1141 TTCCGCCATGCTCATCTCGGCATGACAGGGGCGCGGATGACCGAAGCTGCTCTCAGAG 1200
QY 1198 CTCTTCGAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTTTGGT 1257
Db 1201 CTCTTCGAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTTTGGT 1260
QY 1258 ATGGCAAAATCCAAGCAACCGGTCGGCAAGTTAA 1293
Db 1261 ATGGCAAAATCCAAGCAACCGGTCGGCAAGTTAA 1296

RESULT 6
LOCUS 115326 115326 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5463175.
ACCESSION 115326
VERSION 115326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;
FEATURES
1. .1296
source
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 97.1%; Score 1255.2; DB 5; Length 1296;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 ATGCTGTGAGAACCAACAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCAAG 60
Db 1 ATGGCTGAGAACCAACAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCAAG 60
QY 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCCGGAACCCCTCCTGGC 120
Db 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCCGGAACCCCTCCTGGC 120
QY 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAAGGCTCATCCGCTGTCCTATGTC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAAGGCTCATCCGCTGTCCTATGTC 180
QY 181 ATCCCGGGAACCTTGACGAGCGTGGCAGTGGCTCCTTTGACCCGAT -GGGCGGTGTGTA 239
Db 181 ATCCCGGGAACCTTGACGAGCGTGGCAGTGGCTCCTTTGACCCGAT -GGGCGGTGTGTA 240
QY 240 ATCCGGTTTACGTA-TTTCACCAACATCATG-CCTGGTTGATTGCTTTCGTTAGCCGA 297
Db 241 ATCCGGTTTACGTA-TTTCACCAACATCATG-CCTGGTTGATTGCTTTCGTTAGCCGA 300
QY 298 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360

QY 358 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATCGAGCCCATCTGATCCGCCATGAAGT 417
Db 361 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATCGAGCCCATCTGATCCGCCATGAAGT 420
QY 418 CATCTGACCGTATATCTGTGGAGAGCAGACTTCCCAAGGACCCGCGAGGTGGGACTG 477
Db 421 CATCTGACCGTATATCTGTGGAGAGCAGACTTCCCAAGGACCCGCGAGGTGGGACTG 480
QY 478 CCGGCTCTCAACGGTGTTCGACGACGATCTCTAGCCCGCATGCGTTCCGGGATTTCCGAT 537
Db 481 CCGGCTCTCAACGGTGTTCGACGACGATCTCTAGCCCGCATGCGTTCCGGGATTTCCGAT 540
QY 538 CCGAATCTGTGCGATGCGTTTACCAAGGGCATCTTATAGAAGAGAACGCTCAGACGATT 597
Db 541 CCGAATCTGTGCGATGCGTTTACCAAGGGCATCTTATAGAAGAGAACGCTCAGACGATT 600
QY 598 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGGCTTTTATCCGCGAACCGTGGCGAATT 657
Db 601 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGGCTTTTATCCGCGAACCGTGGCGAATT 660
QY 658 GTATCTCGCGGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAACC 717
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QY 718 ACGAAGCGGCTTTCGCGCTTGATGACAGCGGTTGTCGACGCGCGCACACTCGAATCA 777
Db 721 ACGAAGCGGCTTTCGCGCTTGATGACAGCGGTTGTCGACGCGCGCACACTCGAATCA 780
QY 778 CTTGCTTAATTCGCTAGCGGATGACATCCGCTCGATACCGAACGTTGATATCATATGTC 837
Db 781 CTTGCTTAATTCGCTAGCGGATGACATCCGCTCGATACCGAACGTTGATATCATATGTC 840
QY 838 ATCGCGAATCCGAAGCGCTCCACGCAATTCGAGACGACCGATGCGTCAGGAAATTCATC 897
Db 841 ATCGCGAATCCGAAGCGCTCCACGCAATTCGAGACGACCGATGCGTCAGGAAATTCATC 900
QY 898 GCGACACTATGAAATGGGGCTTCGCGTGGCGGTTACGGTTGAGTTGCGTGGGCTCACA 957
Db 901 GCGACACTATGAAATGGGGCTTCGCGTGGCGGTTACGGTTGAGTTGCGTGGGCTCACA 960
QY 958 GCGCTCCTAACTGGAACGTCGCGCATGCTCTATACGACGCTCGAAGAACTCTTTCCA 1017
Db 961 GCGCTCCTAACTGGAACGTCGCGCATGCTCTATACGACGCTCGAAGAACTCTTTCCA 1020
QY 1018 GCGCTCGCGCTCGAGTTCCTGAAGAACGATATTTCCAAATGATGGGTTCCCGCCGAGC 1077
Db 1021 GCGCTCGCGCTCGAGTTCCTGAAGAACGATATTTCCAAATGATGGGTTCCCGCCGAGC 1080
QY 1078 ATCCCGGATTGCTTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1137
Db 1081 ATCCCGGATTGCTTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1140
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Db 1141 TTCCGCCATGCTCATCTCGGCATGACAGGGGCGCGGATGACCGAAGCTGCTCTCAGAG 1200
QY 1198 CTCTTCGAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTCGCAACCAACCGCTTTTGGT 1257
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QY 1258 ATGGCAAAATCCAAGCAACCGGTCGGCAAGTTAA 1293
Db 1261 ATGGCAAAATCCAAGCAACCGGTCGGCAAGTTAA 1296

RESULT 7
LOCUS AR016594 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 7 from patent US 5776760.
ACCESSION AR016594
VERSION AR016594.1 GI:3972871
KEYWORDS Unknown.
SOURCE

ORGANISM	Unknown.	Unclassified.	REFERENCE	1 (bases 1 to 1296)	DB 5:	length 1296:
AUTHORS	Barry.G.Francis and Kishore.G.Murthy.					
TITLE	Glyphosate tolerant plants					
JOURNAL	Patent: US 5776760-A 7 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..1296					
BASE COUNT	287 a 344 c 332 g					
ORIGIN	/organism="unknown"					
Query Match	89.8%;	Score 1160.8;	DB 5:	length 1296:		
Best Local Similarity	95.0%;	Pred. No. 0:				
Matches 1231;	Conservative 0;	Mismatches 62;	Indels 3;	Gaps 3;		
Qy	1	ATGTCGTGAGAACACAAAAAGTAGGCATCCTCGAGCCGGAATCGTCGGCGGTATGCACG	60			
Db	1	ATGGCTGAGAACACAAAAAGTAGGCATCCTCGAGCTGGAATCGTTGGTGTATGCACAT	60			
Qy	61	CGCTGTATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGTATTGACCCGGAACCCCTCTGGC	120			
Db	61	CTTTTGTATGCTTCAAGGTCGTGGATTCAAAGTCACCTTGTATTGACCCGGAACCCCTCTGGC	120			
Qy	121	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTTCAACGGCTCATCCGTCGTCCCTATGTCC	180			
Db	121	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTTCAACGGCTCATCCGTCGTCCCTATGTCC	180			
Qy	181	ATCCGGGAAACTTGAAGAGGTCGCGAAGTGGCTCTTGTACCCGAT--GGGCGGTGTGCA	239			
Db	181	ATCCGGGAAACTTGAAGAGGTCGCGAAGTGGCTCTTGTACCCGATGGGGCCGTGTGCA	240			
Qy	240	ATCCGGTTTCAGCTA-TTTTCCAAACCATATG-CCTGGTTGATTTCGCTTCTTTAGCCGGA	297			
Db	241	ATCCGGTTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTTCGCTTCTTTAGCCGGA	300			
Qy	298	AGACCAACAAGGTGAAGGACAGCGGAAGCACTCCGCAATCTCATCAAGTCACAGGTG	357			
Db	301	AGACCAACAAGGTGAAGGACAGCGGAAGCACTCCGCAATCTCATCAAGTCACAGGTG	360			
Qy	358	CCTCTGATCAAGTCAATTGGCGGAGGAGGCTCATCGGAGCCATCTGATCCGCCATCAAGGT	417			
Db	361	CCTCTGATCAAGTCAATTGGCGGAGGAGGCTCATCGGAGCCATCTGATCCGCCATCAAGGT	420			
Qy	418	CATCTGACCGGTATATCGTGGAGAGCAGACATTCGCCAAGGACCCGGAGGTGGGAACGTG	477			
Db	421	CATCTGACCGGTATATCGTGGAGAGCAGACATTCGCCAAGGACCCGGAGGTGGGAACGTG	480			
Qy	478	CGGCGTCTCAACGGTGTTCGACCCAGATCCTCAGCCCGCATGCGTTCGCGGATTTTCGAT	537			
Db	481	CGGCGTCTCAACGGTGTTCGACCCAGATCCTCCTGCTGATGCTTTTTCGCGTTCGAT	540			
Qy	538	CCGAACCTTGTCCCATGCGCTTTTACCAAGGGCATCTTATAGAAGAGAACCGGTACACAGATT	597			
Db	541	CCTAACTTGTCCGATGCTTTTACCAAGGGCATCTTATAGAAGAGAACCGGTACACAGATT	600			
Qy	598	AATCCGGAAGGGCTCGTGACCCCTCTTGTTCGCGGTTTTTATCGCGAAGCGGTGGCGAATTC	657			
Db	601	AATCCGGAAGGGCTCGTGACCCCTCTTGTTCGCGGTTTTTATCGCGAAGCGGTGGCGAATTT	660			
Qy	658	GTATCTGCGCGTGTCAATCGGCTTTGAGACTCAAGGTAGGGCGCTTAAAGGCATTTACACCC	717			
Db	661	GTATCTGCGCGTGTCAATCGGCTTTTGAAGACTCAAGGTAGGGCTGTCTCTCAAGGCATTTACACCC	720			
Qy	718	ACGAAGCGGCTTCTGGCGTGTGATCGACGGCTTGTGCGAGCGCGGCGACACTCCAAATCA	777			
Db	721	ACTAAGCGGCTTCTGGCGTGTGATCGACGGCTTGTGCGAGCTGGTGCACACTCTAAATCA	780			
Qy	778	CTTGCATTAATCGCTAGGGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	837			
Db	781	CTTGCATTAATCGCTAGGGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	840			

Qy	838	ATCGGAATCCGGAACCCGCTCCACGCAATTCGACGACCGGATGCGTTCAGGAAATTCATC	897			
Db	841	ATCGGAATCCGGAACCCGCTCCACGCAATTCGACGACCGGATGCGTTCAGGAAATTCATC	900			
Qy	898	CGACACCTATGAAATGGGCTTCGCTGGCGGGTACGGTTGAGTTGCGTGGGCTCACA	957			
Db	901	CGACACCTATGAAATGGGCTTCGCTGGCGGGTACGGTTGAGTTGCGTGGGCTCACA	960			
Qy	958	GCGGCTCCTAACTGGAACGTCGGCATGTGCTCTATAGCACGCTCGGAAATCTCTTCCA	1017			
Db	961	GCTGCTCCTAACTGGAACGTCGGCATGTGCTCTATAGCACGCTCGGAAATCTCTTCCA	1020			
Qy	1018	GCCTCGCGCTTCGAGTTCTGAAGAACGATATTCCTCAATGGATGGGTTTCGCTCTAGC	1077			
Db	1021	GCCTCGCGCTTCGAGTTCTGAAGAACGATATTCCTCAATGGATGGGTTTCGCTCTAGC	1080			
Qy	1078	ATCCGGATTGCTCCCGGTGATGGCGGGCAACCCGACACCCGACGTAATCTATGCT	1137			
Db	1081	ATTCCTGATTTCTCTCCAGTGATTTGGTGTGCACTCGTACCCGAGGTAACTATGCT	1140			
Qy	1138	TTGGGCATGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG	1197			
Db	1141	TTTGGTCAGGTCATCTCGGTATGACAGGTGCTCAATGACTGCACACTCTGCTCAGAG	1200			
Qy	1198	CTCTCGCAGCGGAAAGACCTCAATTCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT	1257			
Db	1201	CTCTCGCAGCGGAAAGACCTCAATTCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT	1260			
Qy	1258	ATTGGCAATCCAAGCAACGGGTCGGCAAGTTAA	1293			
Db	1261	ATTGGCAATCCAAGCAACGGGTCGGCAAGTTAA	1296			
RESULT 8						
115327						
LOCUS	115327	1296 bp	DNA			
DEFINITION	Sequence 7 from patent US 5463175.					
ACCESSION	115327					
VERSION	115327.1	GI:1250235				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1296)					
AUTHORS	Barry,G.F. and Kishore,G.M.					
TITLE	Glyphosate tolerant plants					
JOURNAL	Patent: US 5463175-A 7 31-OCT-1995;					
FEATURES	Location/Qualifiers					
source	1..1296					
BASE COUNT	287 a	344 c	332 g			
ORIGIN	/organism="unknown"					
Query Match 89.8%; Score 1160.8; DB 5; Length 1296;						
Best Local Similarity 95.0%; Pred. No. 0;						
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps						
Qy	1	ATGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGCGGAGTCTGGCGGTATGCACG	60			
Db	1	ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAAATCGTTGGTATGCACT	60			
Qy	61	GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCGAACCCCTCTGGC	120			
Db	61	GCTTTGATGCTTCACGTCGTGGATTTCAANGTCACCTTGATTGACCGAACCCCTCTGGC	120			
Qy	121	GAAGTGCATCGTTTGGGAATCCGGGATGCTTTCAACGGCTCATCCGTCGTCCCTATGTC	180			
Db	121	GAAGTGCATCGTTTGGGAATCCGGGATGCTTTCAACGGCTCATCCGTCGTCCCTATGTC	180			
Qy	181	ATCGCGGAAACTTTCAGACGCTGCGGAAGTGGCTCTCTTGACCCGAT-TGGCGCTTGCA	239			
Db	181	ATCGCGGAAACTTTCAGACGCTGCGGAAGTGGCTCTCTTGACCGATGGGCGCTTGCA	240			

Qy 240 ATCCGGTTCAAGTAA-TTTTCCAAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCCGGA 297
Db 241 ATCCGGTTCAAGTAA-TTTTCCAAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCCGGA 300
Qy 298 AGACCAACAAGGTGAAGGACGCGGAAAGACATCTCCCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAACAAGGTGAAGGACGCGGAAAGACATCTCCCAATCTCATCAAGTCCACGGTG 360
Qy 358 CCTGTGATCAAGTCAATTTGGCGAGGAGCTGATGCGAGCCCATCTGATCCGCCATGAAGGT 417
Db 361 CCTGTGATCAAGTCAATTTGGCGAGGAGCTGATGCGAGCCCATCTGATCCGCCATGAAGGT 420
Qy 418 CATCTGACCGTATATCTGTGGAGAAAGACATCTCGCAAGACCGCGGAGGTGGGAAGT 477
Db 421 CATCTGACCGTATATCTGTGGAGAAAGACATCTCGCAAGACCGCGGAGGTGGGAAGT 480
Qy 478 CGGCTCTCAACGGTGTTCGCAACGACATCTCAGCCCGCATGCTGCGGGATTTCCAT 537
Db 481 CGGCTCTCAACGGTGTTCGCAACGACATCTCAGCCCGCATGCTGCGGGATTTCCAT 540
Qy 538 CCGAATTTGTGCGATGGGTTTACCAAGGGCATTTCTTATAGAAGAGACGGTTCACACGATT 597
Db 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTTATAGAAGAGACGGTTCACACGATT 600
Qy 598 AATCCGAAGGGTCTGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGCGGTGGGGAATTC 657
Db 601 AATCCGAAGGGTCTGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGCGGTGGGGAATTT 660
Qy 658 GTATCTCGCGCTGTTCATCGCGCTTTGAGACTCAAGTATAGGGCGCTTAAAGGATTTACAACC 717
Db 661 GTATCTCGCGCTGTTCATCGCGCTTTGAGACTCAAGTATAGGGCGCTTAAAGGATTTACAACC 720
Qy 718 ACGAAGCGGTTCTGGCGGTTGATGCGAGCGTTGTCGCGAGCGCGCACACTCGAAATCA 777
Db 721 ACTAACGGTGTCTGGCTGTGATGCGAGCTGTTCTGCGAGTGTGCGACACTCTAAATCA 780
Qy 778 CTTCGTAATTCGCTAGGGGATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTC 837
Db 781 CTTCGTAATTCGCTAGGGGATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Qy 838 ATCCGAATCCGAAGCGCTCCAGCATTCGAGACCGCATGCGTCAAGGAAATTCATC 897
Db 841 ATCCGAATCCGAAGCGCTCCAGCATTCGAGACCGCATGCGTCAAGGAAATTCATC 900
Qy 898 GCGACACTATGGAATGGGGCTTCGCGTGGCGGTGAGTTGAGTTGCTGCTGGGCTCACA 957
Db 901 GCGACACTATGGAATGGGGCTTCGCGTGGCGGTGAGTTGAGTTGCTGCTGGTCTCACA 960
Qy 958 GCGGCTCTACTGGAACGTTGGCGATGTGCTCTATACGACCGCTCGAANAATCTTTCCA 1017
Db 961 GCTGCTCTACTGGAACGTTGGCGATGTGCTCTATACGACCGCTCGAANAATCTTTCCA 1020
Qy 1018 GCGCTCGCGCTCGAGTCTGAGAACGATTTCCAAATGAGTGGGTTCCGCGCCGAGC 1077
Db 1021 GCGCTCGCGCTCGAGTCTGAGAACGATTTCCAAATGAGTGGGTTTCGTCCTAGC 1080
Qy 1078 ATCCCGGATTCGCTCCCGCTGATTGGCGGGCAACCCGACACCCGAGTAACTATGCT 1137
Db 1081 ATTCCTGATCTCTTCAGTGATTGGTGTGCAACTGCTACACCCGAGTAACTATGCT 1140
Qy 1138 TTTCGGCATGTCTATCTCGGATGACAGGGGCGCGATGAGCGCAACCGCTCGTCTCAGAG 1197
Db 1141 TTTGGTCACGGTCTATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG 1200
Qy 1198 CTCTCCGAGCGGAAAGACCTCAATGCACATTTTCGGCTTCGCAACCAACCGCTTTGGT 1257
Db 1201 CTCTCCGAGCGGAAAGACCTCAATGCACATTTTCGGCTTCGCAACCAACCGCTTTGGT 1260
Qy 1258 ATTCGCAAAATCCAAAGCAACCGGTCGCGCAAGTTAA 1293
Db 1261 ATTCGCAAAATCCAAAGCAACCGGTCGCGCAAGTTAA 1296

RESULT 9
AR016595
LOCUS AR016595 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5776760.
ACCESSION AR016595
VERSION AR016595.1 GI:3972872
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1296)
AUTHORS Barry.G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 8 07-JUL-1998;
FEATURES Location/Qualifiers
1..1296
source /organism="unknown"
BASE COUNT 271 a 359 c 305 g 361 t
ORIGIN
Query Match 71.8%; Score 928.8; DB 5; Length 1296;
Best Local Similarity 83.8%; Pred. No. 3e-244;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;
Qy 1 ATGCTGTGAGAACCAACAAAAGTAGGCATCGCTGGAGCCGAATCGTCGGCGGTATGCACG 60
Db 1 ATGCTGTGAGAACCAACAAAAGTTGGTATCGCTGGAGCTGGANTCGTTGGTGTTCGACT 60
Qy 61 CGCTGTGATGCTTTCAGCGCCGCGGATTTCAAAGTTCACCTTTGATTTGACCCCAACCCCTCTGGC 120
Db 61 GCTTTGATGCTTTCACACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACAGGT 120
Qy 121 GAAGGTGCATCGTTTGGGAATCCCGGATGCTTCAACGCTCATCGTCGTCCTCCATGTCC 180
Db 121 GAAGGTGCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCTCCGTTGTTTCCAAATGTCC 180
Qy 181 ATGCGGGAACCTTGACGAGCGTCCGGAAGTGGCTCTTGGACCCGATGGG-CCGTTGTCA 239
Db 181 ATGCGGGAACCTTGACTAGCTTCCAAAGTGGCTTCTTGGACCAATGGTCCATTTGTC 240
Qy 240 ATCCGTTTCACTTA-TTTTCCAAACCATCATGCGC-TGGTTGATTTCCGTTTCTGTTAGCCGGA 297
Db 241 ATCCGTTTCACTTA-TTTTCCAAACCATCATGCGCTTGGTTGATTTGCTTTCTGCTGGA 300
Qy 298 AGACCAACAAGGTGAAGGACGCGGAAAGACATCTCCCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAACAAGGTGAAGGACGCGGAAAGACATCTCCCAATCTCATCAAGTCCACGTGTG 360
Qy 358 CCTGTGATCAAGTCAATTTGGCGAGGAGCTGATGCGAGCCCATCTGATCCGCCATGAAGGT 417
Db 361 CCTGTGATCAAGTCAATTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAGGT 420
Qy 418 CATCTGACCGTATATCTGTGGAGAAAGACATCTCGCAAGACCGCGGAGGTGGGAAGT 477
Db 421 CACCTTACCGTGTACCGTGGAGAAAGACAGACTTCGCAAGGACCGCTGGAGGTGGGAAGT 480
Qy 478 CGGCTCTCAACGGTGTTCGCAACGACATCTCAGCCCGCATGCTGCGGGATTTCCAT 537
Db 481 CGTGTCTCAACGGTGTTCGTAACCTCTCAGCCGCTGATGCAATGCGGTGATTTCCAT 540
Qy 538 CCGAATTTGTGCGATGGGTTTACCAAGGGCATTTCTTATAGAAGAGACGGTTCACACGATT 597
Db 541 CCTAACTTGTCTACGCTTTTACCAAGGGATCTTATCAGAGAGAGAGGTTCACACCATC 600
Qy 598 AATCCGAAGGGTCTGTGACCCCTCTTGTTCGGCGTTTATTCGCGAAGCGGTGGGGAATTC 657
Db 601 AACCCACAAGGTCGCTGACTCTCTTGTTCGTCGTTTTCATCGCTTAACGCTGGAGAGTTC 660
Qy 658 GTATCTCGCGCTGTTCATCGCGCTTTGAGACTCAAGTATAGGGCGCTTAAAGGATTTACAACC 717
Db 661 GTGCTGCTGCTGTATTCGGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCACC 720

Qy	718	ACGAACGGCGTTCTTGGCCGTTGATGACAGGGGTTGTCCGAGCGCGGCACACTCGAAATCA	777
Db	721	ACCAACGGGTGTTCTTCTTGTATGACAGCTGTTGTTGCAGCTGGTGACACTCCAAGTCT	780
Qy	778	CTTGCTTAATTTCGCTAGCGCATCACATCCCGTTCGATACCGAACCTGGATATCATATCGTC	837
Db	781	CTTGCTTAATCCCTTGGTGATGACATCCATGGATACCGAACCTGGATACCACTACGTC	840
Qy	838	ATCCGGAATCCGGAACCGCTCCAGCGAATTCGAGCAGCCGATGGCTCAGGAAATTCATC	897
Db	841	ATCGCAACCCAGAAGCTGCTCCAGTATTCCAACTACCGATGCTTCGGAAGTTTCATC	900
Qy	898	GCAGACCTATGGAATGGGGCTTCGCTGGGGGTACGGTTGAGTTGCTTGGGCTCACCA	957
Db	901	GCTACTCTATGGAGATGGGCTTCGCTGTTGCTGGAACCGTTGAGTTGCGTGGTTCACCT	960
Qy	958	GCGCTCCTAACTGGAACCTGGCATGTCGCTATATCGCACGCTCGAAGAACCTCTCTTCCA	1017
Db	961	GCTGCTCTAACTGGGAAGCGTCTCAGCTTCTCTACACTCAGCTCGTAAGTTGCTTCCA	1020
Qy	1018	GCCTCCCGCTCGAGTTCCTGAAGAAGCATATTCCTCAATGGATGGGTTCCGGCCGAGC	1077
Db	1021	GCTCTCGCTCTGCCAGTTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCCGTCCAAGC	1080
Qy	1078	ATCCGGATTTCGCTCCCGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1137
Db	1081	ATCCACGATTTCCCTTCAGTGATGGTCTGCTGCTACCCGTACTCCGACAGCTTATCTAGCT	1140
Qy	1138	TTCCGGCATGGTCATCTCGGCATGACAGGGCGCCGATGACCGCAACGCTGCTCTCAGAG	1197
Db	1141	TTCCGGTCACGGTCACCTCCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTCTGAG	1200
Qy	1198	CTCCTCCGAGCGCAAAAGACCTCAATTCGACATTTTCGCCCTTCGCACCAACCGCTTTGGT	1257
Db	1201	CTCCTCCGAGGTGAGAAGACCTCTATGCACATCTCTCCTATTCGCACCAACCGTTCCGGT	1260
Qy	1258	ATTGGCAATTCGAAGCAACGGGTCCGGCAAGTTAA	1293
Db	1261	ATTGGTAAGTCCAAGCAAACTGGTCTCGATCTTAA	1296
RESULT 10			
115328			
LOCUS	115328	1296 bp	DNA
DEFINITION	Sequence 8 from patent US 5463175.		
ACCESSION	115328		
VERSION	115328.1	GI:1250236	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	271 a	359 c	305 g
ORIGIN	/organism="unknown"		
Query Match			
Best Local Similarity	71.8%;	Score 928.8;	DB 5; Length 1296;
Matches 1086;	Conservative	0; Mismatches 207;	Indels 3; Gaps
Qy	1	ATGCTCTGAGAACCACAAAAGTAGGCATCGCTGGAGCGCGGAATCGTCGGCGTATGCACG	60
Db	1	ATGCTCTGAGAACCACAAAAGTGGTATCGCTGGAGCTGGCAATCGTTGGTGTTCGACT	60
Qy	61	GCCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCGCAACCCCTCTGCGC	120

Db	61	CTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACACAGGT	120
Qy	121	GAAGGTGCATCGTTTGGGAAATCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC	180
Db	121	GAAGTGCCTTCTTTCGGTAACGCTGGTTGCTTTCACGGTTCCTCCGTGTGTTCCAATGTCC	180
Qy	181	ATGCCGGGAAACTTTCACGAGCGTGCAGAGTGGCTTCTTTGACCCGATGGG-CGGTGTCTCA	239
Db	181	ATGCCAGGAACTTGCATAGCGTTCCTCAAAAGTGGCTTCCTTGACCCAAATGGGTTCCTATG	240
Qy	240	ATCCGGTTCAGCTA-TTTTCCAACTCATATGCC-TGGTTGATTTCGGTTTCTGTATAGCCGGA	297
Db	241	ATCCGTTTCAAGCTATCTTCCAACTCATATGCCCTTGGTTGATTTCGGTTTCTGTCTTGGGGA	300
Qy	298	AGACCAACAAAGTGAAGGAGCAGGCGAAAGACATCCGCAATCTCATCAAGTCCACGGTG	357
Db	301	AGACCAACAAAGTGAAGGAGCAAGCTAAGGCACATCCGTAACCTCATCAAGTCCACATGTG	360
Qy	358	CCTCTGATCAAGTCATTTGGGGGAGGAGGCTGATGGAGGCGCATCTGATCCCGCATGAAGGT	417
Db	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTATGCCACCTTATATCCGTCAGCAAGT	420
Qy	418	CATCTGACCGTATATCGTTGAGAGGACAGACTTTCCGCAAGGACCCGCGAGGTTGGGAACTG	477
Db	421	CACCTTACCCTGTACCGTGGAGAGCGACTTCGCGCAAGGACCGTGGAGGTTGGGAACTT	480
Qy	478	CGGCGTCTCAACGGTCTTCGACGACAGATCCCTCAGCGCGGATGGCTTCGCGGATTTCCGAT	537
Db	481	CGTCGTCCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTTCCGTTGATTTCCGAT	540
Qy	538	CCGAACCTTGTTCGATGCGGTTTACCAAGGCGATTCCTATAGAGAGAGACGGTTCACACGATT	597
Db	541	CCTTAACCTTGTCTCACGCCCTTTACCAAGGCGAATCCCTTATCGAAGGAGAACGGTTCACACCATC	600
Qy	598	AATCCGCAAGGGCTCGTAGCCCTCTTGTTTTCGGCGTTTTATCGCGAACGGTGGCGAATTC	657
Db	601	AACCCACAAGGTCGTGTGACTCTCTTGTTCGTCTGTCTCATCGCTAACGGTGGAGAGTTC	660
Qy	658	GTATCTCGCGCTGTCATTCGGCTTTGAGACTGAAGCTTAGGGCGCTTTAAAGGCAATTAACAACC	717
Db	661	GTGTCCTGCTGCTTATCCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACACCACC	720
Qy	718	ACGAACGGGCTTCTGGCGGCTTGATGACGCGGTTGTGCGACCGGGCGCACACTCGAATCA	777
Db	721	ACCAACCGGCTTCTGCTGTGTGATGACGCTGTGTGTTCGAGCTGGTGTGACACTCCCAAGTCT	780
Qy	778	CTTGCTAAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTTGGATATCATATCGTC	837
Db	781	CTTGCTTAACCTCCCTTGGTATGACATCCCATTCGGAATCCGAAACGTTGATACCCATCGTG	840
Qy	838	ATCCGGAATCCGGAAGCGCTCCACGCAATCCGACGACCGGATGGCTCAGGAAATTCATC	897
Db	841	ATCCGCAACCCAGAGCTGCTCCACGTATTCACACTACCGATGCTTCTGGGAAAGTTTCATC	900
Qy	898	CGGACACCTATGGAATAGGGGCTTCGCTGGGGGTGACGGTTGAGTTGCTGTGGGCTCACCA	957
Db	901	GCTACTCCTATGGAGATGGGCTCTTCGCTGTTCGTGGAACCGCTTGAGTTCCGCTCTCACT	960
Qy	958	GCCGCTCCTTAACCTGGAACGTCGCGATGTGCTCTATACCGACGCTCGAAACACTTCTTCCCA	1017
Db	961	GCTGCTCCTTAACCTGGAAGCGTGCTACGTTCTCTACATCTACGCTCGTGAAGTTCGTTCCCA	1020
Qy	1018	CCCTTCGCGCTCGGATGTTCTGAAGAACGATATTCCAAATGGATGGGGTTCGCGCCGACG	1077
Db	1021	GCTCTCGCTCCTTCCAGTTCCTGAAGAACGTTACTTCAAAGTGGATGGGTTTCCGTCCAAGC	1080
Qy	1078	ATCCCGGATTCGCTCCCGTGATTGGCCGGGCGMACCCGAGCACCCGACGTTAATCTATGCT	1137
Db	1081	ATCCACGATTCCTTCCAGTGATTGGTTCGTGCTACCCGCTACTCCACGAGTTTATCTACGCT	1140
Qy	1138	TTCCGCCATGGTCATCTCGGATGACAGGGGGCGCGATGACCGCAACGCTCGTCTCAGAG	1197
Db	1141	TTCCGTCACGGTCACCTCGGTATGACTGGTGTCTCAATGACGCAACCCCTCGTTTCTTGAG	1200

Qy	1198	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTCCGCCCTTTCGCAACCAACCGGTTTGGT	1257
Db	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTCGCAACCAACCGGTTTCGGT	1260
Qy	1258	ATTGGCAATCCAAAGCAACCGGTCGGCAAGTTAA	1293
Db	1261	ATTGGTAAGTCCAAAGCAAACTGGTCTGCATCCCTAA	1296
RESULT 11			
LOCUS	AR016604	1296 bp	DNA
DEFINITION	Sequence 17 from patent US 5776760.		PAT
ACCESSION	AR016604		
VERSION	AR016604.1		GI:3972881
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry, G. Francis and Kishore, G. Murthy.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5776760-A 17 JUL-1998;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	360 t
ORIGIN	/organism="unknown"		
Query Match 71.6%; Score 925.6; DB 5; Length 1296;			
Best Local Similarity 83.6%; Pred. No. 2.3e-243;			
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps			
Qy	1	ATGCTGAGAACCAACAAAGTAGGACATCGTGGAGCCGGAATCGTCGGGGTATGACG	60
Db	1	ATGCTGAGAACCAACAAAGTAGGATATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT	60
Qy	61	CGCGTGATGCTTACGCGCGCGGGATTCAAAGTCACCTTGATTGACCCGCAACCCCTCTCGGC	120
Db	61	CGTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGGT	120
Qy	121	GAAGGTGATCGTTTGGGAATCCGGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC	180
Db	121	GAAGGTGCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCCTCCGTTGTTCCAAATGTC	180
Qy	181	ATCGCGGAAACTTCACGAGCGTCCCGAAGTGGCTCTTGACCCGATGGG-CCGTTGTCA	239
Db	181	ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTTCATGTC	240
Qy	240	ATCCGGTTTCAGCTA-TTTCCAAACCATCATGCC-TGGTTGATTGCTTCTCTTAGCCGGA	297
Db	241	ATCCGTTTCGGCTACTTTCCAACCATCATGCGTTGGTTGATTGCTTCTTTCGTTGCTGGA	300
Qy	298	AGACCAACAAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357
Db	301	AGACCAACAAAGGTGAAGGAGCAAGCTTAAGCACTCCGTTAACCTCATCAAGTCCACCTGTG	360
Qy	358	CCCTGATCAAGTCAITTCGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT	417
Db	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTCATGCTAGCCACCTTATCCGTCACGAAGGT	420
Qy	418	CATCTGACCGTATATCTGGGAGAGCAGACTTCGCCAAGGACCGGAGGTTGGGAACCTG	477
Db	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAGGAGCCGTTGGAGTTTCGGAACTT	480
Qy	478	CGGCGCTCTCAACCGGTGTTTCGCACGACAGATCCTCAGCGCCGATGCGTTGCGGGATTTTCGAT	537
Db	481	CGTCTCTCAACGGGTGTTCTACTCAATCCTCAGCGCTGATGATTCGCTGATTTTCGAT	540
Qy	538	CCGAACCTTGTCCGATGCGTTTACCAAGGCAATCTTATAGAAGAGAACGGTTCACACGATT	597

Db	541	CCTAACTTGTCTCAGCCCTTTACCAAGGAATCTCTTTATTCGAAGAGAACGGTTCACACCATC	600
Qy	598	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTCATTCGCAACCGGTGGCGAATTC	657
Db	601	AACCCACAAGGCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC	660
Qy	658	GTATCTGCGCGTGTCAATCGGCTTTTGAGACTGAAGGTAGGCGCTTTAAAGGCATTTACAACC	717
Db	661	GTGTCTGCTCGTGTATCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACCAACC	720
Qy	718	ACGAACGGCGTTCCTGCCGCTTGATGACGCGGTTGTGCGACGCGCGGCACACTCGAATCA	777
Db	721	ACCAACGGGTGTTTGTCTGTGTGATGACGCTGTGTTGCGAGCTGGTGACACTCCAAGTCT	780
Qy	778	CTTGCTAATTCGCTAGCGGATGACATCCCGTTCGATACCGAAGCTGGATATCATATCGTC	837
Db	781	CTTGCTAATTCGCTAGCGGATGACATCCATTCGATACCGAAGCTGGATACCATCTCGTG	840
Qy	838	ATCGGAATCCGAAGCGCTCTCCAGCATTCGACGACCGCATGCGTCAGGAAATTCATC	897
Db	841	ATCGCAACCCAGAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC	900
Qy	898	CGACACCTATGGAATGGGGCTTCGCGTGGGGGTAGGTTGAGTTCGCTGGGCTCACA	957
Db	901	GCTACTCCTATGGAGATGGGCTTTCCTGCTTGTGCGAACCCTTGAGTTCGCTGGTCTCACT	960
Qy	958	GCGGCTCCTAACTGGAACGTCGCGCATGCTCTATAGCACGCTCGAATACTTCTTCCA	1017
Db	961	GCTGCTCCTAACTGGAAGGTGCTCAGCTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA	1020
Qy	1018	GCCTCGCGCTCGGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCCGGCCGAGC	1077
Db	1021	GCTCTCGCTCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCGCTCCAAGC	1080
Qy	1078	ATCCGGATTCGCTCCCGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT	1137
Db	1081	ATCCCGGATTCGCTTCCAGTGATTGGTCTGTGCTACCCGCTACTCCAGACGTTATCTAGCT	1140
Qy	1138	TTCCGCCATGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG	1197
Db	1141	TTCCGTCACGCTACCTCGGTATGACTGGTCTCCATGACCGCAACCGCTGTTCTTGAG	1200
Qy	1198	CTCTCGCAGCGGAAAGACCTCAATCGACATTTTCGCGCTTCGCACCAACCCGCTTTGGT	1257
Db	1201	CTCCTCGCAGGTGAAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGCTTCGGT	1260
Qy	1258	ATTGCGAATCCAAAGCAACGGGTCGCGCAAGTTAA	1293
Db	1261	ATTGGTAAGTCCAAAGCAAACTGGTCTGCATCCCTAA	1296
RESULT 12			
LOCUS	115337	1296 bp	DNA
DEFINITION	Sequence 17 from patent US 5463175.		
ACCESSION	115337		
VERSION	115337.1	GI:1250245	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 17 OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	360 t
ORIGIN	/organism="unknown"		
Query Match 71.6%; Score 925.6; DB 5; Length 1296;			

Best Local Similarity 83.68; Pred. No. 2.3e-243;			
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;			
Qy	1	ATGCTGAGAACCAACAAAAATAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGACAG	60
Db	1	ATGCTGAGAACCAACAAAGTTGGTATCGCTGGAGCTGGAAATCGTTGGTGTTCGACT	60
Qy	61	CGCTGATGCTTTCAGCGCCCGGGATTCAAAGTTCACCTTTGATTTGACCCGAACCCCTCTGGC	120
Db	61	GCTTTGATGCTTTCACGCTGCTGGATTCAAAGTTACCTTTGATTTGATTCCAAACACCAAGT	120
Qy	121	GAAGTGATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC	180
Db	121	GAAGTGCTCTTTTCGGTAAACCGTGTTCCTTCAACGGTTCCTCGTTGTTCCAAATGTC	180
Qy	181	ATCGCGGAAACTTTCAGCAGGGCTGCGGAAGTGGCTCTTGACCCGATGGG-CCGTTGTCA	239
Db	181	ATCGCAGAACTTCAGCTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTTGTC	240
Qy	240	ATCGGGTTCAGCTA-TTTTCCAAACCATCATGGC-TGGTTGATTCGGTTCCTTTAGCCGGA	297
Db	241	ATCGGTTTCGGCTACTTTTCCAAACCATCATGGCTGGTTGATTCGTTCTTCTGCTCTGGA	300
Qy	298	AGACCAACAGGTTCAGGAGCAGCGGAAACGACTCCGCAATCTCATCAAGTCCACGGTG	357
Db	301	AGACCAACAGGTTCAGGAGCAAGCTTAAGGCATTCGCTAACCTCATCAAGTCCACGCTG	360
Qy	358	CCTGTGATCAAGTCATTCGGCGGAGGAGCTGATGGAGGCCATCTGATCCGCCATCAAGGT	417
Db	361	CCTTTGATCAAGTCCTTTGGCTGAGGAGCTCATGCTACCCACTTATCCGTCACGAAGT	420
Qy	418	CATCTGACCGTATATCTGTTGAGAACAGCAGACTTCGCCAAGAGCCGCGAGTTGGGAATG	477
Db	421	CACCTTACCCTGTACCGTGGAGAGCAGACTTCGCCAGGACCGGTGGAGTTGGGAAT	480
Qy	478	CGGCTCTCAACGGTTTCGACAGCAGATCCTCAGCGCGGATGCGTTCCGGGATTTCCAT	537
Db	481	CGTCTCTCAACGGTTTCGTAACAATCTCAGCGCTGATGCAATCCGTCGATTTCCAT	540
Qy	538	CCGAACCTTTCGCGATCGCTTTACCAAGGCCATCTTATAGAGAGAACCGGTACACAGAT	597
Db	541	CCTAACTGTCTACGCCCTTTACCAAGGAATCCTTATCGAAGAGACGGTACACCATC	600
Qy	598	AAATCCGAAGGGCTGCTGACCCCTCTTGTTCGGGCTTTTATCGGGAACGGTGGGAAATC	657
Db	601	AACCCACAAGGCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTTAACGGTGGAGATTC	660
Qy	658	GTATCTCGCGGTGTCATCGGCTTTGAGACTTCAGAGTACGGGCGCTTAAAGGCATTCACAC	717
Db	661	GTGTCTGCTCTGTATCCGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC	720
Qy	718	ACGAAGCGGTTCTGGCCGTTGATCGACGGTTGTGCGACGCGGCGGCACACTCGAANATCA	777
Db	721	ACCAAGCGTGTCTTGCTGTTGATGCCAGCTGTGTTGACGCTGGTGCACACTTCCAAGTCT	780
Qy	778	CTTGCTAATTCGCTAGCGCATACATCCCGTTCGATACCGAACCGTATCATATCTGTC	837
Db	781	CTTGCTAATCCCTTGGTGATGACATCCATTGGATACCGAAGCTGGATACCATCTGTCG	840
Qy	838	ATCGGAATCCGGAAGCCGCTCCACCGATTCGAGCAGCCGATGCGTCAGGAAATTCATC	897
Db	841	ATCGCCACCAAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTCATC	900
Qy	898	CGCACACCTATGGAATGGGCTTTCGCGTGGCGGTACGGTTGAGTTCGCTGGGCTCAC	957
Db	901	CCTACTCTATGGAGATGGGCTTCGCTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT	960
Qy	958	CGCGCTCTAATCGGAACGCTCGGCATGTGCTCTATAGCGACGCTCGGAAACCTTCTTCCA	1017
Db	961	GCTGCTCTAATCGGAAGCGTCTCACGTTCTCTACACTCGCGCTCGTTAAGTGTGCTTCCA	1020
Qy	1018	GCCCTCGCGCTTCGAGTTCCTGGAAGACGATATTTCCAAATGGATGGGTTCCGCGCCGAG	1077

Db	1021	GCCTCTCGGCTTCCTGCCAGTTCCTTCCAGGACGCTTACCTCCAGTGGGATGGGCTTTCCTGCCGCTCAAGC	1080
QY	1078	ATCCCGGATTCGCTCCCGCTGATTGGCCGGGCAACCGGACACCGGACGTAATCTATGCT	1137
Db	1081	ATCCCGGATTCCTTCCAGTGATGGTCTGTGCTACCGCTACTCCAGACGTTATCTACGCT	1140
QY	1138	TTTCGGCATTGGTCATCTCGGCATGACAGGGGCGCCGATGACCCGACACGCTGCTGTCAGAG	1197
Db	1141	TTTCGGTTCAGGTCACCTCGGTATGACTGGTGTCTCCAAATGACCGCAACCCCTCGTTTCTGAG	1200
QY	1198	CTCCTCGCAGGCGAAGACCTCAANTCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT	1257
Db	1201	CTCCTCGCAGGTCGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAACCGCTTTCCGT	1260
QY	1258	ATTGGCAATCCAAAGCAACGGTCCGGCAAGTTAA	1293
Db	1261	ATTGTAAGTCCAAAGCAAACTGGTCTGCATCCTAA	1296
RESULT	13		
LOCUS	A59869	1631 bp	DNA
DEFINITION	Sequence 1 from Patent WO9706269.		PAT 06-MAR-1998
ACCESSION	A59869		
VERSION	A59869.1	GI:3715060	
KEYWORDS			
SOURCE	Arabidopsis sp.		
ORGANISM	Arabidopsis sp.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Kossidae; Capparales; Brassicaceae; Arabidopsis.		
AUTHORS	Jepson, J.		
TITLE	INDUCIBLE HERBICIDE RESISTANCE		
JOURNAL	Patent: WO 9706269-A 1 20-FEB-1997;		
FEATURES	ZENEGA LTD (GB)		
source	Location/Qualifiers		
	1..1631		
	/organism="Arabidopsis sp."/		
	/db_xref="taxon:29726"		
BASE COUNT	342 a 454 c 381 g 454 t		
ORIGIN			
	Query Match 66.3%; Score 857.6; DB 5; Length 1631;		
	Best Local Similarity 80.2%; Pred. No. 1 1e-224;		
	Matches 1079; Conservative 0; Mismatches 214; Indels 53; Gaps		
QY	1	ATGCTGTGAGAACACAAAAAGTTCAGCATCGCTGGAGCCGGAATCGTCGGCGATGACG	60
Db	274	ATGGCTGAGAACACAAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACT	333
QY	61	CGCGTGATGCTTCAGCGCCGCGGATTCAAAGTTCACCTTGATTGACCCGGAACCTCCTGGC	120
Db	334	GCTTTGATGCTTCAGCGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT	393
QY	121	GAAGTGTGATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTC	180
Db	394	GAAGTGTGCTTCTTCGGTAAACGCTGGTGGCTTCAACGGTTCCTCCGTTGTTCCANTGCC	453
QY	181	ATCCCGGGAACCTTCACGAGCGGTCCGGAAGTGGCTCCT	218
Db	454	ATGCCAGGAACCTTACTAGCGTTCCAAAGTGCCTCTGGATCCTGTGTGAATCAAGC	513
QY	219	----TGACCCGATGGCGGTTGTCAATCCGGTTACGTA--TTTCCAAACCATGATGCC--TG	272
Db	514	TTACCGATCCAATGGGTCCATGTGTCATCCCTTTCAGTACTTTTCCAAACCATCATGCGCTG	573
QY	273	GTTGATTCGCTTCTGTTAGCCGAAGACCAACAGGTGAAGGACGACGCGGAAGACCT	332
Db	574	GTTGATTCGCTTCTGCTTGGTGAAGACCAACAGGTGAAGGACGACGCTAAGGACCT	633
QY	333	CGCAATCTCATCAAGTCCACGGTGCCTCTTGATCAAGTCAATGGCGGAGGAGGCTGATGC	392

Db	634	CCGTAACCTCATCAAGTCCACCTGTGSCCTTTTGATCAAGTCCCTGGCTGAGGAGCTGATGCG	693
Qy	393	CAGCCATCTGATCCGCCATGAAGGTCACTCGACCTATATCGTGGAGAGAGACTTCCGC	452
Db	694	TAGCCACCTTATCCGTACAGAGGTCACTTACCGTGTACCGTGGAGAGAGACTTCCGC	753
Qy	453	CAAGGACCGGAGGTTGGGAACCTCGCGCTCTCAACGGTGTTCGACGCGAGATCCTCAG	512
Db	754	CAAGACCGTGGAGTTGGGAACCTCGCTGCTCAACGGTGTTCGACTCAATCCTCAG	813
Qy	513	CGCGATCGGTTGGGGATTTTCGATCCGAACCTTTCGCGATCGGTTTACCAAGGCAATCT	572
Db	814	CGCTGATGCATTTGGTGATTTTCGATCCCTAACTTGTCTCACGCCCTTACCAAGGAACTCT	873
Qy	573	TATGAACAGAACGGTTCACAGATTAATCCGCAAGGGTCTGTGACCCCTCTGTTGGCG	632
Db	874	TATCGAAGAACGGTTCACACCATCAACCCACAGGTCGTGACTCTCTTGTTCGTCG	933
Qy	633	TTTTATCGGAACGGTGGCGAATTTCGTATCTCGCGTGTCTATCGGCTTTGAGACTGAAGG	692
Db	934	TTTCATCGCTAACGGTGCAGAGTTCGTCTCTGCTCGTGTATTCGGATTCGAGACTGAAGG	993
Qy	693	TAGGCGCTTAAAGCATTTACACCAAGAACGGGTTCTGCGCGTTGATG-----	742
Db	994	TCGTGCTCTCAAGGGTATCACACACCAACCGGTTCTTCTGCTGTGATGCTGCAGTGT	1053
Qy	743	-----CAGCGTGTTCGCGAGCGCGGCACACTCGAAATCACTTGTCTAATT	787
Db	1054	GTGAATTCAGCTTACTGCACTTGTTCGAGCTGTGTCACACTCCNAGTCTCTTGTCTACT	1113
Qy	788	CGCTAGGCGATGACATCCCGTCGATACCGAACGTGGATATCATATCGTCATCGGAAATC	847
Db	1114	CCCTTGGTGATGACATCCCATTTGGATACCGAACGTGGATACCACTGTCGCAACACC	1173
Qy	848	CGGAAGCGCTCCACGCATTCGAGGACCGGATCGTTCAGGAATATTCATCGGACACCTA	907
Db	1174	CAGAAGTGCCTCCACGATATCCAACTACCGGATGCTTCTGGAAGTTTCATCGTACTCCTA	1233
Qy	908	TGGAATGGCGTTCGCGTGGCGGTACGGTTGAGTTGCTGGCTGACGCTCACAGCGCTCCTA	967
Db	1234	TGGAGATGGGTCTTCGTGCTGTAACCGTGTGAGTTGCTGGTCTACTGCTGCTCCTA	1293
Qy	968	ACTGGAACGTGGCGATGCTCTATAGCAGCGTTCGAAACCTCTTCCAGCCCTCGCGC	1027
Db	1294	ACTGGAACGTGCTCAGCTTCTCTACACTCGTCTGCTGCTGAAGTTGCTTCCAGCTCTCGCTC	1353
Qy	1028	CTGCGAGTTCTGAGAACGATATTCCTCAATGGATGGGGTTCCGGCGGAGCATCCCGGAT	1087
Db	1354	CTGCCAGTTCTGAGAACGTTTACTCCAAAGTGGATGGGTTTCGGTCCCAAGCATCCAGAT	1413
Qy	1088	CGCTCCCGCTGATTTGGCGGGCAACCGCGACACCGACGTAATCTATGCTTTTCGGCCATG	1147
Db	1414	CCCTTCCAGTATTTGGTGTCTACCGGTACTCCAGAGTTATCTACGCTTTCGCTCAG	1473
Qy	1148	GTATCTCGGCGATGACAGGGCGCGATGACCGCAACGCTCGTCTCAGAGCTCTCGCAG	1207
Db	1474	GTACCTCGGTATGACTGGTGTCTCCAAATGACCGCAACCCCTGTTCTGAGCTCTCGCAG	1533
Qy	1208	GCGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAACCCGCTTTGGTATTGGCAAT	1267
Db	1534	GTGAGAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGTATTGGTAAGT	1593
Qy	1268	CCAAGCAACCGGTCCGGCAAGTTAA	1293
Db	1594	CCAGCAACCTGCTCCTGCATCCTAA	1619

RESULT 14
PSEAKSD
LOCUS
DEFINITION Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.

ACCESSION	M69158
VERSION	M69158.1
KEYWORDS	GI:150981
SOURCE	ketoglutarate semialdehyde dehydrogenase.
ORGANISM	Pseudomonas putida
REFERENCE	1 (bases 1 to 3430)
AUTHORS	Burlingame, R.P., Maruya, A., Allyn, A.H., Allyn, D. and Backman, K.C.
TITLE	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of Pseudomonas putida
JOURNAL	Unpublished (1991)
FEATURES	Location/Qualifiers
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BASE COUNT	562 a 1140 c 1157 g 571 t
ORIGIN	

Query Match	6.5%	Score	84.2;	DB	2;	Length	3430;		
Best Local Similarity	46.2%	Pred.	No. 2.7e-12;						
Matches	537;	Conservative	0;	Mismatches	608;	Indels	18;	Gaps	7;
QY	23	TAGGCATCGCTGGAGCGGGAATCGTCGGCTGATGCACGCGCTGATGTCAGCGCGCGCG	82						
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QY	83	GATTCAAAGTCACCTTGATTGACCCGAACCTCTCTGGCGAAGGTGCATCGCTTTGGGAATG	142						
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QY	143	CCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCATCCATCCCGGGAACCTTGACGAGCG	202						
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RESULT 15

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PSEKSDA
LOCUS PSEKSDA 2289 bp DNA BCT 26-APR-1993
DEFINITION Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.
ACCESSION M69159
VERSION M69159.1 GI:151317
KEYWORDS ketoglutarate semialdehyde dehydrogenase.
SOURCE Pseudomonas putida (strain ATCC 12633) DNA.
ORGANISM Pseudomonas putida
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.
REFERENCE 1 (bases 1 to 2289)
AUTHORS Burlingame,R.P., Maruya,A., Ally,A.H., Ally,D. and Backman,K.C.
TITLE Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
putida
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..2289
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gene

CDS

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BASE COUNT 378 a 766 c 734 g 411 t
ORIGIN
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Query Match 4.8%; Score 61.8; DB 2; Length 2289;
Best Local Similarity 54.7%; Pred. No. 3.9e-06;
Matches 123; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 8 AGAACCAACAAAAAGTAGGCATCGCTGGAGCGCGGAATCGTGGCGGTATGCACGCGCGCTGA 67
Db 1732 ACAATCGCCACGACATAACCCGTCATCGCGCGCGGAATCATCGCGCTCGCCCTGC 1791
Qy 68 TGCTTCAGCGCGCGGATTCAAAAGTCACCTTGATTGACCCGAACCTCTCTGGCGAAGGTG 127
Db 1792 AACTGGCGCGCTGGCGGTGACGGTCTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1851
Qy 128 CATCTTTTGGGAATCCGGATGCTTCAACGGCTCATCGCTCGTCCCTATGTCCTCATGCCG 187
Db 1852 CTCCTTGGCAATCCGGGATCTGGCGACGAGCAGGTGTTCCCATCGCGGATTTGT 1911
Qy 188 GAAACTTCACGAGCGTCCCGAAGTGGCTCCTTGACCCCATGGCC 232
Db 1912 CGATCTGAAAGCGTTGCCCTGCCATGCTCATGACCCCATGGGGC 1956
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Search completed: January 1, 2001, 03:14:54
Job time: 29178 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 22:06:32 ; Search time 263.11 Seconds
(without alignments)
1846.117 Million cell updates/sec

Title: US-08-484-274-4
Perfect score: 1293
Sequence: 1 ATGCTGAGNACCACAAANA.....AAACGGGTCCGGCAAGTTAA 1293

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289.8	99.8	1689	13 Q20832	Glyphosate oxidoreductase
2	1256.8	97.2	1692	13 Q22705	Glyphosate oxidoreductase
3	1253.6	97.0	1321	13 Q20833	Manipulated glyphosate
4	1159.2	89.7	1321	13 Q20834	Modified glyphosate
5	928.8	71.8	1296	13 Q20835	Synthetic glyphosate
6	928.8	71.8	8418	20 X57309	Sugar beet T-DNA c
7	857.6	66.3	1631	18 T85664	CPT1-GOX gene fusi
8	641.8	49.6	8798	20 X57308	Sugar beet T-DNA c
9	640.2	49.5	8012	20 X57305	Sugar beet T-DNA c
c 10	35.4	2.7	534720	19 V30458	Rhizobium species
c 11	35.4	2.7	536165	19 V30459	Rhizobium species
c 12	34	2.6	405	20 X98168	Nucleotide sequenc

c 13	34	2.6	603	20 X98167	Nucleotide sequenc
c 14	34	2.6	1137	20 X98164	Nucleotide sequenc
c 15	34	2.6	42235	20 X98035	Nucleotide sequenc
c 16	33	2.6	2241	21 Z51469	Vector pVgXR-5A/5
c 17	33	2.6	2295	21 Z51470	Vector pVgXR-5A/5
c 18	33	2.6	2301	21 Z51471	Control vector pVg
c 19	33	2.6	2455	21 Z45836	cDNA of intestinal
c 20	33	2.6	2821	21 Z45837	cDNA of intestinal
c 21	32.8	2.5	1140	20 X36611	Pseudomonas oxidat
c 22	32.6	2.5	534720	19 V30458	Rhizobium species
c 23	32.6	2.5	536165	19 V30459	Rhizobium species
c 24	32.4	2.5	922	19 V15073	Hybrid DNA compris
c 25	31.4	2.4	1436	11 Q03319	cDNA of Elmeria te
c 26	31.4	2.4	1755	19 V03306	Bacterium OC9a pho
c 27	31.4	2.4	2241	18 V06244	Modified ecdysone
c 28	31.4	2.4	2970	14 Q37556	DHR23alpha cDNA cl
c 29	31.4	2.4	5534	12 Q13574	Eck gene, Drosoph
c 30	31.2	2.4	1116	20 X81700	DNA encoding a fru
c 31	31.2	2.4	3358	20 V70229	Human receptor tyr
c 32	31.2	2.4	35099	19 V27112	Adenovirus 17. Ma
c 33	31	2.4	1531	18 T46195	Maize insecticidal
c 34	31	2.4	5059	20 X84332	Human colon cancer
c 35	30.8	2.4	611	21 Z80753	HIV-1 Group M env
c 36	30.8	2.4	1800	20 X56121	Complete nucleotid
c 37	30.8	2.4	34094	20 Z30163	Modified glyphosat
c 38	30.6	2.4	1321	13 Q20834	Pseudomonas PROC p
c 39	30.4	2.4	1113	21 Z58692	Maize retinoblasto
c 40	30.4	2.4	3747	19 V05714	Maize retinoblasto
c 41	30.4	2.4	3747	19 V17081	Neisseria gonorrhoe
c 42	30.2	2.3	1359	21 Z53148	Neisseria meningit
c 43	30.2	2.3	1359	21 Z53150	Laccase-LCC2 gene.
c 44	30.2	2.3	2880	17 T15599	Human proteasome s
c 45	30	2.3	624	16 T02335	

ALIGNMENTS

RESULT 1

ID Q20832	Q20832	standard; DNA; 1689 BP.
XX	Q20832;	
AC	Q20832;	
DT	01-MAY-1992	(first entry)
DE	Glyphosate oxidoreductase gene.	
DE	Glyphosate oxidoreductase gene.	
KW	Recombinant; GOR; resistance; ss.	
XX	Bacterial isolate LBAA.	
OS	Bacterial isolate LBAA.	
FH	Key	Location/Qualifiers
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FT	misc_feature	389..390
FT		/tag= d
FT		/note= "in the alternative sequence C is present here"
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PN	W09200377-A.	
XX	09-JAN-1992.	
PD	09-JAN-1992.	
XX	24-JUN-1991;	91WO-US04514.
PF	24-JUN-1991;	91US-0717370.
XX	24-JUN-1991;	91US-0717370.
PR	24-JUN-1991;	91US-0717370.

Db 1261 attggttaagtcacaaagactggctcctgcatectaa 1296
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RESULT 6
X57309
ID X57309 standard; DNA; 8418 BP.
XX
AC X57309;
XX
DT 26-JUL-1999 (first entry)
XX
DE Sugar beet T-DNA containing cp4/epsps #2.
XX
KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
XX
OS Beta vulgaris.
XX
PN W09923232-Al.
XX
PD 14-MAY-1999.
XX
PF 29-OCT-1998; 98WO-EP06859.
XX
PR 31-OCT-1997; 97US-0112003.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Mannerloef M, Steen P, Tenning PP;
XX
DR WPI; 1999-313347/26.
XX
XX Glyphosate resistant transgenic sugar beet plants
XX
XX Claim 15; Page 36-41; 55pp; English.
XX
CC This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
CC mediated transformation with a gene allowing expression of cp4/epsps
CC in plants, where the plant lacks both right and left T-DNA border
CC sequences. The transgenic sugar beet plants of the invention are capable
CC of tolerating herbicide treatment with glyphosate (also known as
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
SQ Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;

Query Match 71.8%; Score 928.8; DB 20; Length 8418;
Best Local Similarity 83.8%; Pred. No. 2.4e-287;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

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Db 7275 atgccaggaaaacttgactagagttccaaagtggcttcttgacccaatgggtccattgtcc 7334
Qy 240 ATCCGGTTTACGCTA-TTTTCCAAACCATATGCC-TGGTTGATTCGCTTCTGTTAGCCGGA 297
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Db 7335 atccgcltccagctacttltccaaacccaatcgaacttggttgattcgcttcttcttgcttgcgta 7394
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Db 8055 gctgctcctaactggaaagcgtgctcacgttctctcacatcagcgtcgtgaagtgtctcca 8114
Qy 1018 GCGCTCGCGCTGCGAGTTCTGAAGAAGCATATTCAAATGATGGGTTCGCGCGGAGC 1077
|| || |||||||| || || |||||||| || || |||||||| || || |||||||| || |||
Db 8115 gctctcgtcctcgcagttctgaagaagttactccaagtgagatgggtttccggtccaagc 8174
Qy 1078 ATCCCGGATTCGCTCCCGTGTATTTGGCGGGCAACCGGACACCCGACGATATCTATGCT 1137
||||| |||||||| || || |||||||| || || |||||||| || || |||||||| || |||
Db 8175 atcccaagattcctctccagtgattggtcgttaccgttactccagaagttatctacgt 8234
Qy 1138 TTTGCGCATGCTCANCTCGGATGACAGGGCGCGGATCACCGCAACCGTCCGCTCAGAG 1197
|| || |||||||| || || |||||||| || || |||||||| || || |||||||| || |||
Db 8235 ttcggtcgcagtcacactcgggtatgactgggtgctcaagtcacgcacccctcttctgag 8294
Qy 1198 CTCTTCGCGGCGGAAAGACCTCAATTCGACATTTTCGCCCTTCGCCACCAACCGCTTGTGT 1257
||||| || || |||||||| || || |||||||| || || |||||||| || || |||||||| || |||
Db 8295 ctctcgcaggtgagaagacctctatcgacatctctccattcgcacccaacccgtttcgtt 8354
Qy 1258 ATTGGCAANTTCAACGAACGGGTCCGCGAAGTTAA 1293
||||| || || |||||||| || || |||||||| || || |||||||| || || |||||||| || |||
Db 8355 attggttaagtcacaaagactggctcgtcctcctaa 8390
RESULT 7
T85664

ID	T85664 standard; DNA; 1631 BP.
XX	AC
XX	AC
XX	T85664;
XX	
DT	21-NOV-1997 (first entry)
XX	CPT1-GOX gene fusion.
XX	
KW	expression cassette; inducible promoter; alca; alcr; alda; regulator;
KW	alcohol dehydrogenase; herbicide resistance gene; glyphosate;
KW	N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EFSPS;
KW	5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1;
KW	Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
XX	
XX	Chimeric Arabidopsis.
OS	Synthetic.
XX	
PN	W09706269-AL.
XX	
PD	20-FEB-1997.
XX	
PF	02-AUG-1996; 96WO-GB01883.
XX	
PR	03-AUG-1995; 95GB-0015941.
XX	
XX	(ZONE) ZENECA LTD.
XX	
PI	Jepson I;
XX	
DR	WPI; 1997-154273/14.
XX	
PT	Chemically inducible cassette for expressing herbicide resistance
PT	gene in plants - and derived plants, partic. for resistance to
PT	glyphosate, avoids constitutive expression and minimises development
PT	of herbicide tolerant weeds
XX	
PS	Example 3; Fig 7; 59pp; English.
XX	
CC	A chemically inducible plant gene expression cassette which comprises an
CC	inducible promoter linked to a gene (I) that confers resistance to a
CC	herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-
CC	glycine (glyphosate) or its salts, but may also be a gene for resistance
CC	to, e.g. chloracetanilides, glufosinate, sulphonyl ureas, imidazolidones,
CC	etc. The inducible promoter (e.g. alca, alcr, alda or other alcr-induced
CC	gene promoter) is operatively linked to an alcr regulator sequence.
CC	Induced expression of (I) avoids the risk that constitutive expression
CC	may interfere with plant development; allows volunteer plants to be
CC	controlled by herbicide applied without inducer and minimises the chance
CC	that herbicide-resistant strains of weeds will arise. The expression
CC	cassette is strictly controlled and suitable for general use in plants
CC	(both mono- and dicotyledons). The alca/alcr gene switch was exemplified
CC	with genes conferring resistance to glyphosate. The switch was used to
CC	drive inducible expression of glyphosate oxidase (GOX) in plants.
CC	Switchable GOX was expressed alone or in conjunction with constitutive
CC	expression of 5-enol-pyruvylshikimate 3-phosphate (EFSPS) CP4. Construct
CC	were optimised for expression in mono- and dicotyledonous crop species.
CC	The present sequence comprises a fusion of the GOX gene fused to the
CC	chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This
CC	sequence was ligated into pWJ1 (see T85666) and used in construction of
CC	dicot vectors.
XX	
SQ	Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match	66.3%;	Score 857.6;	DB 18;	Length 1631;
Best Local Similarity	80.2%;	Pred. No. 7.3e-265;		
Matches 1079;	Conservative	0;	Mismatches 214;	Indels 53; Gaps 4

QY	1	ATGCTGTGAGAACACAAAAAGCTAGGCATCGCTGGAGCGCGGAATCGTCGGCGTATGCACG	60
Db	274	ATGCTGTGAGAACACCAAGAGTGTGATCGCTGGAGCGCGGAATCGTCGGCGTATGCACG	333
QY	61	GCGCATGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGTAGCCCGCAACCCCTCTGGC	120

Db 1414 cccctccagtgattggtgctaccccglaclccceagagtgattatcagcgttllcggtcag 1473

QY 1148 GTTCATCTCGCATGACAGGGCGCGATGACCGCAACCTCTCTCAGAGCTCCTCGCAG 1207

Db 1474 gtccactcgggtatgctggtgctcaatgacgcgcaacctcgtttctgagctccctcgca 1533

QY 1208 GGGNAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTTGGTATTGGCAAT 1267

Db 1534 gtagaagacctctatcacatctctccattcgcacccaaccttctcggtattggttaagt 1593

QY 1268 CCAAGCAACGGTCCGGCAAGTTAA 1293

Db 1594 ccaagcaactggtcgtcatcctaa 1619

RESULT 8

X57308

ID X57308 standard; DNA: 8798 BP.

AC X57308;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX

PN WO9292322-A1.

XX

PD 14-MAY-1999.

XX

PP 29-OCT-1998; 98WO-EP06859.

XX

PR 31-OCT-1997; 97US-0112003.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Mannerloef M, Steen P, Tenning PP;

XX

DR WPI; 1999-313347/26.

XX

PT Glyphosate resistant transgenic sugar beet plants

XX

PS Claim 11; Page 31-36; 55pp; English.

XX

CC This invention describes a novel sugar beet plant, including its

CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase

CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium

CC mediated transformation with a gene allowing expression of cp4/epsps

CC in plants, where the plant lacks both right and left T-DNA border

CC sequences. The transgenic sugar beet plants of the invention are capable

CC of tolerating herbicide treatment with glyphosate (also known as

CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.

XX

SQ Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;

Query Match 49.6%; Score 641.8; DB 20; Length 8798;
Best Local Similarity 83.2%; Pred. NO. 2.5e-195;
Matches 766; Conservative 0; Mismatches 152; Indels 3; Gaps 3;

QY 1 ATGCTGAGAACCAAAAAGTAGGATCGCTGGAGCGGNATCGTCGGCGTATGCAGG 60

Db 7205 atggctgagaaccacaagaagttggtatcgctggagctggaatcgttggtttgcact 7264

QY 61 GCGCTGATCTTCACGCGCGGGATTCAAAGTCACCTTGATTCAGCCCAACCTCCTGGC 120

Db 7265 gctttgatgcttcaacgctcgtggaaggttaccttggattgattccaaacccacaggt 7324

QY 121 GAAGGTGCATCGCTTTGGGAATCCCGGATGCTTTCAACGGCTCATCGTCCCTATGTCC 180

Db 7325 gaaggtgcttcttcggttaacgctggttgctcaacgggtctcctcgttgcttccaatgtcc 7384

QY 181 ATGCGCGGANAAGTTGACGAGCGTCCGGAAGTGGCTTCCTTGACCCCGATGGG-CCGTTGTCA 239

Db 7385 atgcaggaacttgactagcgttccaaagtggctcttgaaccaatgggtccattgtcc 7444

QY 240 ATCCCGTTTCAGCTA-TTTTCCAAACCATCATGCGC-TGGTTGATTTTCGTTTTCGTAGCCGGA 297

Db 7445 atccgtttcagctactttlccaaacctatcgcttggttgatcttcttgcgttgcgtgga 7504

QY 298 AGACCAACAAGGTGAAGGAGCAGCGAAGACCTCCGCAATCTCATCAAGTCCACGGTG 357

Db 7505 agaccaacaaggtgaaggagcaagctaaagcactcctgaacctcatcaagtcacactgtg 7564

QY 358 CCTCTCATCAAGTCAATGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAGGT 417

Db 7565 cctttgatcaagctccttggtgagggagctgatgtagccaccttatccgtcacagaggt 7624

QY 418 CATCTCACCGTATATCTGTGGACAAGCACACTTTCCGCCAAGCGCGGAGGTTTGGGAACGT 477

Db 7625 cactttaccgtgtaccgttgagaagacagacttcgcaagagacgttggaaggttgggaactt 7684

QY 478 CGGCTCTCAACGGTGTTCGACACGAGATCTTCAGCGCGGATGCGTTCGGGATTTCCGAT 537

Db 7685 cgtcgtctcaacgctgttctgtactcaaatcctcagcgctgatgcttgcgtgatttcgat 7744

QY 538 CCGAATCTGTGCGATGCGTTTACCAAGGGCATCTTTAGAGAAGAACGGTCCACAGGATT 597

Db 7745 cctaaactgtctcacgcctttaccaagggaaaccttatcgaagagaacggtcacaccatc 7804

QY 598 AATCCGCAAGGCTGCTGACCCCTCTTTGTTTCGGCGTTTATTCGCAACGGTCGCAATTC 657

Db 7805 aaccaccaaggtcctcgtgactctctgttcgcgttccatcgctcaacggttggaagttc 7864

QY 658 GTATCTGCGGTGTCATCGGCTTTGAGACTGAAAGTAGGGCGCTTAAAGGCATTTACAACC 717

Db 7865 gtgctcgtcgtgttatcggtatcgactgagactgaggtcgtcctcaaggttatcaccacc 7924

QY 718 ACGAAGCGGTTCTGCGCGTTGATGACGAGGTTGTGCGAGCGCGGCACACTCGAANTCA 777

Db 7925 accaacggtgtcttctgtctgtatgctcagctgttctgagctggtgacactccaagttc 7984

QY 778 CTTGCTAATTTGCTAGGCGATGACATCCGCTCGATACCGAACGTCGATATCATTCGTC 837

Db 7985 ctltgctaaactccttgggtgatgacatcccatccttggtatccgaacgttggaacacatcgtg 8044

QY 838 ATCGGAATTCGGAAGCGCTCCACGCATTCGACGACCGGATGCGTCAAGAAAATTCATC 897

Db 8045 atcgccaacccagaagctgctccacgtattccaaactaccgatgcttctggaaggttccgg 8104

QY 898 GCGACACCTATGGAANTGGG 918

Db 8105 tccaaattgtttacatgtg 8125

RESULT 9

X57305

ID X57305 standard; DNA: 8012 BP.

XX

AC X57305;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps fragment.

XX

KW Sugar beet; transformation; T-DNA; Insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX WO9923232-A1.
PN
XX
PD
XX
XX
PF
XX
XX
PR
XX
XX
PA
PA
XX
PI
XX
XX
DR
XX
XX
PT
XX
XX
PS
XX
CC This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
CC mediated transformation with a gene allowing expression of cp4/epsps
CC in plants, where the plant lacks both right and left r-DNA border
CC sequences. The transgenic sugar beet plants of the invention are capable
CC of tolerating herbicide treatment with glyphosate (also known as
CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
SQ Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;

Query Match 49.5%; Score 640.2; DB 20; Length 8012;
Best Local Similarity 84.3%; Pred. No. 7.9e-195;
Matches 756; Conservative 0; Mismatches 138; Indels 3; Gaps 3;

QY 1 ATGCTCAGAACCAAAAAGTAGGATCGCTGGAGCGGAATCGTGGCGGTATGCAAG 60
DB 7116 atggctgagaaacacaaagaggttggtgctggagctggaatcggtgtgttgcaact 7175
QY 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTGATTCACCGGAACCCCTCCGTC 120
DB 7176 gcttgatgcttcaacgctgctgattcaaggttacccttgattgatccaaacccaccaggt 7235
QY 121 GAAGGTCATCGTTTGGGAATGCGCGATGCTTCAACGGCTCATCGCTCGTCCCTATGTCC 180
DB 7236 gaaggctgctctcttcggttaacgctggttgcctcaacggttccctcgtgttccaaatgcc 7295
QY 181 ATGCGCGGAACCTTGACGAGCGTGCAGAGTGGCTCTTACCGCGGATGGG-CCGTTGTCA 239
DB 7296 atgcaggaaacttgactagcgttccaaagtggcttcttgacccaaagggtccattgcc 7355
QY 240 ATCCGGTTACGCTA-TTTCACCAACCATCATGCC-TGGTTGATTCGCTTTCTTAGCCGGA 297
DB 7356 atccggttccagcttcccttccaaacatacgtccttggttgattcgttcttgcgtgcga 7415
QY 298 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACCTCCGCAATCTCATCAAGTCCACCGTG 357
DB 7416 agaccaaacaagtggaaggaagactaaggaactccgttaactcctcaagatccactgtg 7475
QY 358 CCTGTGATCAAGTCATTTGGCGGAGGAGGCTGTGATCGAGGCCATCTGATCCGCCATGAAGGT 417
DB 7476 ccttbtgatcaagcttcttgcgtgagaggtgtagtgcagacacttaccgttcacgaaggt 7535
QY 418 CATCTGACCCATATATCGTGAGAGCAGACTTCGCCAGGACCCCGAGGTTTGGAACTG 477
DB 7536 cacttaccgtgtaccgttggaagcagactctgcgaagaccgttgaggttgggaactt 7595
QY 478 CGGCGTCTCAACGCTGTTCGCGAGCGAGACTCCTCAGCGCCCATGCTGTCGGGATTTCCAT 537
DB 7596 cgtcgtctcaacggttctgtactactcaaatcctcagcgtgatgctgattgttcgat 7655
QY 538 CCGAAGCTGTGCGCATGCGTTTACCAGGGCATTTCTTATAGAGAGAACGGTCAACAGATT 597

DB 7656 cctaactgtctcaagcctttaccaaggaataccttatcgaagagaacggttcacaccalc 7715
QY 598 AATCCGCAAGGGCTCGTGACCTCTTTCGCGCGTTCCTTATCGCGAACGGTGGCGAATTC 657
DB 7716 aaccacaaggtctcgtgactctcttcttctcgtcttcatcgtcaacggtggaagagctc 7775
QY 658 GTATCTCGCGGTGTATCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAACC 717
DB 7776 gtgtcgtcgtgttatcggattcggactcgaagctcgtgctctcgaaggttatcaccacc 7835
QY 718 ACGAACGGGCTTCGCGCGTGTGATCGAGCGTTCGCGAGCGCGCGCACACTCGAAATCA 777
DB 7836 accaacggtgtcttctgctgtgtagcagctgtgttgcaagctgtgcacactccaagctc 7895
QY 778 CTTGCTAATTTCGCTAGCGGATGACATCCGCTCCGATACCGAACCTGGATATCATATCGTC 837
DB 7896 ctfgtaactcccttggtagatgacatccattggatccaccgaacgtggatccacatcgtg 7955
QY 838 ATCCGGAATCCGGAAGCGCTCCACGATTCGACGACCGATCGCTCAGGAAAATTC 894
DB 7956 atcgccaaccagaagctgtctccacgtatttccaaactaccgactgtctcttggaagctc 8012

RESULT 10
V30458/c
ID V30458 standard; DNA; 534720 BP.
XX
AC V30458;
XX
DT 14-OCT-1998 (first entry)
XX
DE Rhizobium species plasmid pNGR234a.
XX
KW Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
KW degradation; metabolism; host range; nitrogen fixation; nodulation;
XX
OS Rhizobium sp.
XX
FH Key Location/Qualifiers
FT CDS 417796..418671
FT FT /*tag= a
FT FT /standard_name= "ORF K1"
FT FT /product= "oligopeptide permease"
FT FT /note= "homologous to the OppC gene"
FT CDS 418673..419680
FT FT /*tag= b
FT FT /standard_name= "ORF K2"
FT FT /product= "oligopeptide permease"
FT FT /note= "homologous to the Oppd gene"
FT CDS 419677..420738
FT FT /*tag= c
FT FT /standard_name= "ORF K3"
FT FT /product= "oligopeptide permease"
FT FT /note= "homologous to the Oppf gene"
FT CDS 420774..422159
FT FT /*tag= d
FT FT /standard_name= "ORF K4"
FT FT /product= "encapsulation-like protein"
FT FT /note= "homologous to the CapA gene"
FT CDS 422628..424031
FT FT /*tag= e
FT FT /standard_name= "ORF K5"
FT FT /product= "aminotransferase-like protein"
FT FT /note= "homologous to the BioA gene"
FT CDS 424056..425594
FT FT /*tag= f
FT FT /standard_name= "ORF K6"
FT FT /product= "(semi)aldehyde dehydrogenase-like protein"
FT CDS complement (426949..428028)
FT FT /*tag= g
FT FT /standard_name= "ORF K7"

```
FT /product= "transposase homologue"
FT /note= "homologous to the tnp gene"
FT 428292..429623
FT /*tag= h
FT /standard_name= "ORF K8"
FT /product= "glutamate dehydrogenase-like protein"
FT /note= "homologous to the GluDI gene"
FT complement (430538..431284)
FT /*tag= i
FT /standard_name= "ORF K9"
FT /product= "transposase homologue"
FT complement (431296..432840)
FT /*tag= j
FT /standard_name= "ORF K10"
FT /product= "transposase homologue"
FT /note= "homologous to the Tnp gene"
FT complement (433880..434110)
FT /*tag= k
FT /standard_name= "ORF K11"
FT /product= "protein of unknown function"
FT /note= "homologous to the FixJ gene"
FT complement (434107..434433)
FT /*tag= l
FT /standard_name= "ORF K12"
FT /product= "protein of unknown function"
FT complement (434517..434711)
FT /*tag= m
FT /standard_name= "ORF K13"
FT /product= "ferrodoxin/ferrodoxin-like protein"
FT /note= "homologous to the FdxN gene"
FT complement (434753..436234)
FT /*tag= n
FT /standard_name= "ORF K14"
FT /gene= "nifB"
FT /product= "protein involved in FeMo co-factor
FT biosynthesis"
FT complement (436460..438130)
FT /*tag= o
FT /standard_name= "ORF K15"
FT /gene= "nifA"
FT /product= "positive regulator of nif, fix and other
FT genes"
FT complement (438297..438590)
FT /*tag= p
FT /standard_name= "ORF K16"
FT /gene= "fixX"
FT /product= "protein required for nitrogenase activity"
FT complement (438605..439912)
FT /*tag= q
FT /standard_name= "ORF K17"
FT /gene= "fixC"
FT /product= "protein required for nitrogenase activity"
FT complement (439923..441032)
FT /*tag= r
FT /standard_name= "ORF K18"
FT /gene= "fixB"
FT /product= "protein required for nitrogenase activity"
FT complement (441042..441899)
FT /*tag= s
FT /standard_name= "ORF K19"
FT /gene= "fixA"
FT /product= "protein required for nitrogenase activity"
FT complement (442316..442636)
FT /*tag= t
FT /standard_name= "ORF K20"
FT /product= "protein of unknown function"
FT complement (443313..443879)
FT /*tag= u
FT /standard_name= "ORF K21"
FT /product= "protein of unknown function"
FT 444337..445029
FT /*tag= v
FT /standard_name= "ORF K22"
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FT /product= "ferrodoxin-like protein"
FT /note= "homologous to the NifQ gene"
FT 445088..446602
FT /*tag= w
FT /standard_name= "ORF K23"
FT /gene= "dctA"
FT /product= "C4-dicarboxylate transport protein"
FT /note= "homologous to the DctAI gene"
FT 446599..447843
FT /*tag= x
FT /standard_name= "ORF L1"
FT /product= "cytochrome P450-like protein"
FT /note= "homologous to the CamC gene"
FT 447844..448500
FT /*tag= y
FT /standard_name= "ORF L2"
FT /product= "gamma-hexachlorocyclohexane-dechlorinase-like
FT protein"
FT /note= "homologous to the LinA gene"
FT 448497..450203
FT /*tag= z
FT /standard_name= "ORF L3"
FT /product= "putative protein with degradative function"
FT 450341..451396
FT /*tag= aa
FT /standard_name= "ORF L4"
FT /product= "luciferase alpha-subunit-like protein"
FT /note= "homologous to the LuxA gene"
FT 452980..454494
FT /*tag= ab
FT /standard_name= "ORF L6"
FT /gene= "nifD"
FT /product= "alpha-subunit of FeMo protein of nitrogenase"
FT 454590..456131
FT /*tag= ac
FT /standard_name= "ORF L7"
FT /gene= "nifK"
FT /product= "beta-subunit of FeMo protein of nitrogenase"
FT 456187..457677
FT /*tag= ad
FT /standard_name= "ORF L8"
FT /product= "protein involved in FeMo co-factor
FT biosynthesis"
FT 457687..459096
FT /*tag= ae
FT /standard_name= "ORF L9"
FT /product= "protein involved in FeMo co-factor
FT biosynthesis"
FT /note= "homologous to the FixF gene"
FT 459093..459575
FT /*tag= af
FT /standard_name= "ORF L10"
FT /product= "protein of unknown function"
FT /note= "homologous to the NifX gene"
FT 459579..460067
FT /*tag= ag
FT /standard_name= "ORF L11"
FT /product= "protein of unknown function"
FT 460501..460920
FT /*tag= ah
FT /standard_name= "ORF L12"
FT /product= "protein similar to part of the Fe protein
FT of nitrogenase"
FT /note= "homologous to the NifH gene"
FT 461228..461545
FT /*tag= ai
FT /standard_name= "ORF L13"
FT /product= "protein of unknown function"
FT 463201..464739
FT /*tag= aj
FT /standard_name= "ORF L14"
FT /product= "peptidase-like protein"
```

```
FT CDS /note= "homologous to the bI-MPP gene"
FT 464736..466079
FT /*tag= ak
FT /standard_name= "ORF 115"
FT /product= "processing protease-like protein"
FT /note= "homologous to the PP gene"
FT 466590..467021

Query Match 2.7%; Score 35.4; DB 19; Length 534720;
Best Local Similarity 50.9%; Pred. No. 4.7;
Matches 135; Conservative 0; Mismatches 126; Indels 4; Gaps 2;

QY 994 ACGACACCTCGAATCTTCTC-CAGCCCTCGCCCTCGAGTCTCTGAAGAACGATATTC 1052
Db 395468 ACGCACACTCGAGCATTCCTCGTCAATGACCTCTTCCCGGGCGGATGCAAAAGAAGCATC 395409

QY 1053 CAAATGGATGGGTTCGGCGGAGCATCCCGATTCCTCCCGTGAATGGCCGGGCAAC 1112
Db 395408 CTATTGGTCTGGGTCTGCGCCCAATGACCGGACGCGGATGCGTCAATCGACATTC 395352

QY 1113 CCGACACACCGACGTAATCTATGCTTTTCGGCCCATGCTCTCGGCATGACAGGGGGGCC 1172
Db 395351 GAAGATCGCGGTCTCTTCTTAACACCGGACGCGGACGCGCTTGGCTGGACGATGAGCTC 395292

QY 1173 GATGACCGAAGCTCTCTCAGAGCTCTCGAGGCGAAGAACCTCAATCGACATTC 1232
Db 395291 CGGCTCTCGCGGCTCTATCTGCGGACCTGGTATCTGCGCGAAGCCGAGATCGACGCCAC 395232

QY 1233 GCCTTCGCGACCAACCGCTTTGGT 1257
Db 395231 CGACCTCGCGTACGCCGCTACGCT 395207

RESULT 11
V30459/c
ID V30459 standard; DNA; 536165 BP.
XX V30459;
XX
XX 06-JUL-1999 (first entry)
XX
XX Rhizobium species symbiotic plasmid pNGR234.
XX
XX Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
XX degradation; metabolism; host range; nitrogen fixation; nodulation;
XX legume; plant; ds.
XX
XX Rhizobium sp.
XX
XX WO9802560-A2.
XX
XX 22-JAN-1998.
XX
XX 10-JUL-1997; 97WO-1B00950.
XX
XX 20-MAY-1997; 97GB-0010395.
XX 12-JUL-1996; 96EP-0730001.
XX
XX (MOLE-) INST MOLECULAR BIOTECHNOLOGY.
XX (BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
XX
XX Broughton WJ, Frelberg CB, Perret XP, Rosenthal A;
XX WPI; 1998-110606/10.
XX
XX New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to
XX develop products for modifying plant characteristics, e.g. nitrogen
XX fixation, synthesis of compounds and stress response
XX
XX Claim 1; Fig 3; 228pp; English.
XX
XX This is the nucleotide sequence of the plasmid pNGR234a isolated from
XX Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the
```

```
CC nucleotide sequence are claimed. The nucleotide sequences or ORFs can
CC be used e.g. in the transportation of compounds to and from an organism
CC which is a host to at least one of the nucleotide sequences, ORFs or
CC proteins, the degradation and/or metabolism of organic, inorganic,
CC natural or xenobiotic substances in a host organism or the modification
CC of the host range, nitrogen fixation abilities; for obtaining a synthetic
CC minimal set of ORFs required for functional Rhizobium-legume symbiosis,
CC especially for nodulation efficiency on host plants.
XX
XX Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
SQ

Query Match 2.7%; Score 35.4; DB 19; Length 536165;
Best Local Similarity 50.9%; Pred. No. 4.7;
Matches 135; Conservative 0; Mismatches 126; Indels 4; Gaps 2;

QY 994 ACGACACCTCGAATCTTCTC-CAGCCCTCGCCCTCGAGTCTCTGAAGAACGATATTC 1052
Db 395468 ACGCACACTCGAGCATTCCTCGTCAATGACCTCTTCCCGGGCGGATGCAAAAGAAGCATC 395409

QY 1053 CAAATGGATGGGTTCGGCGGAGCATCCCGATTCCTCCCGTGAATGGCCGGGCAAC 1112
Db 395408 CTATTGGTCTGGGTCTGCGCCCAATGACCGGACGCGGATGCGTCAATCGACATTC 395352

QY 1113 CCGACACACCGACGTAATCTATGCTTTTCGGCCCATGCTCTCGGCATGACAGGGGGGCC 1172
Db 395351 GAAGATCGCGGTCTCTTCTTAACACCGGACGCGGACGCGCTTGGCTGGACGATGAGCTC 395292

QY 1173 GATGACCGAAGCTCTCTCAGAGCTCTCGAGGCGAAGAACCTCAATCGACATTC 1232
Db 395291 CGGCTCTCGCGGCTCTATCTGCGGACCTGGTATCTGCGCGAAGCCGAGATCGACGCCAC 395232

QY 1233 GCCTTCGCGACCAACCGCTTTGGT 1257
Db 395231 CGACCTCGCGTACGCCGCTACGCT 395207

RESULT 12
X98168/c
ID X98168 standard; DNA; 405 BP.
XX X98168;
XX
XX 25-OCT-1999 (first entry)
XX
XX Nucleotide sequence of ORF33512 encoding a virulence factor.
XX
XX Human pathogen; virulence polypeptide; virulence factor;
XX pathogenic infection; Pseudomonas aeruginosa infection; ss.
XX
XX Pseudomonas aeruginosa.
XX
XX WO9927129-A1.
XX
XX 03-JUN-1999.
XX
XX 25-NOV-1998; 98WO-US25247.
XX
XX 25-NOV-1997; 97US-0066517.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
XX Rahme LG, Tan M, Tsongalis J;
XX WPI; 1999-357851/30.
XX
XX Virulence factors useful in developing disease treatments
XX
XX Disclosure; Fig 4; 228pp; English.
XX
XX The present sequence represents a Pseudomonas aeruginosa nucleic acid
XX sequence. P. aeruginosa is an opportunistic human pathogen present in
```


GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 19:09:36 ; Search time 157.96 Seconds
(without alignments)
1238.001 Million cell updates/sec

Title: US-08-484-274-4
Perfect score: 1293
Sequence: 1 ATCTGTGAGAACACACAAAA.....AAACGGGTCCGGCAAGTTAA 1293

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA.*
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2: /cgn2_6/ptodata/2/lna/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/lna/5C_COMB.seq.*
4: /cgn2_6/ptodata/2/lna/5D_COMB.seq.*
5: /cgn2_6/ptodata/2/lna/6_COMB.seq.*
6: /cgn2_6/ptodata/2/lna/PCTRUS_COMB.seq.*
7: /cgn2_6/ptodata/2/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1293	100.0	1293	2	US-08-484-274A-4
3	1293	100.0	1689	1	US-08-391-339-3
4	1260	97.4	1692	2	US-08-484-274A-3
5	1255.2	97.1	1296	1	US-08-391-339-6
6	1255.2	97.1	1296	2	US-08-484-274A-6
7	1160.8	89.8	1296	1	US-08-391-339-7
8	1160.8	89.8	1296	2	US-08-484-274A-7
9	928.8	71.8	1296	1	US-08-391-339-8
10	928.8	71.8	1296	2	US-08-484-274A-8
11	925.6	71.6	1296	1	US-08-391-339-17
12	925.6	71.6	1296	2	US-08-484-274A-17
13	56.2	4.3	69	1	US-08-391-339-30
14	56.2	4.3	69	2	US-08-484-274A-30
15	54.6	4.2	69	1	US-08-391-339-33
16	54.6	4.2	69	2	US-08-484-274A-33
17	50.6	3.9	65	1	US-08-391-339-28
18	50.6	3.9	65	2	US-08-484-274A-28
19	48.2	3.7	61	1	US-08-391-339-31
20	48.2	3.7	61	2	US-08-484-274A-31
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22	47.6	3.7	62	2	US-08-484-274A-27
23	47.2	3.7	68	1	US-08-391-339-32
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25	33	2.6	41	1	US-08-391-339-29
26	33	2.6	41	2	US-08-484-274A-29

c	27	33	2.6	2241	5	US-09-144-759-17	Sequence 17, Appl
c	28	33	2.6	2295	5	US-09-144-759-19	Sequence 19, Appl
c	29	33	2.6	2301	5	US-09-144-759-21	Sequence 21, Appl
c	30	31.6	2.4	8931	5	US-09-028-934-28	Sequence 28, Appl
c	31	31.4	2.4	2970	6	PCW-US92-06391-1	Sequence 1, Appl
c	32	31.2	2.4	3358	3	US-08-469-537A-104	Sequence 104, App
c	33	31	2.4	1531	2	US-08-449-986-1	Sequence 1, Appl
c	34	31	2.4	1531	3	US-08-756-855-1	Sequence 1, Appl
c	35	30.2	2.3	2880	1	US-08-462-484-3	Sequence 3, Appl
c	36	30.2	2.3	2880	2	US-08-441-147-3	Sequence 3, Appl
c	37	30.2	2.3	2880	6	PCT-US95-07536-3	Sequence 3, Appl
c	38	29.6	2.3	1300	4	US-08-440-845D-8	Sequence 8, Appl
c	39	29.2	2.3	471	1	US-08-474-177-1	Sequence 1, Appl
c	40	29.2	2.3	471	2	US-08-487-033-1	Sequence 1, Appl
c	41	29.2	2.3	471	3	US-08-480-810-1	Sequence 1, Appl
c	42	29.2	2.3	471	3	US-08-508-735-1	Sequence 1, Appl
c	43	29.2	2.3	471	4	US-08-848-251-1	Sequence 1, Appl
c	44	29.2	2.3	471	4	US-08-486-047-1	Sequence 1, Appl
c	45	29.2	2.3	471	5	US-09-120-130-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-391-339-4
; Sequence 4, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B44F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
US-08-391-339-4

Query Match 100.0%; Score 1293; DB 1; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAAATCGTCGGGGTATGCACG 60
Db 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAAATCGTCGGGGTATGCACG 60

Qy 61 GCGTGTATGCTTACAGCGCGCGGATTCAAAGTCACTTGTATGACCCGCAACCCCTCCTGGC 120
Db 61 GCGTGTATGCTTACAGCGCGCGGATTCAAAGTCACTTGTATGACCCGCAACCCCTCCTGGC 120

Qy 121 GAAGTGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180
Db 121 GAAGTGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180

Qy 181 ATGCCGGGAAACTTGCAGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGCGGTGTGCAA 240
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Db 241 TCCGCTTCAAGTATTCACCAACCATCATCGCTGGTGTATTCGCTTCTGTAGCCGGAAGA 300

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Db 301 CCAACAAAGTGAAGGAGCAGCGGAAAGCACTTCCGCAATCTCATCAAGTCCACGGTGCCT 360

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Qy 421 CTGACCGTATATCTGGAGAGCAGACTTCCGCAAGCAGCGGAGTGGGAACCTGCGG 480
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Qy 481 CGTCTCAACGGTGTTCGACCCAGATCTCAGCCCGCATGCGGTTCGCGGATTCGATCCG 540
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Qy 541 AACTTGTGCGATCGTTCACCAAGGCACTTCTATAGAGAGACGGTTCACACCATTAAT 600
Db 541 AACTTGTGCGATCGTTCACCAAGGCACTTCTATAGAGAGACGGTTCACACCATTAAT 600

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Qy 661 TCTCGCGGTGTATCGCGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 720
Db 661 TCTCGCGGTGTATCGCGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 720

Qy 721 AACCGCGTTCGCGCGTGTATGACAGCGTTCGCGAGCGCGGCGCACACTCGAAATCACTT 780
Db 721 AACCGCGTTCGCGCGTGTATGACAGCGTTCGCGAGCGCGGCGCACACTCGAAATCACTT 780

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Db 781 GCTAATTCGCTAGCGATGACATCCCGCTCGATACCGAAGTGGATATCATATGCTCATC 840

Qy 841 GCGAATCCGGAAGCGGTTCACGCAATTCGACGACCGCATCGGTGAGGAAATTCATCGCG 900
Db 841 GCGAATCCGGAAGCGGTTCACGCAATTCGACGACCGCATCGGTGAGGAAATTCATCGCG 900

Qy 901 ACACCTATGAAATGGGGCTTCGCGTGGCGGTTACGGTTCAGTTCGCTGGGCTCACAGCC 960
Db 901 ACACCTATGAAATGGGGCTTCGCGTGGCGGTTACGGTTCAGTTCGCTGGGCTCACAGCC 960

Qy 961 GCTCCTAACTGGAACGTGCGCATGCTCTATACGACGCGCTCGAAACCTTCTTCCAGCC 1020
Db 961 GCTCCTAACTGGAACGTGCGCATGCTCTATACGACGCGCTCGAAACCTTCTTCCAGCC 1020

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Db 1021 CTCGCGCCTCGGAGTTCGAAGAACGATATTCCAAATCGATGGGTTCGCGCCGAGCATC 1080

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Qy 1141 GGCCATGTCTATCTCGGCATGACAGGGCGCGGATGACCGAACGCTCTCTCAGAGCTC 1200
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Db 1201 CTCGAGCGGAAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGTAT 1260

Qy 1261 GGCAAAATCAAGCAAAACGGGTCCGGCAAGTTAA 1293
Db 1261 GGCAAAATCAAGCAAAACGGGTCCGGCAAGTTAA 1293

RESULT 2
US-08-484-274A-4
; Sequence 4, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barcy, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
US-08-484-274A-4

Query Match 100.0%; Score 1293; DB 2; Length 1293;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTCAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAAATCGTCGGGGTATGCACG 60
Db 1 ATGCTCAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAAATCGTCGGGGTATGCACG 60

QY 61 GCGCTCATCTTACGCGCGGGATTCAAAGTCACCTTGATTGACCGCAACCCCTCTCGC 120
Db 61 GCGCTGATGCTTACGCGCGGGATTCAAAGTCACCTTGATTGACCGCAACCCCTCTCGC 120
QY 121 GAAGGTGATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCGTGGTCCCTATGTCC 180
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QY 481 CGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATGCTTGGGGATTTTCGATCGG 540
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QY 841 GCGAATCCGGAAGCGCTCCAGCGATTCCGAGACCGATGCGTCAGGAAATTCATCGCG 900
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QY 1081 CCGGATTCGCTCCCGGATTTGGCGGGCAACCCGGACACCCGAGCTAATCTATGCTTTC 1140
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Db 1141 GCCCATGCTCATCTCGGGCATACAGGGGGCGGCGCGATGACCGCAACGCTCGTCTCAGAGCTC 1200
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QY 1261 GCGAATCAAGCAACGCGTCCGGCAAGTTAA 1293
Db 1261 GCGAATCAAGCAACGCGTCCGGCAAGTTAA 1293
RESULT 3
US-08-391-339-3
; Sequence 3, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESS: Monsanto Co. B4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-391-339-3
Query Match 100.0%; Score 1293; DB 1; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 120 ATGCTCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 179
QY 61 GCGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTTGATTTGACCCGCAACCCCTCTCGC 120
Db 180 GCGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTTGATTTGACCCGCAACCCCTCTCGC 239
QY 121 GAAGGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTGGTCCCTATGTCC 180

Db 240 GAAGTGCATCGTTCGGAATGCCGGATGCTTCACAGGCTCATCCGTGCTCCCTATGTCC 299
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Db 360 TCCGGTTCAGCTATTTCCAAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA 419
Qy 301 CCAACAAAGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGCTGCT 360
Db 420 CCAACAAAGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGCTGCT 479
Qy 361 CTGATCAAGTCATTTGGCGAGGAGGCTGATCGAGCCATCTGATCCGCCATGAAGTCA 420
Db 480 CTGATCAAGTCATTTGGCGAGGAGGCTGATCGAGCCATCTGATCCGCCATGAAGTCA 539
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Qy 541 AACTTGTGCGATGCGTTTACCAAGGGATCTTATAGAAGAACGCGTCAACGATTAAT 600
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Qy 661 TCTCGCGTGCATCGCTTTGACACTGAAGTAGGGCTTAAAGGCATTTACAACACG 720
Db 780 TCTCGCGTGCATCGCTTTGACACTGAAGTAGGGCTTAAAGGCATTTACAACACG 839
Qy 721 AACGGCGTTCGCGGTTGATGACAGCGTTGTGCGAGCGGCGACACTCGAAATCACTT 780
Db 840 AACGGCGTTCGCGGTTGATGACAGCGTTGTGCGAGCGGCGACACTCGAAATCACTT 899
Qy 781 GCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGAATATCATTCGTATC 840
Db 900 GCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGAATATCATTCGTATC 959
Qy 841 GCGAATCCGGAAGCGCTCCACGATTCGAGCAGCGATGCTCAGGAAATTCATCCG 900
Db 960 GCGAATCCGGAAGCGCTCCACGATTCGAGCAGCGATGCTCAGGAAATTCATCCG 1019
Qy 901 ACACCTATGGAATAGGGCTTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACAGCC 960
Db 1020 ACACCTATGGAATAGGGCTTTCGCGTGGCGGTACGGTTGAGTTGCGTGGGCTCACAGCC 1079
Qy 961 GCTCCTAATTCGGAACGTCGCGATGCTCTATACGACAGCTTCGAAACCTTCACAGCC 1020
Db 1080 GCTCCTAATTCGGAACGTCGCGATGCTCTATACGACAGCTTCGAAACCTTCACAGCC 1139
Qy 1021 CTCGCGCTCGGAGTCTGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGCATC 1080
Db 1140 CTCGCGCTCGGAGTCTGAAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGCATC 1199
Qy 1081 CCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCTTC 1140
Db 1200 CCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGTAATCTATGCTTC 1259
Qy 1141 GCGCATGCTCATCTCGGCATTCAGAGGGCGCGGATGACCGAAGCTTCGTCAGAGCTC 1200
Db 1260 GCGCATGCTCATCTCGGCATTCAGAGGGCGCGGATGACCGAAGCTTCGTCAGAGCTC 1319
Qy 1201 CTCGAGCGGAAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTTGGTATT 1260
Db 1320 CTCGAGCGGAAAGACCTCAATCGACATTTCCGCCCTTCGCAACCAACCGCTTTGGTATT 1379

Qy 1261 GCAGAAATCAAGCAACGGTCCGGCAAGTTAA 1293
Db 1380 GCAGAAATCAAGCAACGGTCCGGCAAGTTAA 1412

RESULT 4

US-08-484-274A-3
; Sequence 3, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBI130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-484-274A-3

Query Match 97.4%; Score 1260; DB 2; Length 1692;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Qy 1 ATGTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
Db 120 ATGTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 179
Qy 61 GCGCTGATGCTTCAGCCCGCGGATTCAAAGTCACCTTGATTGACCCGAAACCCCTCCTGGC 120
Db 180 GCGCTGATGCTTCAGCCCGCGGATTCAAAGTCACCTTGATTGACCCGAAACCCCTCCTGGC 239
Qy 121 GAAGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
Db 240 GAAGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 299
Qy 181 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGCTCTTGACCCGAT-TGGCCGCTGTCA 239
Db 300 ATGCCGGGAAACTTGACGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGGCCCTTGTCA 359
Qy 240 ATCCGGTTCAGCTA-TTTTCCAACCATCATG-CCTGGTTGATTTCGCTTTCTGTTAGCCGA 297
Db 360 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTTCGCTTTCTGTTAGCCGA 419
Qy 298 AGACCAACAAGTGAAGGAGCAGCGGCAACGACTCCGCAATTCATCAAGTCCACCGT 357
|||||

Db 420 AGACCAAAAGGTGAAGGAGCAGCGGAAGCACTCCGCAATCTCATCAAGTCCACGGTG 479
Qy 358 CCTCTGATCAATCATYTCGCGGAGAGGCTGATGCGAGCCATCTGATCGGCATGAAGT 417
Db 480 CCTCTGATCAATCATYTCGCGGAGAGGCTGATGCGAGCCATCTCATCGGCATGAAGT 539
Qy 418 CATCTGACCGTATATCTGTTGGAGAACACACTTCGCCAAGGACCGGGAGGTGGAACTG 477
Db 540 CATCTGACCGTATATCTGTTGGAGAACACACTTCGCCAAGGACCGGGAGGTGGAACTG 599
Qy 478 GGGCTCTCAACGGTGTTCGCAACGCAGATCTCTACGCGCGATGCTTTCGGGATTTTCGAT 537
Db 600 GGGCTCTCAACGGTGTTCGCAACGCAGATCTCTACGCGCGATGCTTTCGGGATTTTCGAT 659
Qy 538 CGGAATTTGTCGATCGCTTTACCAAGGGCATTTCTATAGAGAGAACCGGTACACAGATT 597
Db 660 CGGAATTTGTCGATCGCTTTACCAAGGGCATTTCTATAGAGAGAACCGGTACACAGATT 719
Qy 598 AATCGCAAGGGCTGCTGACCTCTTGTTCGGCGTTTATCGCAACGGTGGCAATTC 657
Db 720 AATCGCAAGGGCTGCTGACCTCTTGTTCGGCGTTTATCGCAACGGTGGCAATTC 779
Qy 658 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAAC 717
Db 780 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAAC 839
Qy 718 AGCAAGCGGTTTCTGCGCGTTGATGACAGCGGTTTTCGAGCGCGGCACACTTCGAATCA 777
Db 840 AGCAAGCGGTTTCTGCGCGTTGATGACAGCGGTTTTCGAGCGCGGCACACTTCGAATCA 899
Qy 778 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGACGTGGATATCATATCGTC 837
Db 900 CTTGCTAATTCGCTAGGCGATGACATCCGCTCGATACCGACGTGGATATCATATCGTC 959
Qy 838 ATCGGAATTCGGAAGCGGCTCCAGCATTCGAGACCGCATGCTCAGGAAATTTCAATC 897
Db 960 ATCGGAATTCGGAAGCGGCTCCAGCATTCGAGACCGCATGCTCAGGAAATTTCAATC 1019
Qy 898 GCGACACTATGGAATGGGGTTTCGCGTGGCGGTACGGTTGAGTTGCTGGGCTCACA 957
Db 1020 GCGACACTATGGAATGGGGTTTCGCGTGGCGGTACGGTTGAGTTGCTGGGCTCACA 1079
Qy 958 GCGGCTCTAATCGAAACGTCGCATCTGCTATACGACGCTCGAANACTTCTTCCA 1017
Db 1080 GCGGCTCTAATCGAAACGTCGCATCTGCTATACGACGCTCGAANACTTCTTCCA 1139
Qy 1018 GCGCTCGGCGCTCGAGTTCTGAAGAAGCATATTCGCAATGGATGGGTTCGCGCGGAGC 1077
Db 1140 GCGCTCGGCGCTCGAGTTCTGAAGAAGCATATTCGCAATGGATGGGTTCGCGCGGAGC 1199
Qy 1078 ATCCCGGATTCGCTCCCGTGAATGGCGGGCAACCCGACACCGACGTAATCTATGCT 1137
Db 1200 ATCCCGGATTCGCTCCCGTGAATGGCGGGCAACCCGACACCGGACGTAATCTATGCT 1259
Qy 1138 TTGCGCATGTGTCATCTCGGATGACAGGGCGCGGATGACGCAACGCTCGTCTCAGG 1197
Db 1260 TTGCGCATGTGTCATCTCGGATGACAGGGCGCGGATGACGCAACGCTCGTCTCAGG 1319
Qy 1198 CTCTCTCGAGCGGAAAGACCTTCAATGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1257
Db 1320 CTCTCTCGAGCGGAAAGACCTTCAATGACATTTTCGCCCTTCGCAACCAACCGCTTGGT 1379
Qy 1258 ATTGGCAATCAAGCAACGGTTCGCGCAAGTTAA 1293
Db 1380 ATTGGCAATCAAGCAACGGTTCGCGCAAGTTAA 1415

RESULT 5

US-08-391-339-6

; Sequence 6, Application US/08391339

; Patent No. 5463175

; GENERAL INFORMATION:

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co., B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-391-339-6

Query Match 97.1%; Score 1255.2; DB 1; Length 1296;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGTCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60

Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60

Qy 61 GGGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGCAACCTCCTGGC 120

Db 61 GGGCTGATGCTTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGCAACCTCCTGGC 120

Qy 121 GAAGTGATGCTTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCGTCCTATGTCC 180

Db 121 GAAGTGATGCTTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCGTCCTATGTCC 180

Qy 181 ATCCCGGAAACTTCACGAGCGTCCGAAAGTGGCTCCTTGACCCGAT-CGGCGCTTGTC 239

Db 181 ATCCCGGAAACTTCACGAGCGTCCGAAAGTGGCTCCTTGACCCGATGGGCGCTTGTC 240

Qy 240 ATCCCGTTCAGCTA-TTTCACACCATCATG-CCTGGTGTGATTTCGCTTTCTGTAGCCGA 297

Db 241 ATCCCGTTCAGCTA-TTTCACACCATCATG-CCTGGTGTGATTTCGCTTTCTGTAGCCGA 300

Qy 298 AGACCAACAGGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357

Db 301 AGACCAACAGGTGAAGGAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360

Qy 358 CCTCTGATCAAGTCAATTCGCGGAGGAGGCTGATGCGAGGCATCTGATCGGCCATGAAGT 417

Db 361 CCTCTGATCAAGTCAATTCGCGGAGGAGGCTGATGCGAGGCATCTGATCGGCCATGAAGT 420

Qy 418 CATCTGACCGGTATATCGTGAGAGACAGACTTCGCCAAGAGACCCGCGAGGTTCGGAACTG 477
Db 421 CATCTGACCGGTATATCGTGAGAGACAGACTTCGCCAAGAGACCCGCGAGGTTCGGAACTG 480
Qy 478 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGGATCGGTTCGCGGATTCGAT 537
Db 481 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGGATCGGTTCGCGGATTCGAT 540
Qy 538 CCGAACTTGTTCGATCGGTTCACCAAGGGATTCCTTATAGAAGAGACCGGTTCACACGAT 597
Db 541 CCGAACTTGTTCGATCGGTTCACCAAGGGATTCCTTATAGAAGAGACCGGTTCACACGAT 600
Qy 598 AATCCGAAGGGTCTGTGACCGCTTTCGCGGCTTTATCGGAAAGCGGTTCACACGAT 657
Db 601 AATCCGAAGGGTCTGTGACCGCTTTCGCGGCTTTATCGGAAAGCGGTTCACACGAT 660
Qy 658 GTATCTCGCGGTCTATCGCGCTTTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAAAC 717
Db 661 GTATCTCGCGGTCTATCGCGCTTTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAAAC 720
Qy 718 ACGAAACGGCTTTCGCGGTTCGACGCGGTTCGACGCGCGGCGCACACTCCAAATCA 777
Db 721 ACGAAACGGCTTTCGCGGTTCGACGCGGTTCGACGCGCGGCGCACACTCCAAATCA 780
Qy 778 CTTCGTAATTCGCTAGCGATGACATCCCGCTCGATACCGAAACGTTGATATCATATCCTC 837
Db 781 CTTCGTAATTCGCTAGCGATGACATCCCGCTCGATACCGAAACGTTGATATCATATCCTC 840
Qy 838 ATCCGGAATCCGGAAGCGCTCCACGATTCGACGACCGATGCGTTCAGGAAATTCATC 897
Db 841 ATCCGGAATCCGGAAGCGCTCCACGATTCGACGACCGATGCGTTCAGGAAATTCATC 900
Qy 898 GCGACACTTATGGAATGGGGTTCGCGGTTCGCGGTTCGCTGAGTTTCGCTGGGCTCACA 957
Db 901 GCGACACTTATGGAATGGGGTTCGCGGTTCGCGGTTCGCTGAGTTTCGCTGGGCTCACA 960
Qy 958 GCGGCTCTTAAGTGAACGTTGCGCATGTGCTCTATACGACGCTCGAAACTTCCTTCCA 1017
Db 961 GCGGCTCTTAAGTGAACGTTGCGCATGTGCTCTATACGACGCTCGAAACTTCCTTCCA 1020
Qy 1018 GCGGCTCTGCGGTTCGAGTTCGAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC 1077
Db 1021 GCGGCTCTGCGGTTCGAGTTCGAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC 1080
Qy 1078 ATCCCGGATTCGCTTCGCGGTTCGAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC 1137
Db 1081 ATCCCGGATTCGCTTCGCGGTTCGAGAACGATATTCGAAATGGATGGGTTCCGCGCGAGC 1140
Qy 1138 TTCCGCGCATGCTATCTCGCATGACAGGGGCGCGATGACCGAACGCTCGTCTCAGAG 1197
Db 1141 TTCCGCGCATGCTATCTCGCATGACAGGGGCGCGATGACCGAACGCTCGTCTCAGAG 1200
Qy 1198 CTCTCCGCGCGAAAGACCTCAATCGACATTCGCGCTTCGCAACCAACCGCTTTCGT 1257
Db 1201 CTCTCCGCGCGAAAGACCTCAATCGACATTCGCGCTTCGCAACCAACCGCTTTCGT 1260
Qy 1258 ATTGGCAATCCAGCAACCGGTTCGCGCAAGTTAA 1293
Db 1261 ATTGGCAATCCAGCAACCGGTTCGCGCAAGTTAA 1296

RESULT 6

US-08-484-274A-6
; Sequence 6, Application US/08484274A
; Patent No. 576760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6

Query Match 97.1%; Score 1255.2; DB 2; Length 1296;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGCTCAGAACCAACAAAGTAGGATCGCTCGAGCCGGAATCGTCGGCGTATGCACG 60
Db 1 ATGCTCAGAACCAACAAAGTAGGATCGCTCGAGCCGGAATCGTCGGCGTATGCACG 60
Qy 61 GCGGTGATGCTTTCAGCGCCGCGGATTCAAAGTCACTTGTATGACCGGAACCCCTCTGCG 120
Db 61 GCGGTGATGCTTTCAGCGCCGCGGATTCAAAGTCACTTGTATGACCGGAACCCCTCTGCG 120
Qy 121 GAAGGTGATGCTTTCGGAATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180
Db 121 GAAGGTGATGCTTTCGGAATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180
Qy 181 ATGCGCGGAACTTCAGAGCGTCCGAAAGTGGCTTCCTTGACCCGAT-GGGCCCTTGTCA 239
Db 181 ATGCGCGGAACTTCAGAGCGTCCGAAAGTGGCTTCCTTGACCCGATGCGGCGCTTGTCA 240
Qy 240 ATCCGGTTCAGCTA-TTTCACCAACCATCATG-CCTGGTGTGATTCGCTTCTGTTAGCCGGA 297
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTCTGTTAGCCGGA 300
Qy 298 AGACCAACAAAGGTGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Db 301 AGACCAACAAAGGTGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Qy 358 CCTCTGATCAAGTTCATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
Db 361 CCTCTGATCAAGTTCATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 418 CATCTGACCGGTATATCGTGAGAGACAGACTTCGCCAAGAGACCCGCGAGGTTCGGAACTG 477
Db 421 CATCTGACCGGTATATCGTGAGAGACAGACTTCGCCAAGAGACCCGCGAGGTTCGGAACTG 480
Qy 478 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGGATCGGTTCGCGGATTCGAT 537
Db 481 CGCGCTCTCAACGGTGTTCGACGACGATCTCAGCCCGGATCGGTTCGCGGATTCGAT 540
Qy 538 CCGAACTTGTTCGATCGGTTCACCAAGGGATTCCTTATAGAAGAGACCGGTTCACACGAT 597
Db 541 CCGAACTTGTTCGATCGGTTCACCAAGGGATTCCTTATAGAAGAGACCGGTTCACACGAT 600

QY 598 AATCCGCAAGGCGCTGTCGACCTCTTGTTCGGCGTTTATCCGCAACGGTCCGCAATTC 657
Db 601 AATCCGCAAGGCGCTGTCGACCTCTTGTTCGGCGTTTATCCGCAACGGTCCGCAATTC 660
QY 658 GTATCTGGCGGTGTCATCGCGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAAC 717
Db 661 GTATCTGGCGGTGTCATCGCGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAAC 720
QY 718 AGCAAGCGGTTCTGGCGGTGATCGAGCGTTGTCGAGCGCGGCGACACTCGAATCA 777
Db 721 AGCAAGCGGTTCTGGCGGTGATCGAGCGTTGTCGAGCGCGGCGACACTCGAATCA 780
QY 778 CTTGCTAATTCCTAGGCGATCACATCCGCTCGATACCGAAGCTGCGATATCATATCGTC 837
Db 781 CTTGCTAATTCCTAGGCGATGACATCCGCTCGATACCGAAGCTGCGATATCATATCGTC 840
QY 838 ATCGGGAATCCGGAAGCGCTCCAGCGATTCCGAGACCGATGCGTCAGGAAATTCATC 897
Db 841 ATCGGGAATCCGGAAGCGCTCCAGCGATTCCGAGACCGATGCGTCAGGAAATTCATC 900
QY 898 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTAGCGTTGAGTTGCGTGGGCTCACA 957
Db 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTAGCGTTGAGTTGCGTGGGCTCACA 960
QY 958 GCCGCTCCTAAGTGAAGCGTCGCGATGCTCTATACGACGCTCGAAGAACTTCTTCCA 1017
Db 961 GCCGCTCCTAAGTGAAGCGTCGCGATGCTCTATACGACGCTCGAAGAACTTCTTCCA 1020
QY 1018 GCCCTCGGCGCTCGAGTTCTGAAGAAGCATATTCGAATGATGGGTTCCGGCGGAGC 1077
Db 1021 GCCCTCGGCGCTCGAGTTCTGAAGAAGCATATTCGAATGATGGGTTCCGGCGGAGC 1080
QY 1078 ATCCCGGATTCGCTCCCGTGATTTGGCGGGCAACCGGACACCGACGTAATCTATGCT 1137
Db 1081 ATCCCGGATTCGCTCCCGTGATTTGGCGGGCAACCGGACACCGGACGTAATCTATGCT 1140
QY 1138 TTCGCGCATGTCATCTCGCATGACAGGGCGCGGATCACCGCAACGCTCGTCTCAGAG 1197
Db 1141 TTCGCGCATGTCATCTCGCATGACAGGGCGCGGATCACCGCAACGCTCGTCTCAGAG 1200
QY 1198 CTCCTCGAGGGAAGAACCTCAATCGACATTTCCGCCCTTCGCAACCAACGGCTTTGCT 1257
Db 1201 CTCCTCGAGGGAAGAACCTCAATCGACATTTCCGCCCTTCGCAACCAACGGCTTTGCT 1260
QY 1258 ATTGGAATCCAGCAACGGGTCGGCAAGTTAA 1293
Db 1261 ATTGGAATCCAGCAACGGGTCGGCAAGTTAA 1296

RESULT 7

US-08-391-339-7
; Sequence 7, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B44F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339

; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-391-339-7

Query Match 89.8%; Score 1160.8; DB 1; Length 1296;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;

QY 1 ATGTCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGCGTATGCAAG 60
Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTATGCAACT 60
QY 61 GCGCTGATGCTTCAGCGCCGCGGATTTCAAAGTCACCTTGAATGACCCGCAACCTCTGCG 120
Db 61 GCTTTGATGCTTCAACGTCGTGGATTTCAAAGTCACCTTGAATGACCCGCAACCTCTGCG 120
QY 121 GAAGGTGCACTCTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGCTCCCTATGTCC 180
Db 121 GAAGGTGCACTCTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGCTCCCTATGTCC 180
QY 181 ATCCGCGGGAACCTTGACGAGCGTGGCGAAGTGGCTCTTGGAGCCGATG -GGGCGGTTGTCA 239
Db 181 ATCCGCGGGAACCTTGACGAGCGTGGCGAAGTGGCTCTTGGAGCCGATG -GGGCGGTTGTCA 240
QY 240 ATCCGCTTCAGCTA-TTTCACCAACCATCATG-CCTGTTGATTCGCTTCTGTTAGCCGA 297
Db 241 ATCCGCTTCAGCTA-TTTCACCAACCATCATG-CCTGTTGATTCGCTTCTGTTAGCCGA 300
QY 298 AGACCAAAACAGGTGAGGAGCAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAAAACAGGTGAGGAGCAGCGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
QY 358 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 417
Db 361 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
QY 418 CATCTGACCGTATATCGTGGAGAACGACACTTTCGCAAGAGCCGCGAGGTTGGGAATC 477
Db 421 CATCTGACCGTATATCGTGGAGAACGACACTTTCGCAAGAGCCGCGAGGTTGGGAATC 480
QY 478 CGGCGTCTCAACGGTCTTCGCGACGAGATCTTCAGCGCCGATGCGTTGCGGATTCGAT 537
Db 481 CGGCGTCTCAACGGTCTTCGCGACGAGATCTTCAGCGCCGATGCGTTGCGGATTCGAT 540
QY 538 CCGAACTTGTGCTGCTGTTTACCAAGGCGATTCTTATAGAGAGAACGGTCCACAGATT 597
Db 541 CCTAACTTGTGCTGCTGTTTACCAAGGCGATTCTTATAGAGAGAACGGTCCACAGATT 600
QY 598 AATCCGCAAGGCGCTCGTGACCTCTTGTTCGGCGTTTATCCGCAACGGTCCGCAATTC 657
Db 601 AATCCGCAAGGCGCTCGTGACCTCTTGTTCGGCGTTTATCCGCAACGGTCCGCAATTC 660
QY 658 GTATCTGCGCGTGTCACTCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAAC 717
Db 658 GTATCTGCGCGTGTCACTCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAAC 717

Db	661	GTATCTCGCGCTGTATCGGTTTGTGAGACTGAAGTGGTGTCTCTCAAGAGCATTTACAACC	720
Qy	718	ACGAACGGCGTTCTGGCCGTTTCATCGACGGGTTGTGCAGACGGCGCACACTCGAAATCA	777
Db	721	AC"AAACGGTGTCTGGCTGTTCATCGACGTTGTTCGTGAGCTGGTGCACACTCTAAATCA	780
Qy	778	CTTTGCTAATTTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	837
Db	781	CTTTGCTAATTTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840
Qy	838	ATCGCGAATTCGGGAACCGCTCCACGCATTTCCGACGACCGATGGGTTCAGGAAAAATTCATC	897
Db	841	ATCGCGAATTCGGGAACCGCTCCACGCATTTCCGACGACCGATGGGTTCAGGAAAAATTCATC	900
Qy	898	GCACACACTATGGAATTGGGGCTTCGCGTGGCGGTTACGGTTGAGTTCCGCTGGGCTCACAC	957
Db	901	GCACACACTATGGAATTGGGTCTTCGTGTTCGTGCTACTGTTGAGTTTGCTGGTCTCACAC	960
Qy	958	GC CGCTCCTAACTGGAACGTCGGGATGTGCTCTATACGCACGCTCGAANAACCTCTTCCCA	1017
Db	961	GCTGCTCCTAACTTGGAAAGTCGGCATGTGCTCTATACGCACGCTCGAANAACCTCTTCCCA	1020
Qy	1018	GCCTTCGCGCTCGCAGTTC"TGAAAGACGATATCCAAATGAGTGGGTTC"CCGCGCCGAC	1077
Db	1021	GCCTTCGCGCTCGCAGTTC"TGAAAGACGATATCCAAATGAGTGGGTTC"CGTCTAGC	1080
Qy	1078	ATCCCGGATTCGCTCCCGCTGATTTGGCGGGCAACCCGGACACCCGACGTAATCATGCT	1137
Db	1081	A"TTCC"TA"TTCTTC"TCAGTGAT"TGCTCGTGAAC"TCGTACACCGACGTAATCTATGCT	1140
Qy	1138	TTCGGCCATGGTCATCTCCGGCATGACAGGGGCGCGGATGACCGCAACGCTCGTCTCAGAG	1197
Db	1141	TTT"GGT"CAAGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAAC"TC"CGTCTCAGAG	1200
Qy	1198	CTCCTTCGACGGCGAAAGACCTCAATTCGACATTTTCGCCCTTC"TGCAACCAACCGCTTTTGGT	1257
Db	1201	CTCCTTCGACGGCGAANAAGACCTCAATTCGACATTTTCGCCCTTC"TGCAACCAACCGCTTTTGGT	1260
Qy	1258	ATTGGCAAAATCCAAAGCAACCGGTCCGGCAAGTTAA	1293
Db	1261	ATTGGCAAAATCCAAAGCAACCGGTCCGGCAAGTTAA	1296

RESULT	8	
US-08-484-274A-7		
: Sequence 7, Application US/08484274A		
: Patent No. 5776760		
: GENERAL INFORMATION:		
: APPLICANT: Kishore, Ganesh M.		
: APPLICANT: Barry, Gerard F.		
: TITLE OF INVENTION: Glyphosate Tolerant Plants		
: NUMBER OF SEQUENCES: 33		
: CORRESPONDENCE ADDRESS:		
: ADDRESSEE: Arnold, White & Durkee		
: STREET: P.O. Box 4433		
: CITY: Houston		
: STATE: Texas		
: COUNTRY: USA		
: ZIP: 77210-4433		
: COMPUTER READABLE FORM:		
: MEDIUM TYPE: Floppy disk		
: COMPUTER: IBM PC compatible		
: OPERATING SYSTEM: PC-DOS/MS-DOS		
: SOFTWARE: PatentIn Release #1.0, Version #1.25		
: CURRENT APPLICATION DATA:		
: APPLICATION NUMBER: US/08/484,274A		
: FILING DATE: 07 June 1996		
: CLASSIFICATION: 435		
: ATTORNEY/AGENT INFORMATION:		
: NAME: Patterson, Melinda L.		
: REGISTRATION NUMBER: 33,062		
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A		
: TELECOMMUNICATION INFORMATION:		

Db 841 ATCCGGAATCCGAAAGCCCTCCACGCATTCGACGACCGATCCGTCAGGAAATTCATC 900
QY 898 GCGACACCTATGAAATGGGGCTTCGGGTGGGGGTACGGTTGAGTTGCTGGGCTCACA 957
Db 901 GCGACACCTATGAAATGGGGCTTCGGTTGCTGGTACTGTTGAGTTTCTGGTCTCACA 960
QY 958 GCGGCTCCTAACTGGAAGCTGGCATGTCCTATACGACGCTCGGAAACTTCCTTCCA 1017
Db 961 GCTGCTCCTAACTGGAAGCTGGCATGTCCTATACGACGCTCGGAAACTTCCTTCCA 1020
QY 1018 GCGCTCGGCTCGGAGTTCTGAAGAACGATATTCMAATGGATGGGTTCGGCGCGAGC 1077
Db 1021 GCGCTCGGCTCGGAGTTCTGAAGAACGATATTCMAATGGATGGGTTCGGCTCAGC 1080
QY 1078 ATCCGGGATTCGCTCCCGCTGATTTGGCCGGGCAACCCGGACACCGACATATCTATGCT 1137
Db 1081 ATTCCTGATTCCTTCCAGTATGGTCTGCAACTCGTACACCGACGCTAATCTATGCT 1140
QY 1138 TTCGCCATGGTCATCTCGGCATGACAGGGCGCGCATGACCGCAACGCTCTCTCAGAG 1197
Db 1141 TTGCTCAGGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCTCTCAGAG 1200
QY 1198 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTGCGCCCTTCGCACCAAAACGCTTTGCT 1257
Db 1201 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTGCGCCCTTCGCACCAAAACGCTTTGCT 1260
QY 1258 ATTGCAATCCCAAGCAACGGGTCGGCAAGTTAA 1293
Db 1261 ATTGCAATCCCAAGCAACGGGTCGGCAAGTTAA 1296

RESULT 9

US-08-391-339-8
: Sequence 8, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. B4JF
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-8
Query Match 71.8%; Score 928.8; DB 1; Length 1296;
Best Local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;
QY 1 ATGCTGTGAGAACACAAAAAAGTAGGCATCGGTGGAGCGGAATCGTCGCGGTATGCACG 60
Db 1 ATGGCTGTGAGAACACAAAGAGGTTCGTATCGCTGGAGCTTGAATCGTTGGTTTGCACCT 60
QY 61 GCGCTGATGCTTCAGCGCCCGCGGATTCAAAGTACCTTGTATGACCGCAACCCCTCTTGGC 120
Db 61 GCTTTGATGCTTCACGCTGCTGGATTCAGAGTTACCTTGTATGATCCAAACCCACCAAGT 120
QY 121 GAAGGTGCAATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCTC 180
Db 121 GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTTCCGTTGTTCCTCAATGTCTC 180
QY 181 ATGCCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGG-CGGTTGTCA 239
Db 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTTGCTC 240
QY 240 ATCCCGTTTCAGCTA-TTTCACCAACCATCATGCC-TGGTTGATTCGGTTTCTGTTAGCCGGA 297
Db 241 ATCCCGTTTCAGCTACTTTCACCAACCATCATGCCTTGGTTGATTCGGTTTCTGTGCTGGA 300
QY 298 AGACCAAAACAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACCTGTG 360
QY 358 CTTCTGATCAAGTCATTTGCGGAGGAGGTGATGCGAGCGCATCTGATCGCCCATGAAGGT 417
Db 361 CTTTGTATCAAGTCTTGGCTGAGGAGGTGATGCTAGCCACCTTATCCGTACAGAGGT 420
QY 418 CATCTGACCGTATATCGTGGAGAACAGACTTTCGCAAGGACCGCGGAGGTTCGGAACTG 477
Db 421 CACCTTACCGTGTACCGTGGAGAACAGACTTTCGCAAGGACCGCGTGGAGGTTCGGAACTT 480
QY 478 GCGGCTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCCGATCGCTTGGCGGATTTCCGAT 537
Db 481 CGTGTCTCAACGGTGTTCGTAACAATCCTCAGCGCTGATGCAATGGGTGATTTCCGAT 540
QY 538 CGGAATTTGTCGATCGCTTTACCAAGGCAATCTTTATAGAAGAGAACGCTCACAGATT 597
Db 541 CCTAATTTGTCACGCTTTACCAAGGCAATCTTTATCGAAGAGAACGCTCACACCATC 600
QY 598 AATCCCAAGGGCTCGTGACCTCTTTGTTTGGCGGTTTATTCGCGAACGGTTCGCGAATTC 657
Db 601 AACCACAAAGGTCTCGTGACTCTCTTTGTTTGGTTCGTTTCATCGCTAACCGGTGGAGGTTT 660
QY 658 GTATCTGCGGTCTCATCGCTTTGAGACTTGAAGGTAGGGCGCTTAAGCGCATTTACAACC 717
Db 661 GTGTCTGCTGTGTTATCGGATTCGAGACTGAAGGTGAGTCTCTCAAGGGGTATCACACCC 720
QY 718 AGAAGCGGCTTCTGGCGGTTGATGACGCGGTGTGCGACGCGCGCACACTCGAAATCA 777
Db 721 ACCAAGGTGTCTTGTCTGTTGATGACGCTGTTGTTGACGCTGGTGCACACTCCAAGTCT 780
QY 778 CTTGCTTAATTCGTAGGCGATGACATCCCGCTCGATACCGAACGGTGGATATCATATCGTC 837
Db 781 CTTGCTAATTCCTTGGTGTGATGACATCCCATTTGGATACCGAACGGTGGATACCATCGTG 840
QY 838 ATCCGGAATCCGGAACCCCTCCACCCATTCGACACCGATCGCGTACAGAAATTCATC 897
Db 841 ATCCGCAACCCAGAGCTCTCCACGATATTCACACTACCGATGCTCTTCTGAAAGTTTCATC 900
QY 898 GCGACACCTATGGAATGGGCTTCGCGTGGGGGTACGGTTGAGTTGCTGGGCTGCACA 957
Db 901 GCTACTCTTATGGAGATGGGTCTTCTCGTGTTCGTAACCGCTTGGATTCTGCTGCTCACT 960

QY 1138 TTCGGCCATGTCATCTCGGCATGACAGGGGCGCGATGACCGCAACGGTCGCTCTCAGAG 1197
Db 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTCTCAATACCGCAACCGTCGTTTCTCAG 1200
QY 1198 CTCCTCGCAGGGGAAAGACCTCAATCGACATTTCCGCCCTTCGCCACCAACCGCTTTCGT 1257
Db 1201 CTCCTCGCAGGGTGAGAGACCTCTATCGACATCTCTCCANTTCGCACCAACCGCTTCGT 1260
QY 1258 ATTGGCAATCCCAAGCAACGGGCTCCGCCAAGTTAA 1293
Db 1261 ATTGGTAAGTCCCAAGCAAACTGGTCTGCATCCTAA 1296

RESULT 11
US-08-391-339-17
; Sequence 17, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1296
US-08-391-339-17

Query Match 71.6%; Score 925.6; DB 1; Length 1296;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;
QY 1 ATGCTGAGACCAAAAGTAGGATCGCTGGAGCGGGAATCGTCGGCGATGTCAGG 60
Db 1 ATGCTGAGAACCAAGAAAGTTGCTATCGCTGGAGCTGGAATCGTTGGTTCCT 60
QY 61 CGCGTGATGCTTCAGCGCGCGGATTCAGAGTCACCTTGATTGACCCGNAACCCCTCCTGGC 120

Db 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTTACCTTGATTGATCCAAACCCACCAAGGT 120
QY 121 GAAGGTGCATCTCTTTGGGAATGCCGATGCTTCAACGGGCTCATCGCTCGCTCCCTATGTCC 180
Db 121 GAAGGTGCCTCTTTTCGGTTAACGCTGGTTCCTTCAACGGGTTCCCTCGCTTCAATGTCC 180
QY 181 ATGCGGGGAAATTTGACGAGCGTGCCGAAGTGGCTCTTTGACCCGATGGG - CCGTTGTCA 239
Db 181 ATGCCAGGAATAATTGACTAGCGTTCCAAAGTGGCTTCTTTGACCCAAATGGGTCATGTGCC 240
QY 240 ATCCGGTTTCAGCTA - TTTTCCAAACCATCAAGCC - TGGTTGATTTTCGGTTTCGTAGCCGCA 297
Db 241 ATCCGGTTTCGGCTACTTTCCAAACCATCATGCGCTTGTTGATTTCGTTCTTTCGTGCTGA 300
QY 298 AGACCAACAAGGTGAAGGAGCAGCGCAAGACACTTCGCCCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTTAACTCATCAAGTCCACTGTG 360
QY 358 CCTCTGATCAAGTCATTTGGCGAGGAGGCTGATGGAGGCCATCTGATCCGCCATGAAGT 417
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACTTATTCGTCACGAAGGT 420
QY 418 CATCTCACCGTATATCGTCGAAAGCAGACTTCGCCAAGGACCGCGGAGGTTTGGGAACGT 477
Db 421 CACCTTACCGGTGACCGTGGAGAGCAGACTTCGCCAGGACCGCTGGAGGTTGGGAACFT 480
QY 478 CGGCGTCTCAACGGTGTTCGCACGAGATCCCTCAGCGCCGATGCGCTTTCGGGATTTTCGAT 537
Db 481 CGTCTCTCAACGGTGTTCGTTACTCAATCCCTCAGCGCTGATGCTTTCGCTCATTTTCGAT 540
QY 538 CCGAATTTGTCGATCGCTTTTACCAAGGCAATCTTATAGAGAAACGGTCACACGATT 597
Db 541 CCTAACTTGTCTCACGCCCTTTTACCAAGGGAATCCCTATTCGAAGAGAACGGTCACACCAATC 600
QY 598 AATCCGAAGGCTCGTGACCCCTCTTGTTCGGCGCTTTTATCGCGAAGCGGTGCGCAATTC 657
Db 601 AACCCACAAGGTTCTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACCGTTGGAGAGTTTC 660
QY 658 GTATCTGCGCGTGTATCGGCTTTTTCGACTGAAGGTAGGGCGCTTAAAGGCAATTCACACC 717
Db 661 GTGCTCTCGTGTGTATTCGGATTTCGAGACTGAAGGTTCGTTGCTCAAGGGTATCACCACC 720
QY 718 ACGAAGGGGTTCTGCGCGTTGATGACGGGTTTTCGCGAGCGCGCGCACACTCGAANTCA 777
Db 721 ACCAAGGGTGTCTTCTGCTGTTGATGACAGCTGTGTTCGACAGTGGTCCACACTCCAAGTCT 780
QY 778 CTTCGCTAATTCGCTAGGGGATGACATCCCGCTCGATACCGAAGCTGGGATATCATATCGTC 837
Db 781 CTTCGCTAATTCCTTGGTGGTCTTCTGCTGTTGCTGGAACCGTTGAGTTTCGCTGCTCACT 840
QY 838 ATCGGGAATCCGGAAGCGCTCCACGCCATTCGCGAGACCGGCTCAGGAAATTCATC 897
Db 841 ATCGCAACCCAGAGCTGCTCCACGATTTCCAACTACCGATGCTTCTCGAAAGTTTCATC 900
QY 898 GCGACACCTATGGAATGGGGCTTCGCGTGGGGGTACGGTTGAGTTTCGCTGGGTTCACA 957
Db 901 GCTACTCCTATGAGATGGGTCTTCTGCTGTTGCTGGAACCGTTGAGTTTCGCTGCTCACT 960
QY 958 GCGGCTCCTTAACGTGGAAGCTGCGGATGTCCTTATACGACGCTCGGAAACCTCTTCCA 1017
Db 961 GCTGCTCCTTAACGTGGAAGGCTGCTCAGCTTCTTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020
QY 1018 GCGCTCGGCGCTTCGAGTTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGGCGCGAGC 1077
Db 1021 GCTCTCGCTCCTGCCAGTTCTCAAGAACGTTTACTCCAAGTGGATGGGTTTCGCTCCAAGC 1080
QY 1078 ATCCCGGATTCGCTCCCGTGTATTTGGCGGGCAACCGGAGACACCGACGCTATATCTATGCT 1137
Db 1081 ATCCCGGATTCCTCTTCCAGTGTATGCTGCTGCTAGCCGCTACTCCAGACGCTTATCTACGCT 1140
QY 1138 TTTCCGCGATGGTTCATCTCGGATGACAGGGCGCGGATGACCGCAACCGCTCCTCTCAGAG 1197
Db 1141 TTCGGTCAGGGTCACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCCTTCTGAG 1200

QY 1198 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAAAACCCGTTTGGT 1257
Db 1201 CTCCTCGCAGGTGAGAAAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCCGTTTCGGT 1260
QY 1258 ATTGGCAATCCAAAGCAAAAGCGTCCGGCAAGTTAA 1293
Db 1261 ATTGGTAAGTCCAAGCAAAAGCTGGTCTGTCATCCCTAA 1296

RESULT 12

US-08-484-274A-17
: Sequence 17, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1296

US-08-484-274A-17

Query Match 71.6%; Score 925.6; DB 2; Length 1296;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 1084; Conservative 0; Mismatches 209; Indels 3; Gaps 3;

QY 1 ATGCTGAGAACCAACAAAAGTAGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60
Db 1 ATGGCTGAGAACCAACAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCACAT 60
QY 61 GGGCTGATGCTTACGGCGCGGGATTCAAAGTCACTTGAATGACCCGAAACCTCTCTGGC 120
Db 61 GCTTTGATGCTTCAACGTCGTGATTCAAGGTTACCTTGATTGATCAAAACCCACCAGGT 120
QY 121 CAAGCTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCGTCTGTCCTTATGTCC 180
Db 121 GAAGGTGGCTCTTTCGGTAAACGCTGGTGTCTCAACGGTTCTCTCGTTGTTCCTCAATGTC 180
QY 181 ATGCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCTTACCGCGATGGG -CGGTTGTCA 239
Db 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCATTTGTCC 240

QY 240 ATCCGGTTTCAGCTA -TTTCCAACCATCATGCC -TGGTTGATTTCGTTTCTGTTAGCCGA 297
Db 241 ATCCGTTTCGGCTACTTTTCCAACCATCATGCC -TGGTTGATTTCGTTTCTGTTAGCCGA 300
QY 298 AGACCAAAACAGGTGAAGGAGCAGCGGAAACGACTTCGCAATCTCATCAAGTCCACGGTG 357
Db 301 AGACCAAAACAGGTGAAGGAGCAGCTAAGGCACCTCCGCTAACCTCATCAAGTCCACACTGTG 360
QY 358 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATGGAGCCATCTGATCCGCCATGAAGGT 417
Db 361 CCTTTGATCAAGTCTTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
QY 418 CATCTGACCGGTATATCGTGGAGAAAGACAGCTTCGCCAAGGACCGCGAGGTTGGAACTG 477
Db 421 CACCTTACCGGTGTACCGTGGAGNAGCAGACTTCGCCAGGAGCGGTGGAGGTTGGAACTT 480
QY 478 CGGGCTCTCAACGGGTTCGCGACGACAGATCTCAGCGCGGATGCGTTGCGGGAATTCGAT 537
Db 481 CGTCTCTCAACGGGTTCGCTACTCAATCCTCAGCGCTGATGCAATTCGTTGATTCGAT 540
QY 538 CGAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAGAGAGACGGTCCACAGGAT 597
Db 541 CTTAACTTGTCTACGCTTTTACCAAGGGAATCTCTATCGAAGAGAGACGGTCCACACCATC 600
QY 598 AATCCGCAAGGGTCTGTGACCCCTCTTGTTCGGCGGTTTATCGCGAACCGTGGGAAATTC 657
Db 601 AACCCACAAGGTCGTGAGACTCTCTTGTTCGTCGTTTCATCGCTAAGGGTGGAGAGTTC 660
QY 658 GTATCTCGCGGTGTATCGCGGTTTGGAGACTGAAGTAGGGCGCTTAAAGGCAATTCACAC 717
Db 661 GTGTCTCTGCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
QY 718 ACGAAGCGGTCCTGCGCGTGTGATGACGCGGTTCTGCGAGCGCGCGCACACTCGAATCA 777
Db 721 ACCAAGCGTGTCTTGTCTGTTGATGACGCTGTTTGCAGCTGTGTCACACTTCCAAGTCT 780
QY 778 CTTTCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCTCTC 837
Db 781 CTTGCTAACTCCCTTGGTGATGACATCCCATCCATTCGATACCGAAGCTGGATACCATCTG 840
QY 838 ATCGGAATCCGGAAGCGGCTCCACGCAATTCGAGACCGGATGCGTCAAGAAAATTCATC 897
Db 841 ATCGCAACCCAGAGCTGCTCCACGTAJTCCAACTACCGATGCTTCTGGAAGTTTATC 900
QY 898 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTGAGTTGAGTTCGCTGGGCTCACA 957
Db 901 GCTACTCTATGGAGATGGGTCTTCTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
QY 958 GCGCTCTTAACCTGGAACGTCGCGCATGTGCTCTATACGACGCTCGAATAACTTCTTTCCA 1017
Db 961 GCTGCTCTTAACCTGGAAGCGTGTCTACGCTTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020
QY 1018 GCCTTCGCGCTGGAGTCTTCTGAAGACGATATTTCCAAATGGATGGGTTCCGGCGGAGC 1077
Db 1021 GCTCTGCTCTCTGCCAGTCTTGAAGAACGTTACTTCCAAGTGGATGGGTTCCCGTCCAAGC 1080
QY 1078 ATCCCGGATTCGCTCCCGGTGATTGGCGGCAACCCGACACCCGACGTAATCTATGCT 1137
Db 1081 ATCCCGGATTCCTTCCAGTGATTTGGTGTGCTACCGCTACTCCAGAGGTTATCTACGCT 1140
QY 1138 TTCGGCCATGGTCTATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCTGCTCAGAG 1197
Db 1141 TTCGGTCACGTCACGTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200
QY 1198 CTCTCTCGCAGGCAAAAGACCTCAATCGACATTTTCGGCCCTTCGCAACCAACCCGTTTGGT 1257
Db 1201 CTCTCTCGCAGGTGAGAAAGACCTCTATCCACATCTCTCCATTCGCAACCAACCCGTTTGGT 1260
QY 1258 ATTGGCAAAATCCAAAGCAAAAGCGGTCGGCAAGTTAA 1293
Db 1261 ATTGGTAAGTCCAAGCAAAAGCTGGTCTGTCATCCCTAA 1296

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RESULT      14
US-08-484-274A-30
: Sequence 30, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-33

Query Match      4.2%; Score 54.6; DB 1; Length 69;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 60; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1125 CGTAATCTATGCTTTTCGGCCATGTCATCTCGGCATGACAGGGGGCCCGCATGACGCCAAC 1184
      |||||||
Db 1 CGTAATCTATGCTTTTCGGCCATGTCATCTCGGCATGACAGGGGGCCCGCATGACGCCAAC 60
      |||||||

Qy 1185 GCTCGTCTC 1193
      |||||||
Db 61 TCTCGTCTC 69
```

Search completed: January 1, 2001, 03:17:38
Job time: 29282 sec

GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2000, 18:03:01 ; Search time 3327.86 Seconds
(without alignments)
2402.255 Million cell updates/sec

Title: US-08-484-274-4

Perfect score: 1293

Sequence: 1 ATCTCAGAACCAACAAAA.....AAACGGGTCGGCAAGTTAA 1293

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_estl1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*
- 12: gb_est12:*
- 13: gb_est13:*
- 14: gb_est14:*
- 15: gb_est15:*
- 16: gb_est16:*
- 17: gb_est17:*
- 18: gb_est18:*
- 19: gb_est19:*
- 20: gb_est20:*
- 21: gb_est21:*
- 22: gb_est22:*
- 23: gb_est23:*
- 24: gb_est24:*
- 25: gb_est25:*
- 26: gb_est26:*
- 27: gb_est27:*
- 28: gb_est28:*
- 29: gb_est29:*
- 30: gb_est30:*
- 31: gb_est31:*
- 32: gb_est32:*
- 33: gb_est33:*
- 34: gb_est34:*
- 35: gb_est35:*
- 36: gb_est36:*
- 37: gb_est37:*
- 38: gb_est38:*
- 39: gb_est39:*
- 40: gb_est40:*
- 41: em_estba:*
- 42: em_estfun:*
- 43: em_esthum1:*

44: en_esthum2:*

45: en_esthum3:*

46: en_esthum4:*

47: en_esthum5:*

48: en_esthum6:*

49: en_esthum7:*

50: en_esthum8:*

51: en_esthum9:*

52: en_esthum10:*

53: en_esthum11:*

54: en_esthum12:*

55: en_esthum13:*

56: en_esthum14:*

57: en_esthum15:*

58: en_esthum16:*

59: en_esthum17:*

60: en_esthum18:*

61: en_esthum19:*

62: en_esthum20:*

63: en_estin1:*

64: en_estin2:*

65: en_estin3:*

66: en_estin4:*

67: en_estom:*

68: en_estovi:*

69: en_estov2:*

70: en_estpl1:*

71: en_estpl2:*

72: en_estpl3:*

73: en_estpl4:*

74: en_estpl5:*

75: en_estro1:*

76: en_estro2:*

77: en_estro3:*

78: en_estro4:*

79: en_estro5:*

80: en_estro6:*

81: en_estro7:*

82: en_estro8:*

83: en_estro9:*

84: en_estro10:*

85: en_estro11:*

86: en_estro12:*

87: en_estro13:*

88: gb_gss1:*

89: gb_gss2:*

90: gb_gss3:*

91: gb_gss4:*

92: en_gss1:*

93: en_gss2:*

94: en_gss3:*

95: en_gss4:*

96: gb_gss5:*

97: gb_gss6:*

98: gb_gss7:*

99: gb_gss8:*

100: gb_gss9:*

101: en_gss5:*

102: en_gss6:*

103: en_gss7:*

104: en_gss8:*

105: en_gss9:*

106: en_gss10:*

107: en_gss11:*

108: gb_gss10:*

109: gb_gss11:*

110: en_gss12:*

111: gb_gss12:*

112: gb_gss13:*

113: gb_gss14:*

114: gb_gss15:*

115: gb_gss16:*

116: gb_gss17:*

117: gb_gss18:*
118: gb_gss19:*
119: em_gss13:*
120: gb_gss20:*
121: gb_gss21:*
122: gb_gss22:*
123: gb_gss23:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.4	3.4	434	124	Pl149R
C 2	37.4	2.9	702	96	AQ328054 Leishmania
C 3	36.4	2.8	634	19	AQ328054 nbx00421
C 4	36	2.8	380	22	AW097371 rs43a11.y
C 5	36	2.8	389	22	AW500960 UI-HF-BP0
C 6	36	2.8	895	123	AW501280 UI-HF-BP0
C 7	35.4	2.7	226	5	AL307658 Tetraodon
C 8	35	2.7	360	16	AA644181 ab63a02.s
C 9	35	2.7	360	16	AV190084 AV190084
C 10	35	2.7	382	36	C47876 C47876 Yuj1
C 11	34.8	2.7	171	17	AV386799 AV386799
C 12	34.8	2.7	171	17	AV316270 AV316270
C 13	34.8	2.7	205	18	AV413471 AV413471
C 14	34.8	2.7	251	18	AV418303 AV418303
C 15	34.8	2.7	271	24	AW19954 LjNEST12e
C 16	34.8	2.7	273	18	AV427698 AV427698
C 17	34.8	2.7	300	18	AV406977 AV406977
C 18	34.8	2.7	349	18	AV412853 AV412853
C 19	34.8	2.7	416	18	AV425451 AV425451
C 20	34.8	2.7	423	18	AV407852 AV407852
C 21	34.6	2.7	452	18	AV423367 AV423367
C 22	34.6	2.7	429	18	AV408636 AV408636
C 23	34	2.6	258	39	W09527 W09527
C 24	34	2.6	261	36	D40242 D40242
C 25	34	2.6	425	7	AA871231 AA871231
C 26	34	2.6	433	21	AA542047 AA542047
C 27	34	2.6	614	21	AW254765 AW254765
C 28	33.8	2.6	636	97	AQ447252 AQ447252
C 29	33.8	2.6	296	16	AV139416 AV139416
C 30	33.8	2.6	360	36	C41677 C41677 Yuj1
C 31	33.8	2.6	935	123	CNS03IPN
C 32	33.6	2.6	409	35	BE411304 BE411304
C 33	33.6	2.6	460	15	AU088715 AU088715
C 34	33.6	2.6	724	35	BE454097 BE454097
C 35	33.2	2.6	353	36	C13125 C13125 Yuj1
C 36	33.2	2.6	398	15	AU082174 AU082174
C 37	33.2	2.6	494	14	AL387587 AL387587
C 38	33.2	2.6	676	34	BE248875 BE248875
C 39	33	2.6	472	36	BE516792 BE516792
C 40	33	2.6	884	123	CNS03K34
C 41	32.8	2.5	222	19	AV536254 AV536254
C 42	32.8	2.5	311	24	AW735014 AW735014
C 43	32.8	2.5	400	14	AL364994 AL364994
C 44	32.8	2.5	427	18	AV426876 AV426876
C 45	32.8	2.5	587	25	AW916227 AW916227

ALIGNMENTS

RESULT 1
Pl149R/c

LOCUS DEFINITION	Pl149R	434 bp	DNA	GSS	16-MAR-2000
Leishmania major Friedlin PAC Pl49 right end-sequence, genomic survey sequence.					
ACCESSION	AL160534				
VERSION	AL160534.1	GI:7258935			
KEYWORDS	GSS.				
SOURCE	Leishmania major.				
ORGANISM	Leishmania major				
REFERENCE	1 (bases 1 to 434)				
AUTHORS	Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.				
TITLE	A physical map of the Leishmania major Friedlin genome				
JOURNAL	Genome Res. 8 (2), 135-145 (1998)				
MEDLINE	98146435				
REFERENCE	2 (bases 1 to 41)				
AUTHORS	Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk				
COMMENT	see http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/Lmajor/ The primer sequence can be obtained from alicat@sanger.ac.uk.				
FEATURES	Location/Qualifiers				
source	1. .434				
	/organism="Leishmania major"				
	/strain="Friedlin"				
	/db_xref="taxon:5664"				
	/clone="PAC Pl49"				
BASE COUNT	76 a 131 c 157 g 70 t				
ORIGIN					
Query Match	3.4%;	Score 44.4;	DB 124;	Length 434;	
Best Local Similarity	54.2%;	Pred. No. 0.02;			
Matches	90;	Conservative	0;	Mismatches	76;
				Indels	0;
				Gaps	0;
Qy	34	GGACCGGAATCGTCGGCGTATGCAGCGCGTGTGATGCTTCAGCGCGCGGATTCAAATGC	93		
Db	357	GGCGCGCGCATTCGCGTGTGTCAGCACCGCATCGGCCCTCGCGCGGCGGCGGCGGTC	298		
Qy	94	ACCTTGATGACCGAACCCCTCTCGGCGAAGTGCATCGTTGGGAATGCCGGATGCTTC	153		
Db	297	GTTCTTGTGATCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCATC	238		
Qy	154	AACGGCTCATCGTCGTCCTTCATGTCATGTCGCGGGAATGCGGAACTTGACCA	199		
Db	237	CAGCGCGAGGCGGTGCAGCGCGTATCGTTCCCGCGGCGGCGGCGGCGGCTTCATC	192		
RESULT 2					
AQ328054/c					
LOCUS	AQ328054	702 bp	DNA	GSS	08-JAN-1999
DEFINITION	nbx0042102f CUGI Rice BAC Library Oryza sativa genomic clone				
ACCESSION	nbx0042102f				
VERSION	AQ328054.1	GI:4119904			
KEYWORDS	GSS.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				
REFERENCE	1 (bases 1 to 702)				
AUTHORS	Wing,R.A. and Dean,R.A.				
TITLE	A BAC End Sequencing Framework to Sequence the Rice Genome				
JOURNAL	Unpublished (1998)				
COMMENT	Contact: Wing RA Clemson University Genomics Institute				

Qy 1230 TTTCGGCCCTTCGCACCAAC 1248
197 GACGGCAGGCTCTCCATCTGGGTCGAGAGAGAGCGCCGCTCACCAT 236

note: organ: lung, vector: pIREScript SK⁺, site: 1: Ecom
; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Small cell carcinoma cell line NCI-H69. Average


```

/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/notes="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; Isolate-Miyakojima MG-20"

BASE COUNT      61 a      76 c      55 g      59 t
ORIGIN

Query Match      2.7%; Score 34.8; DB 18; Length 251;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 4 TCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGCGAATCGTCGGCGTATGCACGGCG 63
    || || || || || || || || || || || || || || || || || || || || ||
Db 11 TCGCGGACGACAGAGATTCTGTACCGCGGCGTGC CGCGCTTCATCGGCACCTCACACGGTG 70
    || || || || || || || || || || || || || || || || || || || || ||

QY 54 CTGATGCTTCAGCGCCGGGATTCAAAGTCACCTTGATTGAC 105
    | ||||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 GTTCAGCTTCCCATGACGGCTTCATGCTCCATGCTCCATCATCGAC 112
    || ||||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
AW719954      271 bp      mRNA      EST      19-APR-2000
LOCUS      LJNESt122r Lotus japonicus nodule library 5 and 7 week-old Lotus
DEFINITION      japonicus cDNA 5', mRNA sequence.
ACCESSION      AW719954
VERSION      AW719954.1 GI:7614480
KEYWORDS      EST.
SOURCE      Lotus japonicus.
ORGANISM      Lotus japonicus
Eukaryote; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
1 (bases 1 to 271)
Colebatch,G., Freund,S., Trevasakis,B and Udvardi,M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mplp-golm.mpg.de
Seq primer: T7
High quality sequence stop: 271.
FEATURES
    source
        1..271
            /organism="Lotus japonicus"
            /cultivar="Gifu (B-129)"
            /db_xref="taxon:34305"
            /clone_lib="Lotus japonicus nodule library 5 and 7
            week-old"
            /dev_stage="5 and 7 week-old plants"
            /note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
            Site_2: NotI; The library was prepared using mRNA
            extracted from nodules of 5 and 7 week-old Lotus plants.
            Nodules were induced by, and contained Mesorhizobium
            strain R7A."
BASE COUNT      62 a      89 c      49 g      71 t
ORIGIN

Query Match      2.7%; Score 34.8; DB 24; Length 271;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 4 TCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGCGAATCGTCGGCGTATGCACGGCG 63
    || || || || || || || || || || || || || || || || || || || || ||
Db 96 TCGCGGACGACAGAGATTCTGTACCGCGGCGTGC CGCGCTTCATCGGCACCTCACACGGTG 155
    || || || || || || || || || || || || || || || || || || || || ||

QY 64 CTGATGCTTCAGCGCCGGGATTCAAAGTCACCTTGATTGAC 105
    | ||||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

51

Dn 156 GTTCAGCTTCCCATGACGGCTTCCATGTCTCCCATCGAC 197

RESULT 15
AV427698
LOCUS
DEFINITION AV427698 273 bp mRNA EST 23-MAY-2000
japonicus cDNA clone MWM085c02_r 5', mRNA sequence.
ACCESSION AV427698
VERSION AV427698.1 GI:7787904
KEYWORDS EST.
SOURCE
ORGANISM Lotus japonicus.
Lotus japonicus.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
REFERENCE
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus
JOURNAL DNA Res. 7 (2), 127-130 (2000)
MEDLINE 20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.

FEATURES
source
 1..273
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone_lib="MWM085c02_r"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 xhoI; isolate=Miyakojima MG-20"
BASE COUNT 63 a 91 c 47 g 72 t
ORIGIN

Query Match 2.7%; Score 34.8; DB 18; Length 273;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 4 TCTCAGACCACAAAAAGTAGGCATCGCTGGAGCCCGGATCTGTCGGCGTATGCACGCCG 63
||| |
Db 93 TCGCGGACGACGAAGAATTCTGGTCACCGGGGCTCCGGCTTCATCGGCATCACACGGTG 152
||| |
Qy 64 CTGATGCTTCAGCGCCCGGATTCAAAAGTCAACCTTTGATTGAC 105
||| |
Dn 153 GTTCAGCTTCTCCATGACGGCTTCCATGTCTCCCATCGAC 194
||| |

Search completed: January 1, 2001, 01:12:42
Job time: 25781 sec

Search completed: January 1, 2001, 01:12:42
Job time: 25781 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:14:54 ; Search time 7299.04 Seconds
(without alignments)
775.497 Million cell updates/sec

Title: US-08-484-274-6
Perfect score: 1296
Sequence: 1 ATGGCTGAGNACCACAAAA.....AACGGGTCCGGCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_bal.*
2: gb_baz.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pr1.*
10: gb_pr2.*
11: gb_pr3.*
12: em_fun.*
13: em_hum1.*
14: em_hum2.*
15: em_in.*
16: em_om.*
17: em_or.*
18: em_ov.*
19: em_pat.*
20: em_ph.*
21: em_pl.*
22: em_ro.*
23: em_sts.*
24: em_sy.*
25: em_un.*
26: em_v1.*
27: gb_htg1.*
28: gb_htg2.*
29: gb_in1.*
30: gb_in2.*
31: em_bal.*
32: em_baz.*
33: em_hum3.*
34: em_hum4.*
35: gb_pr4.*
36: gb_htg3.*
37: gb_htg4.*
38: gb_htg5.*
39: gb_htg6.*
40: gb_htg7.*
41: em_htg1.*
42: em_htg2.*
43: em_htg3.*

44: em_hum5.*
45: gb_pl3.*
46: gb_pr5.*
47: gb_htg8.*
48: gb_htg9.*
49: gb_htg10.*
50: gb_htg11.*
51: gb_htg12.*
52: gb_htg13.*
53: gb_htg14.*
54: gb_in3.*
55: gb_htg15.*
56: gb_htg16.*
57: gb_htg17.*
58: em_htg4.*
59: em_htg5.*
60: em_htg6.*
61: em_htg7.*
62: em_hum6.*
63: gb_htg18.*
64: gb_htg19.*
65: gb_ba3.*
66: em_htg8.*
67: em_htg9.*
68: em_htg10.*
69: em_htg11.*
70: em_htg12.*
71: em_htg13.*
72: em_htg14.*
73: em_htg15.*
74: em_htg16.*
75: em_htg17.*
76: em_htg18.*
77: em_htg19.*
78: em_htg20.*
79: em_htg21.*
80: em_htg22.*
81: em_htg23.*
82: gb_pr6.*
83: gb_pr7.*
84: gb_htg20.*
85: gb_htg21.*
86: gb_htg22.*
87: gb_htg23.*
88: gb_ro.*
89: gb_sts1.*
90: gb_sts2.*
91: gb_sy.*
92: gb_un.*
93: gb_v11.*
94: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1296	100.0	1296	5	AR016593	AR016593 Sequence
2	1296	100.0	1296	5	II5326	II5326 Sequence 6
3	1291.2	99.6	1692	5	AR016591	AR016591 Sequence
4	1255.2	96.9	1293	5	AR016592	AR016592 Sequence
5	1255.2	96.9	1293	5	II5325	II5325 Sequence 4
6	1255.2	96.9	1689	5	II5324	II5324 Sequence 3
7	1201.6	92.7	1296	5	AR016594	AR016594 Sequence 7
8	1201.6	92.7	1296	5	II5327	II5327 Sequence 7
9	961.6	74.2	1296	5	AR016595	AR016595 Sequence
10	961.6	74.2	1296	5	II5328	II5328 Sequence 8
11	958.4	74.0	1296	5	AR016604	AR016604 Sequence
12	958.4	74.0	1296	5	II5337	II5337 Sequence 17

13	878.8	67.8	1631	5	A59869	A59869 Sequence 1
14	109.8	8.5	3430	2	PSEAKSD	M69159 Pseudomonas
15	78.8	6.1	2289	2	PSEAKSDA	M69159 Pseudomonas
16	56.2	4.3	69	5	AR016616	AR016616 Sequence
17	56.2	4.3	69	5	AR016619	AR016619 Sequence
18	56.2	4.3	69	5	I15349	I15349 Sequence 30
19	56.2	4.3	69	5	I15352	I15352 Sequence 33
20	50.6	3.9	65	5	AR016614	AR016614 Sequence
21	50.6	3.9	65	5	I15347	I15347 Sequence 28
22	49	3.8	1540	2	EHU17017	U17017 Pctothiorho
23	48.2	3.7	61	5	AR016617	AR016617 Sequence
24	48.2	3.7	61	5	I15350	I15350 Sequence 31
25	47.6	3.7	62	5	AR016613	AR016613 Sequence
26	47.6	3.7	62	5	I15346	I15346 Sequence 27
27	47.2	3.6	68	5	AR016618	AR016618 Sequence
28	47.2	3.6	68	5	I15351	I15351 Sequence 32
29	41.4	3.2	6175	1	AF151698	AF151698 Agrobacte
30	40.4	3.1	12695	1	AE004164	AE004164 Vibrio ch
31	40.2	3.1	23550	2	SCE39	AL049573 Streptomy
32	39.8	3.1	38914	2	MSGB937CS	178820 Mycobacteri
33	37.8	2.9	1020	52	AC033443	AC033443 Giardia 1
34	37.6	2.9	13151	1	AF060871	AF060871 Rhodococ
35	37.4	2.9	1646	4	AAU62918	U62918 Anguilla an
36	37	2.9	10236	1	AE000097	AE000097 Rhizobium
37	37	2.9	236165	5	A79351	A79351 Sequence 2
38	37	2.9	236165	5	A93003	A93003 Sequence 2
39	36.6	2.8	3286	1	AF053760	AF053760 Pseudomon
40	36.4	2.8	3610	2	RLE249196	AJ249196 Rhizobium
41	36.2	2.8	1579	45	ZMB2TUBR	X52879 Maize mRNA
42	36	2.8	13799	1	AE002359	AE002359 Neisseria
43	35.4	2.7	179381	53	AC055863	AC055863 Homo sapi
44	35.2	2.7	3185	2	PSEPEAX	M98033 Pseudomonas
45	35.2	2.7	167922	48	AC022016	AC022016 Homo sapi

ALIGNMENTS

RESULT 1						
LOCUS	AR016593	1296 bp	DNA	PAT	05-DEC-1998	
DEFINITION	Sequence 6 from patent US 5776760.					
ACCESSION	AR016593					
VERSION	AR016593.1	GI:3972870				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1296)					
AUTHORS	Barry.G.Francis and Kishore.G.Murthy.					
TITLE	Glyphosate tolerant plants					
JOURNAL	Patent: US 5776760-A 6 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..1296					
BASE COUNT	286 a 368 c 361 g 281 t					
ORIGIN						
Query Match	100.0%;	Score 1296;	DB 5;	Length 1296;		
Best Local Similarity	100.0%;	Pred. No. 0;				
Matches 1296;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG	60			
Db	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG	60			
Qy	61	CGCGTGATGCTTACGCCCGCGGATTCAAAGTACCTTGATTTGATGACCGAACCCTTCCTGGC	120			
Db	61	CGCGTGATGCTTACGCCCGCGGATTCAAAGTACCTTGATTTGATGACCGAACCCTTCCTGGC	120			
Qy	121	GAAGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180			

Db	121	GAAGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTGTCCTATATGTCC	180
Qy	181	ATGCGCGGAAACTTTGACGAGCGTCCGAAAGTGGCTTCCCTTGACCCGATGGCGCGTTGTCA	240
Db	181	ATGCGCGGAAACTTTGACGAGCGTCCGAAAGTGGCTTCCCTTGACCCGATGGCGCGTTGTCA	240
Qy	241	ATCGCGTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTAGCCGGA	300
Db	241	ATCGCGTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTAGCCGGA	300
Qy	301	AGACCAACAGGTGAAGGACAGCGGAAAGCACTCCCAATCTCATCAAGTCACAGGTG	360
Db	301	AGACCAACAGGTGAAGGACAGCGGAAAGCACTCCCAATCTCATCAAGTCACAGGTG	360
Qy	361	CCTCTGATCAAGTCAATTTGGCGGAGGAGCTGATGCGAGCCCATCTGATCCGCCATGAAGGT	420
Db	361	CCTCTGATCAAGTCAATTTGGCGGAGGAGCTGATGCGAGCCCATCTGATCCGCCATGAAGGT	420
Qy	421	CATCTGACCGTATATCGTGGAGAGACAGTTCGCCAAGAGACCGCGGAGTTGGAACTG	480
Db	421	CATCTGACCGTATATCGTGGAGAGACAGTTCGCCAAGAGACCGCGGAGTTGGAACTG	480
Qy	481	CGGCTCTCAACGGTGTTCGACACGAGATCTCAGCGCCGATGCGTTCGCGGATTTCCAT	540
Db	481	CGGCTCTCAACGGTGTTCGACACGAGATCTCAGCGCCGATGCGTTCGCGGATTTCCAT	540
Qy	541	CCGAACCTTGTCCGATGCGCTTTACCAAGGGCATCTTATAGAGAGAACCGTCAACAGATT	600
Db	541	CCGAACCTTGTCCGATGCGCTTTACCAAGGGCATCTTATAGAGAGAACCGTCAACAGATT	600
Qy	601	AATCGCAAGGGTCTGACCCCTCTTGTTCGGCGTTCGCGGAAACCGTGGCGAATTT	660
Db	601	AATCGCAAGGGTCTGACCCCTCTTGTTCGGCGTTCGCGGAAACCGTGGCGAATTT	660
Qy	661	GTATCTCGCGCTGTCATCGGCTTTAGACTCAAGGTAGGCGGCTTAAAGGCATTTACAAC	720
Db	661	GTATCTCGCGCTGTCATCGGCTTTAGACTCAAGGTAGGCGGCTTAAAGGCATTTACAAC	720
Qy	721	ACGAACGGCTTCTGGCGGTTGATGCAGCGGTTGTGCGAGCGCGCACACTCGAAATCA	780
Db	721	ACGAACGGCTTCTGGCGGTTGATGCAGCGGTTGTGCGAGCGCGCACACTCGAAATCA	780
Qy	781	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATC	840
Db	781	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATC	840
Qy	841	ATCGGAATCCGAAGCGGCTCCAGCGATTCGAGCAGCGATCGGTACAGAAAATTCATC	900
Db	841	ATCGGAATCCGAAGCGGCTCCAGCGATTCGAGCAGCGATCGGTACAGAAAATTCATC	900
Qy	901	CGGACACTATGGAATGGGGCTTCGCGTGGCGGTTACGGTTGAGTTTCGCTGGGCTACA	960
Db	901	CGGACACTATGGAATGGGGCTTCGCGTGGCGGTTACGGTTGAGTTTCGCTGGGCTACA	960
Qy	961	CGCGCTCCTAATCGGAACGTCGCGATGCTCTATAGCACGCTCGGAAACTTCTTCCA	1020
Db	961	CGCGCTCCTAATCGGAACGTCGCGATGCTCTATAGCACGCTCGGAAACTTCTTCCA	1020
Qy	1021	GCCCTCGCGCTCGAGTTCCTGAAGACGATTTCCCAATGGATGGGTTCCGCGCGAGC	1080
Db	1021	GCCCTCGCGCTCGAGTTCCTGAAGACGATTTCCCAATGGATGGGTTCCGCGCGAGC	1080
Qy	1081	ATCCCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGACACCCGACGTAATCTATGCT	1140
Qy	1141	TTGCGGCACGGTCTATCTCGGCATGACAGGGCGCGGATGACCGAAGCGTCTGCTCAGAG	1200
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Qy	1201	CTCCTCCGACGGGAAAGACCTCAATGCACATTTTCGCCCTTCGCAACCAACCGCTTGGT	1260
Db	1201	CTCCTCCGACGGGAAAGACCTCAATGCACATTTTCGCCCTTCGCAACCAACCGCTTGGT	1260

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QY 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296

RESULT 2
I15326.
LOCUS I15326 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5463175.
ACCESSION I15326
VERSION I15326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1296)
TITLE Barry,G.F. and Kishore,G.M.
JOURNAL Glyphosate tolerant plants
PATENT: US 5463175-A 6 31-OCT-1995;
FEATURES Location/Qualifiers
1..1296
/organism="unknown"
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 100.0%; Score 1296; DB 5; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGGTATGCACG 60

QY 61 GCGCTGATCTTTCAGCGCCGCGGATTCAAAGTCACCTTCATTGACCCGAACCTCCTCGGC 120
Db 61 GCGCTGATCTTTCAGCGCCGCGGATTCAAAGTCACCTTCATTGACCCGAACCTCCTCGGC 120

QY 121 GAAGGTGCATCGTTTGGGAATCCCGGATCGTTCAAGGGTCATCCGTCGCTCCCTATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATCCCGGATCGTTCAAGGGTCATCCGTCGCTCCCTATGTCC 180

QY 181 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTTCATGCCCGATGGGGCGGTGTCA 240
Db 181 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTTCATGCCCGATGGGGCGGTGTCA 240

QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTTCGTTTCGTTAGCCGA 300
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QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGGAGCCATCTGATCCGCCATGAAGT 420
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Db 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATGCGTTGCGGGATTTTCGAT 540

QY 541 CGCAACTTCGCGATCGCTTTTACCAAGGCGATTCTTATAGAAGAGAACCGGTACACGATT 600
Db 541 CGCAACTTCGCGATCGCTTTTACCAAGGCGATTCTTATAGAAGAGAACCGGTACACGATT 600

QY 601 AATCCGCAAGGGCTCGTACACCTCTGTTTCGCGCTTTTATCGCGAACCGGTGCGGAATTT 660
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Db 601 AATCCGCAAGGGCTCGTACACCTCTGTTTCGCGCTTTTATCCGGAACGGTTCGCGAATTT 660
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Db 661 GTATCTGCGCGTGTCTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTTACAAC 720

QY 721 ACGAACGGCGTTCCTGGCCGTTGATGCAGGGTGTGTCGAGCGGGCGCACACTCGAATCA 780
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Db 721 ACGAACGGCGTTCCTGGCCGTTGATGCAGGGTGTGTCGAGCGGGCGCACACTCGAATCA 780

QY 781 CTTGCTAATTCGCTAGCGGATGACATCCGCTCGATACCGAAGTGTGATATCATATCGTC 840
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Db 781 CTTGCTAATTCGCTAGCGGATGACATCCGCTCGATACCGAAGTGTGATATCATATCGTC 840

QY 841 ATCGCGAATCCGGAAGCCGCTCCACGATTCGACGACCGATGCGTCGAGGAAATTCATC 900
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Db 841 ATCGCGAATCCGGAAGCCGCTCCACGATTCGACGACCGATGCGTCGAGGAAATTCATC 900

QY 901 GCGACACCTATGGAATGGGGTTCGCGTGGGGGTACGGTTGAGTTTCGTTGGGCTCACA 960
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Db 901 GCGACACCTATGGAATGGGGTTCGCGTGGGGGTACGGTTGAGTTTCGTTGGGCTCACA 960

QY 961 GCGGCTCTTAACCTGGAAACGTGCGCATGTCTATACGACGCTCGAAAACCTTCTTCCA 1020
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QY 1021 GCCCTCGCGCTCGGAGTTCTGAAGAACGATATTCCAATGATGGGGTTCGCGCGGAGC 1080
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Db 1081 ATCCCGGATTCGTTCCCGGTGATTTGGCCGGGCAACCCGACACCCACGCTTAATCTATGCT 1140

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Db 1141 TTCGGCACGGTCATCTCGGCATGACAGGGCGCGCATGACCGCAACGCTCGTCTCAGAG 1200

QY 1201 CTCCTCGAGGCAAAAGACCTCAATCGACATTTCCGCTTCGACACAAACCGCTTTGGT 1260
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Db 1201 CTCCTCGAGGCAAAAGACCTCAATCGACATTTCCGCTTCGACACAAACCGCTTTGGT 1260

QY 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296

RESULT 3
AR016591
LOCUS AR016591 1692 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776760.
ACCESSION AR016591
VERSION AR016591.1 GI:3972868
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1692)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
1..1692
/organism="unknown"
BASE COUNT 381 a 480 c 469 g 361 t
ORIGIN

Query Match 99.6%; Score 1291.2; DB 5; Length 1692;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGGAATCGTTCGGCGTATGCACG 60
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Db 120 ATGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 179
Qy 61 CGCGTGATGCTTACAGCGCGCGGGATTCAAAAGTCACCTTGAATGACCCGAAACCCCTCTGGC 120
Db 180 CGCGTGATGCTTACAGCGCGCGGGATTCAAAAGTCACCTTGAATGACCCGAAACCCCTCTGGC 239
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACAGGCTCATCGTCGTCCCTATGTC 180
Db 240 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACAGGCTCATCGTCGTCCCTATGTC 299
Qy 181 ATGCCGGGAAACTTGAAGGAGCGTCCGGAAGTGGCTCTTGACCGGATGGGCGCGTTGTCA 240
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Qy 241 ATCCGGTTCAGCTATTTTCCAAACCATATGCCCTGGTGTGATTTCGCTTCTGTAGCCGGA 300
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Qy 301 AGACCAACAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 420 AGACCAACAAGGTGAAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 479
Qy 361 CCTCTGATCAAGTCATTGGCGGAGGAGCTCATGGAGCCATCTGATCCGCCATGAAGGT 420
Db 480 CCTCTGATCAAGTCATTGGCGGAGGAGCTCATGGAGCCATCTGATCCGCCATGAAGGT 539
Qy 421 CATCTGACCGTATATCGTGAGAGACGACTTCGCAAGGACCGGGAGGTTGGGAACGT 480
Db 540 CATCTGACCGTATATCGTGAGAGACGACTTCGCAAGGACCGGGAGGTTGGGAACGT 599
Qy 481 CGCGTCTCAACGGTGTTCGCACGACATCTCAGCGCCGATGGGTTGCGGGATTTTCGAT 540
Db 600 CGCGTCTCAACGGTGTTCGCACGACATCTCAGCGCCGATGGGTTGCGGGATTTTCGAT 659
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Db 660 CCGAACTTGTCCGATCGGTTTACCAAGGGCAATCTTATAGAAGAGACGGTCAACGAT 719
Qy 601 AATCCGAAGGGCTCGTGACGCTCTTGTTCGGGCTTTTATCGGAAAGCGGTGGGGAATTT 660
Db 720 AATCCGAAGGGCTCGTGACGCTCTTGTTCGGGCTTTTATCGGAAAGCGGTGGGGAATTC 779
Qy 661 GTATCTGCGGTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAAAC 720
Db 780 GTATCTGCGGTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAAAC 839
Qy 721 ACGAAGCGGCTTCTGGCGGTTGATGCAGCGGTTGTCGAGCGCGGCACACTCGAAATCA 780
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Qy 781 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
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Qy 961 GCCGCTCCTTAACGGAACGCTGCGCATGTGCTCTATAGCGACGCTCGAAGAACTTCTTCCA 1020
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Db 1140 GCCCTCGGGCTCGAGGTTCTGAAGACGATATTCCAATGGATGGGTTCCGGCGGAGC 1199
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Db 1200 ATCCGGGATTCGCTCCCGGTGATTGGCCGGGCAACCCGAGACACCGAGCTAATCTATGCT 1259
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Db 1260 TTCCGCCATGGTCACTTCGGCATGACAGGGCGCGCATGACCGCAACGCTCGTCTCAGAG 1319
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Qy 1261 ATTGGCAATCAACGAAACCGGTCGCGCAAGTTAA 1296
Db 1380 ATTGGCAATCAACGAAACCGGTCGCGCAAGTTAA 1415
RESULT 4
AR016592
LOCUS AR016592 1293 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5776760.
ACCESSION AR016592
VERSION AR016592.1 GI:3972869
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1293)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 4 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..1293
BASE COUNT 286 a 367 c 359 g 281 t
ORIGIN
Query Match 96.9%; Score 1255.2; DB 5; Length 1293;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 ATGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 60
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Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACAGGCTCATCGTCGTCCCTATGTC 180
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Qy 361 CCTCTGATCAAGTCATTGGCGGAGGAGCTCATGGAGCCCATCTGATCCGCCATGAAGGT 420
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Qy 421 CATCTGACCGTATATCGTGAGAGACGACTTCGCAAGGACCGCGGAGGTTGGGAACGT 480
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Qy 481 CGCGTCTCAACGGTGTTCGCACGACGATCCTCAGCGCGGATGGGTTGCGGGATTTTCGAT 540

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LOCUS I15325 1293 bp DNA PAT 02-APR-1996
DEFINITION Sequence 4 from patent US 5463175.
ACCESSION I15325
VERSION I15325.1 GI:1250233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1293)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 4 31-OCT-1995;
FEATURES
source 1..1293
/organism="unknown"
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BASE COUNT	286 a	367 c	359 g	281 t	
ORIGIN					
Query Match					96.9%; Score 1255.2; DB 5; Length 1293;
Best Local Similarity					99.5%; Pred. No. 0;
Matches 1290; Conservative					0; Mismatches 3; Indels 3; Gaps 3;
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Db 1	ATGCTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGGTATGCACG	60			
Qy 61	GGCTGATGCTTCAGCGCCGCGGATTTCAAAGTCACCTTGATTGACCCGAACCTCTCTGGC	120			
Db 61	GGCTGATGCTTCAGCGCCGCGGATTTCAAAGTCACCTTGATTGACCCGAACCTCTCTGGC	120			
Qy 121	GAAGGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180			
Db 121	GAAGGTGATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180			
Qy 181	ATGCCGGGAAACTTTCAGGAGCGTGCCGAAAGTGGCTCCTTGACCCGATGGGGCGGTTGTCA	240			
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Qy 301	AGACCAACAAAGTGAAGGAGGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360			
Db 298	AGACCAACAAAGTGAAGGAGGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357			
Qy 361	CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGGCATCTGATCCGCCATGAAGGT	420			
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Qy 421	CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCCAAGGACCGCGGAGGTTGGGAAC	480			
Db 418	CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCCAAGGACCGCGGAGGTTGGGAAC	477			
Qy 481	CGGCGTCTCAAGGCTGTCGACGAGATCCTCAGCGCGATGCGTTGCGGGATTTCCGAT	540			
Db 478	CGGCGTCTCAAGGCTGTCGACGAGATCCTCAGCGCGATGCGTTGCGGGATTTCCGAT	537			
Qy 541	CGGAACCTTCTGCGATCGCTTTACCAAGGGCATTTCTATAGAAGAGAACGGTCACAGATT	600			
Db 538	CGGAACCTTCTGCGATCGCTTTACCAAGGGCATTTCTATAGAAGAGAACGGTCACAGATT	597			
Qy 601	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCCCGAACGGTGGCGAATTT	660			
Db 598	AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTATCCCGAACGGTGGCGAATTT	657			
Qy 661	GTATCTGCGCGTCTCATCGGCTTTGAGACTGGAAGTGAAGGCGCTTAAAGCAATTACAAAC	720			
Db 658	GTATCTGCGCGTCTCATCGGCTTTGAGACTGGAAGTGAAGGCGCTTAAAGCAATTACAAAC	717			
Qy 721	ACGAACGGGTTCTGCGCGTTTGATGACGAGGGTTGTGCGACGCGCGCACACTCGAAATCA	780			
Db 718	ACGAACGGGTTCTGCGCGTTTGATGACGAGGGTTGTGCGACGCGCGCACACTCGAAATCA	777			
Qy 781	CTTTGCTAATTCGCTTAGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840			
Db 778	CTTTGCTAATTCGCTTAGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	837			
Qy 841	ATCGCAANTCCGGAAGCCGCTCCACGCAATTCGACGACCGGATGCGTCAGGAAATTCATC	900			
Db 838	ATCGCAANTCCGGAAGCCGCTCCACGCAATTCGACGACCGGATGCGTCAGGAAATTCATC	897			
Qy 901	GCGACACCTATGGAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA	960			
Db 898	GCGACACCTATGGAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACA	957			
Qy 961	GCGGCTCCTAACTGGAACGTCGCGATGCTCTATACGACGCTCGAAATCTCTTCCA	1020			

Db 958 GCGCTCCTTAACCTGGAACAGTCGGCATGTGCTCTATACGCACGCCTCGAAACATTCCTTCCA 1017
Qy 1021 GCCTCGCGCTCGAGTCTGAAGAACAGATATTCCAAATGGATGGGTTCCGGCCGAGC 1080
Db 1018 GCCTCGCGCTCGAGTCTGAAGAACAGATATTCCAAATGGATGGGTTCCGGCCGAGC 1077
Qy 1081 ATCCCGATTCGCTCCCGGTGATTGGCCGGCAACCCGGACACCCGACGTAATCTATGCT 1140
Db 1078 ATCCCGATTCGCTCCCGGTGATTGGCCGGCAACCCGGACACCCGACGTAATCTATGCT 1137
Qy 1141 TCCGGCCACGCTCATCTCGGCATGACAGGGCGCGGATGACCGAAGCTCGTCTCAGAG 1200
Db 1138 TCCGGCCATGGTCTATCTCGGCATGACAGGGCGCGGATGACCGAAGCTCGTCTCAGAG 1197
Qy 1201 CTCTCGCAGGGCAAGAACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1260
Db 1198 CTCTCGCAGGGCAAGAACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1257
Qy 1261 ATTTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
Db 1258 ATTTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1293

RESULT 6
LOCUS I15324 1689 bp DNA PAT 02-APR-1996
DEFINITION Sequence 3 from patent US 5463175.
ACCESSION I15324
VERSION I15324.1 GI:1250232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1689)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 3 31-Oct-1995;
FEATURES Location/Qualifiers
source 1. .1689

BASE COUNT 381 a 479 c 468 g 360 t 1 others
ORIGIN

Query Match 96.9%; Score 1255.2; DB 5; Length 1689;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGAACCAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCAAG 179
Db 120 ATGTCTGAGAACCAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCAAG 179

Qy 61 GCCTCATGCTTCAGCGCCCGGATTCAAAGTCAACCTGATTGACCCGACCCCTCTCTGGC 120
Db 180 GCCTCATGCTTCAGCGCCCGGATTCAAAGTCAACCTGATTGACCCGACCCCTCTCTGGC 239

Qy 121 GAAGTGTGATCGTTTGGGAATCGCGATGCTTCAAGGGCTCATCCGTCGCTATGTCC 180
Db 240 GAAGTGTGATCGTTTGGGAATCGCGATGCTTCAAGGGCTCATCCGTCGCTATGTCC 299

Qy 181 ATCCCGGGAACTTTCAGAGCGTCCGGAAGTGGCTCCTTGACCCGATGGGCGCGTGTGCA 240
Db 300 ATCCCGGGAACTTTCAGAGCGTCCGGAAGTGGCTCCTTGACCCGAT - GGGCGGTTGTCA 358

Qy 241 ATCCGGTTTACGCTATTTCCAACCATCATGCCCTGGTTGATTGCTTCTGTTAGCCGGA 300
Db 359 ATCCGGTTTACGCTATTTCCAACCATCATG - CCTGGTTGATTGCTTCTGTTAGCCGGA 416

Qy 301 AGACCAAAACAAAGTGAAGGAGGAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 417 AGACCAAAACAAAGTGAAGGAGGAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 476

Qy 361 CCTCTGATCAAGTCAATTTGGCGGAGAGGCTGATCGAGCCATCTGATCCGCCATGAAGGT 420
Db CCTCTGATCAAGTCAATTTGGCGGAGAGGCTGATCGAGCCATCTGATCCGCCATGAAGGT 536

Qy 421 CATCTGACCGTATATCTGGAGAAAGCAGACTTCGCCAAGAGACCGGAGGTGGGAATCG 480
Db 537 CATCTGACCGTATATCTGGAGAAAGCAGACTTCGCCAAGAGACCGGAGGTGGGAATCG 596

Qy 481 CGGCGTCTCAACGGTGTTCGCACGCAGATCTCAGCGCGGATGCGTTCGCGGATTTCCAT 540
Db 597 CGGCGTCTCAACGGTGTTCGCACGCAGATCTCAGCGCGGATGCGTTCGCGGATTTCCAT 656

Qy 541 CCGAACTTTGTCGATCGGTTTACCAAGGGCATTTCTTATAGAAGAGAACGGTGCACAGATT 600
Db 657 CCGAACTTTGTCGATCGGTTTACCAAGGGCATTTCTTATAGAAGAGAACGGTGCACAGATT 716

Qy 601 AATCCGCAAGGGCTCGTGACCCCTCTTTGTTTCGGCGTTTTATTCGCGAAGCGTGGCGAATTC 660
Db 717 AATCCGCAAGGGCTCGTGACCCCTCTTTGTTTCGGCGTTTTATTCGCGAAGCGTGGCGAATTC 776

Qy 661 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTTACAACC 720
Db 777 GTATCTGCGCGTGTCTATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTTACAACC 836

Qy 721 ACGAAACCGGCTTTGCGCGTTGATCGACGCGTTGTCCAGCGCGCGCACACTCGAAATCA 780
Db 837 ACGAAACCGGCTTTGCGCGTTGATCGACGCGTTGTCCAGCGCGCGCACACTCGAAATCA 896

Qy 781 CTTGCTTAATTCGCTAGGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Db 897 CTTGCTTAATTCGCTAGGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 956

Qy 841 ATCCGGAATCCGGAAGCGCTCCACGCATTCGAGACGCGATGCGTCAGGAAAATTCATC 900
Db 957 ATCCGGAATCCGGAAGCGCTCCACGCATTCGAGACGCGATGCGTCAGGAAAATTCATC 1016

Qy 901 GCGACACTATGGAATGGGCTTTGCGGTGCGGGTACGGTTGAGTTGCGTGGGCTCACA 960
Db 1017 GCGACACTATGGAATGGGCTTTGCGGTGCGGGTACGGTTGAGTTGCGTGGGCTCACA 1076

Qy 961 GCGCTCTACTGGAACGTCGCGCATGCTCTATACGACGCTCGAAAACCTTCTTCCA 1020
Db 1077 GCGCTCTACTGGAACGTCGCGCATGCTCTATACGACGCTCGAAAACCTTCTTCCA 1136

Qy 1021 GCGCTCGCGCTCGGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTCCGGCCGAGC 1080
Db 1137 GCGCTCGCGCTCGGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTCCGGCCGAGC 1196

Qy 1081 ATCCCGGATTCGCTCCCGGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1140
Db 1197 ATCCCGGATTCGCTCCCGGTGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1256

Qy 1141 TTCGGCCACGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1200
Db 1257 TTCGGCCATGGTCTATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1316

Qy 1201 CTCTCGCAGCGCAAAAGACCTCAATGACATTTCCGCCCTTCGCAACCAACCGCTTTGGT 1260
Db 1317 CTCTCGCAGCGCAAAAGACCTCAATGACATTTCCGCCCTTCGCAACCAACCGCTTTGGT 1376

Qy 1261 ATTTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
Db 1377 ATTTGGCAATCCAAAGCAACGGGTCCGGCAAGTTAA 1412

RESULT 7
LOCUS AR016594
DEFINITION Sequence 7 from patent US 5776760.
ACCESSION AR016594
VERSION AR016594.1 GI:3972871
KEYWORDS Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry.G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 7 07-JUL-1998;
FEATURES Location/Qualifiers
source
1..1296
BASE COUNT 287 a 344 c 332 g 333 t
ORIGIN

Query Match 92.7%; Score 1201.6; DB 5; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATCGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCGGAATCGTCGCCCTATGCCAG 60
DB 1 ATCGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC 60
QY 61 GCGCTGATCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGGC 120
DB 61 GCTTTGATGCTTCAACGTCGTGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGGC 120
QY 121 GAAGGTGCATCTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
DB 121 GAAGGTGCATCTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
QY 181 ATCCGGGAAACTTGACGAGCGTCGCGAAGTGGCTTGCCTTGACCCGATGGGGCGTTGTCA 240
DB 181 ATCCGGGAAACTTGACGAGCGTCGCGAAGTGGCTTGCCTTGACCCGATGGGGCGTTGTCA 240
QY 241 ATCCGGTTCCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTGGCTTTCTGTAGCCGA 300
DB 241 ATCCGGTTCCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTGGCTTTCTGTAGCCGA 300
QY 301 AGACCAACAAGGTGAAGGAGCAGGCGAAGACACCTCCGCAATCTCATCAAGTCCACGGTG 360
DB 301 AGACCAACAAGGTGAAGGAGCAGGCGAAGACACCTCCGCAATCTCATCAAGTCCACGGTG 360
QY 361 CCTCTGATCAAGTCTATTCGCGGAGGAGCTGATGGAGCCATCTGATCCGCCATGAAGT 420
DB 361 CCTCTGATCAAGTCTATTCGCGGAGGAGCTGATGGAGCCATCTGATCCGCCATGAAGT 420
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCGCAAGGACCGCGAGGTTGGGAATG 480
DB 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCGCAAGGACCGCGAGGTTGGGAATG 480
QY 481 CGCGCTCTCAACGGTGTTCGCGACGAGATCTCTAGCGCCGATCGCTTGGCGGATTTTCGAT 540
DB 481 CGCGCTCTCAACGGTGTTCGCGACGAGATCTCTAGCGCCGATCGCTTGGCGGATTTTCGAT 540
QY 541 CCGAACTTCTCCGATCGCTTTTACCAAGGCGATTTATATAGAAGAGAACCGTTCACAGATT 600
DB 541 CCGAACTTCTCCGATCGCTTTTACCAAGGCGATTTATATAGAAGAGAACCGTTCACAGATT 600
QY 601 AATCCGAAGGCTCGTGACCTCTGTGTCGCGCTTTTATCGGAACGCGTGGCGAATTT 660
DB 601 AATCCGAAGGCTCGTGACCTCTGTGTCGCGCTTTTATCGGAACGCGTGGCGAATTT 660
QY 661 GTATCTGCGGTGTATCGCGCTTTGAGACTGAAGGTAGGGCTTTAAAGGCAATTACAACC 720
DB 661 GTATCTGCGGTGTATCGCGCTTTGAGACTGAAGGTAGGGCTTTAAAGGCAATTACAACC 720
QY 721 ACGAACGGGTTCTGCCGCTTATGACGAGCGTTTGTCCGAGCGCGGCGACACTCGAATCA 780
DB 721 ACGAACGGGTTCTGCCGCTTATGACGAGCGTTTGTTCGAGCTGGTGCACACTTAATCA 780
QY 781 CTTGCTAATTCGCTAGGCGATCACATCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
DB 781 CTTGCTAATTCGCTAGGCGATCACATCCGCTCGATACCGAAGCTGGATATCATATCGTC 840

QY 841 ATCCGGAATCCGGAAGCCCGCTCCACGCCATTCGACAGACCGATGCGTTCAGAAATTCATC 900
DB 841 ATCCGGAATCCGGAAGCCCGCTCCACGCCATTCGACAGACCGATGCGTTCAGAAATTCATC 900
QY 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTCGGCTCACA 960
DB 901 GCGACACCTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTCGGCTCACA 960
QY 961 GCGGCTCTTAAGTGAAGAGTGGCATGTGCTCTATACGACGCTCGAAACCTCTCTCCA 1020
DB 961 GCTGCTCTTAAGTGAAGAGTGGCATGTGCTCTATACGACGCTCGAAACCTCTCTCCA 1020
QY 1021 GCGCTCGCCCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTCCGGCGAGC 1080
DB 1021 GCGCTCGCCCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTCGCTCAGC 1080
QY 1081 ATCCCGGATTCGCTCCCGCTGATTTGGCGGCAACCGGACACCGACGTAATCTATGCT 1140
DB 1081 ATTCCTGATCTCTCCAGTGTGCTGCGCAACTCGTACACCCGACGTAATCTATGCT 1140
QY 1141 TTCCGCGACGTCATCTCGGCATGACAGGGCGGCCGATGACCGCAACGCTCGTCTCAGAG 1200
DB 1141 TTTCGTCACGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCGTCTCAGAG 1200
QY 1201 CTCCTCGCAGGAAAGAACCTCAATCGACATTTCCGCTTCGACCAACACCGCTTTGGT 1260
DB 1201 CTCCTCGCAGGAAAGAACCTCAATCGACATTTCCGCTTCGACCAACACCGCTTTGGT 1260
QY 1261 ATTGCAAAATCCAAAGCAACGGTCCGCAAGTTAA 1296
DB 1261 ATTGCAAAATCCAAAGCAACGGTCCGCAAGTTAA 1296

RESULT 8
Locus I15327 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 7 from patent US 5463175.
ACCESSION I15327
VERSION I15327.1 GI:1250235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry.G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 7 31-OCT-1995;
FEATURES Location/Qualifiers
source
1..1296
BASE COUNT 287 a 344 c 332 g 333 t
ORIGIN

Query Match 92.7%; Score 1201.6; DB 5; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCTATGCACG 60
DB 1 ATGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC 60
QY 61 GCGCTGATCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGGC 120
DB 61 GCTTTGATGCTTCAACGTCGTGATTCAAAGTCACCTTGATTGACCCCGAACCCCTCCTGGC 120
QY 121 GAAGGTGCATCTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
DB 121 GAAGGTGCATCTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
QY 181 ATCCGGGAAACTTGACGAGCGTCGCGAAGTGGCTTGCCTTGACCCGATGGGGCGTTGTCA 240
DB 181 ATCCGGGAAACTTGACGAGCGTCGCGAAGTGGCTTGCCTTGACCCGATGGGGCGTTGTCA 240

Qy	721	ACGAACGGCGTTCTGGCCGTTGATGCAGCGGTTGTGCGAGCGCGGCACACACTCGAAATCA	780
Db	721	ACCAACGGGTGTTCTGCTGTTGATGCAGCTGTGTGTCAGCTGSGTCACACTCCCAAGTCT	780
Qy	781	CTTGCTAATTCGGCTAGCGGATGACATCCCGCTCGATACCGGAACGTGGATATCATATCGTC	840
Db	781	CTTGCTAATTCGGCTAGCGGATGACATCCCGCTCGATACCGGAACGTGGATATCATATCGTC	840
Qy	841	ATCCGGAATCCGGAAGCCGCTCCACGCATTCGCGACGACCGATCGCTCAGGAAATTCATC	900
Db	841	ATCCGCAACCAAGAAGCTGCTCCACGTAATTCCAACTACCGATGCTTCTGGAAAGTTCATC	900
Qy	901	CGGACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTGCTTCGGCTCGGCTCACA	960
Db	901	GCTACTCTATGGAGATGGGCTCTTCGTTGCTGGAACCGTTGAGTTGCGTGGCTCTCACT	960
Qy	961	GCCGCTCCTAACTGGAACCTGCGCATGTGCTCTATAGCAGCTCGGAAATCTCTTCCCA	1020
Db	961	GCTGCTCTTAAGTGGAAAGCGTGTCTACATCTACAGCTCGTAAGTTGCTTCCCA	1020
Qy	1021	CCCTCGCGCTCCGAGTTCTTGAAGAACGATATTCCAAATGGATGGGTTCCGGCCGAGC	1080
Db	1021	GCTCTGCTCCTGCCAGTTCTTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTTCCAGC	1080
Qy	1081	ATCCGGATTCGCTCCCGTGATTTGCCGGGCAACCCGGACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCCGAATTCCTTCCAGTGATTTGGTCGTGCTACCCGCTACTCCGACAGCTTATCTAGCT	1140
Qy	1141	TTGGCCACAGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTGCTCTCAGAG	1200
Db	1141	TTGGCTCAGGTCACCTCGGATGATGCTGCTGCTCAATGACCGCAACGCTGTTCTGAG	1200
Qy	1201	CTCTCGCAGCGGAAAGACTCAATCGACATTTTCGCCCTTTCGCACCAACCGCTTTGGT	1260
Db	1201	CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAACCGTTTCGGT	1260
Qy	1261	ATTGGCAATCCAAGCAACGGGTCCGGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCCAAGCAAACTGCTCCTGCATCTTAA	1296
RESULT 10			
L15328			
LOCUS	L15328	1296 bp	DNA
DEFINITION	Sequence 8 from patent US 5463175.		
ACCESSION	L15328		
VERSION	L15328.1		
KEYWORDS	GI:1250236		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1296)		
TITLE	Barry, G.F. and Kishore, G.M.		
JOURNAL	Glyphosate tolerant plants		
FEATURES	Patent: US 5463175-A 8 31-OCT-1995;		
	Location/Qualifiers		
	1..1296		
	/organism="unknown"		
BASE COUNT	271 a	359 c	305 g
ORIGIN	361 t		
Query Match			
Best Local Similarity 74.2%; Score 961.6; DB 5; Length 1296;			
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps			
Qy	1	ATGCGCTGAGAACCCACAAAAAGTAGCATCGCTGGAGCCGGAATCGTCGGGCTATGCACG	60
Db	1	ATGCGCTGAGAACCCACAAAAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTTGGCACT	60
Qy	61	CGCGTATGCTTACGGCCGGGATTCAAAGTCACCTTGATTGACCCGGAACCCCTCCCTGCG	120

Qy	1201	CTCCTCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACACCGCTTTGGT	1260
Db	1201	CTCCTCGAGGTGAGAGACCTCTATCGACATCTCTCCATTTCGCACCAACCGTTTCGGT	1260
Qy	1261	ATTGCGAAATCCAAAGCAACCGGTCGGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCCAGCAAACTGGTCTGCATCTAA	1296
RESULT 11			
AR016604	AR016604	1296 bp	DNA
LOCUS	Sequence 17 from patent US 5776760.		PAT
DEFINITION	Sequence 17 from patent US 5776760.		
ACCESSION	AR016604		
VERSION	AR016604.1	GI:3972881	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5776760-A 17 07-JUL-1998;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	309 g
ORIGIN	360 t		
Query Match 74.0%; Score 958.4; DB 5; Length 1296;			
Best Local Similarity 83.7%; Pred. No. 6.9e-247;			
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;			
Qy	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGAGCGCGGAATCGTCGGGTATGCACG	60
Db	1	ATGGCTGAGAACCAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCACAT	60
Qy	61	GGGCTGATGCTTCAGCGCGGCGGATTCAAAGTCACCTTGATTGACCCGAACCTCCTGCG	120
Db	61	GCTTTGATGCTTCACGCTCGTGATTCAGGTTACCTTGATGATCCAAACCCACCAAGT	120
Qy	121	GAAGTGATCGTTTGGGAATCCGGATGCTTTCAACGGCTCATCCGTCGCTATGTCC	180
Db	121	GAAGTGCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCTCGGTTCTTCCAATGTCC	180
Qy	181	ATCCCGGAAACTTCACGAGCGTGCGGAAGTGGCTTTCACCGGATGGGGCGGTGTCA	240
Db	181	ATGCCAGGAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC	240
Qy	241	ATCCGGTTCAGCTATTTCCAAACCATCATGCCCTGCTGTTGATTCGCTTTCTGTAGCCGA	300
Db	241	ATCCGTTTCGGGTACTTTCCAAACCATCATGCCCTGTTGGTGTGATTCGTTCTTGTGCTGA	300
Qy	301	AGACCAAAAGGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAAAAGGTGAAGGAGCAGGCGAAGTAAAGGCACTCCGTAACCTCATCAAGTCCACTGTG	360
Qy	361	CCTGTGATCAAGTCAATTTGGCGGAGAGGCTGATGGAGCCATCTGATCCGCCATGAAGT	420
Db	361	CCTTTGATCAAGTCTCTGGCTGAGGAGGCTGATGTAGCCACCTTATCCGTCACCAAGGT	420
Qy	421	CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGCGGAGTTGGGAACGTG	480
Db	421	CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGACCGTGGAGGTTGGGAACTT	480
Qy	481	CGCGCTCTCAACGGTGTTCGACCGCAGATCTTCAGCGCGATGCGTTGCGGATTTTCGAT	540
Db	481	CGTCTCTCAACGGTGTTCGTAACCTTCAAACTTCCTCAGCGCTGATGATTCGTTGATTCGAT	540
Qy	541	CCGAATTTGTCGATCGGTTTACCAAGGCGATTTCTTATAGAAGACCGGTACACAGATT	600
Db	541	CTTAACCTTTGCTCACGCGCTTTTACCAAGGGAATCCTTTATCGAAGAGAACCGGTACACCATC	600

Db	541	CTTAACCTTTGCTCACGCGCTTTTACCAAGGGAATCCTTTATCGAAGAGAACCGGTACACCATC	600
Qy	601	AATCCGCAAGGGTCGTGACCCCTCTTGTTCGGCGTTTATTCGGGAACCGGTGGCGAATTT	660
Db	601	AACCCACAAGTCTCGTGACTCTCTGTTGCTGCTTCATCGCTAACGGTGGAGAGTTC	660
Qy	661	GTATCTCGCGCTGCTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCAATTTACAAC	720
Db	661	GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGGTGCTCTCAAGGGTATCACCAAC	720
Qy	721	ACGAACGGCTTCTGCGCGTTGATGACAGCGTTGTCGACGCCGCGCACACTCAAAATCA	780
Db	721	ACCAACGGTGTCTGCTGTTGATGACAGCTGTTGTCAGCTGGTGACACTCAAGTCT	780
Qy	781	CTTGCTAAATTCGCTAGCGATGACATCCCGCTCGATACCGAACGTTGATATCATATCATGCTC	840
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGATACCGAACGTTGATATCATATCATGCTC	840
Qy	841	ATCGGAATTCGGAAGCGCTCCACGATTCGAGACGACCGATGCTCAGGAAATTCATC	900
Db	841	ATCGCAACCCAGAAGCTGCTCCACGATTTCCAACTACCGATGCTTCTGGAAGTTCATC	900
Qy	901	GCACACCTATGGAATGGGGCTTCGCGTGGCGGTAGGTTGAGTTGCTGGGCTCACA	960
Db	901	GCTACTCTATGGAGATGGGCTTTCGTTGCTGGAACCGTTGAGTTGCTGGTCTCACT	960
Qy	961	GCGCTCCTAACTGGAAACGTCGCGATGCTCTATACGACACGCTCGAATACTTCTTCCA	1020
Db	961	GCTGCTCCTAACTGGAAAGCGTCTCAGCTTCTACACTCGCGCTCGTAACTTCTTCCA	1020
Qy	1021	GCCTCGCGCTCGAGTTCTGAAGACGATATTCAAATGGATGGGTTCGCGCCGAGC	1080
Db	1021	GCTCTGCTCTCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTCGCTCCAAGC	1080
Qy	1081	ATCCCGATTCGCTCCCGTGATTGGCGGCGACACCCGACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCCGATTCCTTCCAGTATTTGGTCTGCTACCGTACTCCAGACGTTATCTACGCT	1140
Qy	1141	TTCCGCGACCGTCTATCTCGGCATGACAGGGCGCGGATGACCGAAGCTCGTCTCAGAG	1200
Db	1141	TTCCGCTCACGGTCACCTCGGTATGACTGGTGTCTCCATGACCGCAACCCCTGTTCTGAG	1200
Qy	1201	CTCCTCGCAGCGAAAGACCTCAATCGACATTTTCGCGCTTCGCAACCAACCGCTTTGGT	1260
Db	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCAACCAACCGCTTCGGT	1260
Qy	1261	ATTGGCAATTCGAACGCGGTCCGCGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCCAAAGCAACTGGTCTGCTGCAATCTAA	1296
RESULT 12			
IL5337	IL5337	1296 bp	DNA
LOCUS	Sequence 17 from patent US 5463175.		PAT
DEFINITION	Sequence 17 from patent US 5463175.		
ACCESSION	IL5337		
VERSION	IL5337.1	GI:1250245	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1296)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 17 31-OCT-1995;		
FEATURES	Location/Qualifiers		
source	1..1296		
BASE COUNT	267 a	360 c	309 g
ORIGIN	360 t		
Query Match 74.0%; Score 958.4; DB 5; Length 1296;			

Best Local Similarity 83.7%; Pred. No. 6.9e-247;									
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;									
QY	1	ATGGCTGAGAACCAAAAAAGTAGGCTACGCTGGAGCGGAATCGTCGGCGTATGACAG	60						
Db	1	ATGGCTGAGAACCAACAAGAAGTGTGATCGCTGGAGCTGGAATCGTTGGTCTTCCACT	60						
QY	61	GGCTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATGACCCGCAACCCCTCTGGC	120						
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DEFINITION	A59869								
ACCESSION	A59869								
VERSION	A59869.1	GI:3715060							
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Matches 1079; Conservative 0; Mismatches 217; Indels 50; Gaps 2;									
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RESULT 15
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LOCUS Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
DEFINITION gene, complete cds.
ACCESSION M69159
VERSION M69159.1 GI:151317
KEYWORDS ketoglutarate semialdehyde dehydrogenase.
SOURCE Pseudomonas putida (strain ATCC 12633) DNA.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas.
REFERENCE 1 (bases 1 to 2289)
AUTHORS Burlingame,R.P., Maruya,A., Allyn,A.H., Allyn,D. and Backman,K.C.
TITLE Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
putida
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 54.5%; Pred. No. 2e-10;
Matches 158; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Db 1788 CTGCAACTGCGCGCGCTGGGCTGCGGTGACGGTCGTCGACGACGAGGAGCCGCCAT 1847
QY 124 GGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCCATG 183
Db 1848 GGTGCTCGTTCCGCAATCGCGGCATCTGCGGACCGAGCAGGTGTTCCCATCGCGGAT 1907
QY 184 CCGGAAACTTCACGAGCGTGGCGAAGTGGCTTCCTTGACCCCGATGGGCGCGTTGTCAATC 243
Db 1908 TTGTCGATCCTGAACGCTTGCCATGCTCATGAGCCCGATGGGCGCGTTGCGCCTG 1967
QY 244 CGGTTTCAGCTATTTCCAAACCATCATGCCCTGCTGTTGATTGCTTTCTGTT 293
Db 1968 GACTGGAAGTACATGCCGCGCGCCCTGCGCTGTTTCCCGCGCTACTGTT 2017
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Job time: 29203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:32:11 ; Search time 263.11 Seconds
(without alignments)
1850.400 Million cell updates/sec

Title: US-08-484-274-6
Perfect score: 1296
Sequence: 1 ATGCGTGAGNACCACAAAA.....AACGGGTCGGCAAGTTAA 1296

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1294.4	99.9	1321	13 Q20833	Manipulated glypho
2	1288	99.4	1692	13 Q22705	Glyphosate oxidore
3	1252	96.6	1689	13 Q20832	Glyphosate oxidore
4	1200	92.6	1321	13 Q20834	Modified glyphosat
5	961.6	74.2	1296	13 Q20835	Synthetic glyphosa
6	961.6	74.2	8418	20 X57309	Sugar beet T-DNA c
7	878.8	67.8	1631	18 T85664	CPT1-COX gene fusi
8	673	51.9	8798	20 X57308	Sugar beet T-DNA c
9	671.4	51.8	8012	20 X57305	Sugar beet T-DNA c
10	37	2.9	534720	19 V30458	Rhizobium species
11	37	2.9	536165	19 V30459	Rhizobium species
12	35	2.7	38734	20 Z32020	Human METHI relate

C 13	34	2.6	405	20	X98168	Nucleotide sequenc
C 14	34	2.6	603	20	X98167	Nucleotide sequenc
C 15	34	2.6	922	19	V15073	Hybrid DNA compris
C 16	34	2.6	1137	20	X98164	Nucleotide sequenc
C 17	34	2.6	1209	12	Q12569	Protease2 open rea
C 18	34	2.6	1513	12	Q12567	Alkaline protease
C 19	34	2.6	4235	20	X98035	Nucleotide sequenc
C 20	33	2.5	423	18	T80725	Type II topoisomer
C 21	33	2.5	2455	21	Z45836	cDNA of intestinal
C 22	33	2.5	2821	21	Z45837	cDNA of intestinal
C 23	33	2.5	5059	20	X84332	Stealth virus nucl
C 24	32.8	2.5	1140	20	X36611	Pseudomonas oxidat
C 25	32.8	2.5	2830	21	A23429	cDNA encoding huma
C 26	32.6	2.5	534720	19	V30458	Rhizobium species
C 27	32.6	2.5	536165	19	V30459	Rhizobium species
C 28	32.4	2.5	1546	12	Q12568	Protease2 and beta
C 29	32.4	2.5	3172	12	Q12566	Alkaline protease
C 30	31.4	2.4	690	19	V64538	M. tuberculosis im
C 31	31.4	2.4	690	19	V44429	Mycobacterium tube
C 32	31.4	2.4	690	20	Z19339	M. tuberculosis an
C 33	31.4	2.4	690	20	Z19127	M. tuberculosis re
C 34	31.4	2.4	1755	19	V03306	Bacterium OC9a pho
C 35	31.4	2.4	2241	21	Z51469	Vector pVgRXR enco
C 36	31.4	2.4	2295	21	Z51470	Vector pVgRXR-5A/5
C 37	31.4	2.4	2301	21	Z51471	Control vector pVg
C 38	31.2	2.4	1116	20	X81700	DNA encoding a fru
C 39	31.2	2.4	1359	21	Z53148	Neisseria gonorrhoe
C 40	31.2	2.4	1359	21	Z53150	Neisseria meningit
C 41	31.2	2.4	3358	20	V70229	Human receptor tyr
C 42	31.2	2.4	35099	19	V27112	Adenovirus 17. Ma
C 43	31	2.4	1531	18	T46195	Maize insecticidal
C 44	30.8	2.4	611	21	Z80753	Human colon cancer
C 45	30.8	2.4	1837	20	Z16889	Human gene express

ALIGNMENTS

RESULT 1
Q20833
ID Q20833 standard; DNA; 1321 BP.
XX Q20833;
AC Q20833;
XX
DT 01-MAY-1992 (first entry)
DE Manipulated glyphosate oxidoreductase gene.
XX
KW Recombinant; GOR; resistance; ss.
XX
OS Bacterial isolate LBAA.
XX
FH Key Location/Qualifiers
FT CDS 9..1304
FT /*tag= a
FT /note= "encodes wild type glyphosate oxidoreductase"
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PN W09200377-A.
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PD 09-JAN-1992.
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PF 24-JUN-1991; 91WO-US04514.
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PR 24-JUN-1991; 91US-0717370.
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PR 25-JUN-1990; 90US-0543236.
XX
PA (MONS) MONSANTO CO.
XX
PI Kishore GM, Barry GF;
XX
DR WPI, 1992-041559/05.
XX
DR P-PSDB; R20642.

PT Gene encoding glyphosate oxido-reductase enzyme - used to
PT transform plants to produce plants tolerant to glyphosate
XX herbicide
XX
PS
PS
XX

Claim 1; Fig 3; 142pp; English.

CC The sequence is that of the gene encoding a glyphosate oxidoreductase
CC (GOR) enzyme which has been manipulated such that it is suitable for
CC introduction into and expression in plant transformation vectors, but
CC it still encodes the wild type GOR enzyme. It was obtd. from bacterial
CC isolate LBAA. It is used to transform plants such that they express
CC the enzyme sufficiently to enhance the glyphosate tolerance of the
CC plant. Transformed plants resistant to glyphosate can be obtd. so
CC that weeds can be selectively controlled in fields contg. crops.
CC See also Q20832-Q20841 and Q22705.

XX Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;

Query Match 99.9%; Score 1294.4; DB 13; Length 1321;
Best Local Similarity 99.9%; Pred. No. 0;
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DB 1029 gccctcgccgtcgagttcttgaaagacgatattccaaatggatgggttcggtccgagc 1088
QY 1081 ATCCCGGATTCGCTCCCGCTGATTTGGCGCGGCAACCCGACACCGGACGTTATCTATGCT 1140
DB 1089 atcccggaattcgctcccggtgattggccgggcaacccggacacccgacgttaattatgct 1148
QY 1141 TTCGGCCACGGTCACTCTCGGCATGACAGGCGCGCGGATGACGCAACGCTCGTCTCAGAG 1200
DB 1149 ttgggcaagctcatctcgcatgacagggggtgcgcatgacgcaaacgctcgtctccag 1208
QY 1201 CTCTCGCAGCGCAAAAGACCTCAATCGACATTTGCGCCTTTCGCACCAACCGCTTTGGT 1260
DB 1209 ctctcgcagcgcaaaagacctcaatcgacatttcgctccttcgcaccaaacccgcttgg 1268
QY 1261 ATTGGCAAAATCCAAGCAACCGGTCGCGCAAGTTAA 1296
DB 1269 atggcaaatccaagcaaacgggtccggcaagttaa 1304

RESULT 2
Q22705
ID Q22705 standard; DNA; 1692 BP.
XX AC Q22705;
XX AC Q22705;
DT 01-MAY-1992 (first entry)
XX XX
DE Glyphosate oxidoreductase gene.
XX XX
KW Recombinant; GOR; resistance; ss.
XX XX
OS Bacterial isolate LBAA.
FH Key Location/Qualifiers
CDS 120..1415
FT /*tag= a
FT /note= "glyphosate oxidoreductase coding region"
FT misc_feature 350.
FT /*tag= b
FT /note= "not present in alternative sequence"
FT misc_feature 377.
FT /*tag= c
FT /note= "not present in alternative sequence"
FT misc_feature 392.
FT /*tag= d
FT /note= "not present in alternative sequence"
XX WO9200377-A.
XX PN
XX 09-JAN-1992.
XX PD
XX 24-JUN-1991; 91WO-US04514.
XX PF
XX

PR 24-JUN-1991; 91US-0717370.
PR 25-JUN-1990; 90US-0543236.
XX (MONS) MONSANTO CO.
PA Kishore GM, Barry GF;
XX WPI: 1992-041559/05.
DR P-PSDB; R22262.
XX
PT Gene encoding glyphosate oxido-reductase enzyme - used to
PT transform plants to produce plants tolerant to glyphosate
PT herbicide
XX
PS Claim 1; Fig 2; 142pp; English.

The sequence is that of a gene encoding a glyphosate oxidoreductase (GOR) enzyme. It was obtd from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops. This sequence (fig 2) contains apparent discrepancies (see feature table) with a supposedly identical sequence (SEQ ID No.3 in the specification), since it is unclear from the specification which of these is correct, both sequences have been indexed. See also Q0833-Q20841 and Q20832 - the alternative sequence for the GOR gene.

XX Sequence 1692 BP; 381 A; 478 C; 471 G; 361 T; 1 other;

Query Match 99.4%; Score 1288; DB 13; Length 1692;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCGTGAACACAAAAGTAGCATCGCTGGCGGGAATCGTCGGCTATGCCAGC 60
DB 120 atgctggaaccacaaaagtagcatcgctggcggaatcgctgctgtagcgcag 179
QY 61 GCGCTCATGCTTACGCGCGCGGATTCAAAGTCACCTTTGATTCACCCGAACCTCTCTGGC 120
DB 180 ggcgtgatgcttcagcgccgcggattcaaaagtcacattgatgacccgaagcctcctggc 239
QY 121 GAAGTGATCGCTTTGGGAATCGCGGATGCTTCAACGGCTCATCGCTCGCTCATGCTCC 180
DB 240 gaagtgatcgctttgggaatcgcgatgcttcaacggctcatcgctcctcatgtcc 299
QY 181 ATGCGCGGAAACTTGACGAGCGTGCAGAGTGCTTCCCTTGACCCCGATGGCGCGTGTCA 240
DB 300 atgcccggaaaacttgacgagcgtgcgaagtgctccttgaccccgatggcgctgtgca 359
QY 241 ATCCGCTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTTCTGTAGCCGGA 300
DB 360 atccggttcagctattttccaaacatcatgccttggtgatcgctttctgttagccgga 419
QY 301 AGACCAACAAGGTGAAGAGCAGCGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
DB 420 agaccaacaaggtgaagagcagcggaagcactccgcaatctcatcaagtcacgggtg 479
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGCTGATGCGAGCCATCTCATCGCCATGAAGGT 420
DB 480 cctctgaacaagctattggcgagagcgtgatgcgacatctgatccgccatgaagt 539
QY 421 CATCTCACCGTATATCGTGGAAGCAGACTTTCGCAAGCGCGGAGGTTGGGAACGTG 480
DB 540 catctgacggtatalcgtggaagaacagacttcgcaagaagccgcggaggttggaactg 599
QY 481 CGGCGCTCAACGGTGTGCGACGAGATCTCTACGCGCGGATGCGTTCGGGATTTCCGAT 540
DB 600 cgccgtctcaacgggtgttcgcacgcagatccctcagcgcgatgcttgcgggattctgat 659
QY 541 CCGAACTTGTCCGATGCGTTTACCAGGGCATCTTATAGAGAGAACGGTCAACAGTAT 600
DB 1296 attggcaaatccaagcaaaacgggtccggcaagttaa 1415

RESULT 3
Q20832
ID Q20832 standard; DNA; 1689 BP.
XX
AC Q20832;
XX
DT 01-MAY-1992 (first entry)
XX
DE Glyphosate oxidoreductase gene.
XX
KW Recombinant; GOR; resistance; ss.
XX
OS Bacterial isolate LBAA.
XX
FH Key Location/Qualifiers
FT CDS 120..1412
FT /*tag= a
FT /note= "glyphosate oxidoreductase coding region"
FT misc_feature 349..350
FT /*tag= b
FT /note= "in the alternative sequence G is present here"
FT misc_feature 375..376

FT /*tag- C
FT /note- "In the alternative sequence T is present here"
FT misc_feature 389..390
FT /*tag- d
FT /note- "In the alternative sequence C is present here"
XX
PN W09200377-A.
XX
XX
XX 09-JAN-1992.
XX
XX 24-JUN-1991; 91WO-US04514.
XX
XX 24-JUN-1991; 91US-0717370.
XX 25-JUN-1990; 90US-0543236.
XX
XX (MONS) MONSANTO CO.
XX
XX Kishore GM, Barry GF;
XX WPI; 1992-041559/05.
XX P-PSDB; R20642.
XX
XX Gene encoding glyphosate oxido-reductase enzyme - used to
XX transform plants to produce plants tolerant to glyphosate
XX herbicide
XX
XX Claim 1; Page 93; 142pp; English.
XX
XX The sequence is that of a gene encoding a glyphosate oxidoreductase
XX (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used
XX to transform plants such that they express the enzyme sufficiently
XX to enhance the glyphosate tolerance of the plant. Transformed plants
XX resistant to glyphosate can be obtd. so that weeds can be selectively
XX controlled in fields contg. crops. This sequence (SEQ ID No.3 in the
XX specification) contains apparent discrepancies (see feature table)
XX with a supposedly identical sequence (fig 2), since it is unclear
XX from the specification which of these is correct, both sequences have
XX been indexed. See also Q20833-Q20841 and Q22705 - the alternative
XX sequence for the GOR gene.
XX
XX Sequence 1689 BP; 381 A; 477 C; 470 G; 360 T; 1 other;

Query Match 96.6%; Score 1252; DB 13; Length 1689;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGACACACAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGGGTATGCACG 60
Db 120 atgtctgagaaccacaaaagtaggcctgctgagccggaatcgtcgggtatgcacg 179
Qy 61 CGCGTGATGCTTACGCGCCGCGGATTCAAAGTCACTTGAATGACCCGAAACCCCTCTGGC 120
Db 180 gcgctgatgcttcagccgcgagatcaaaagtcacattgattgaccgcgaagccctcctggc 239
Qy 121 GAAGGTGCATGTTGGGATGCGCGATGCTTCAACGCTCATCCGTCGTCCTATGTCC 180
Db 240 gaaggtgcatgcttgggaaatgcgcgagtgcttcaacggtcctcgtcgtccctatgtcc 299
Qy 181 ATGCCGGGAACTTGAAGAGCTGCCGATGGCTTCTTGACCCGATGGGCGCTTGTCA 240
Db 300 atgcgaggaaacttgacgagcgtgcgaagtggtcctcttgaccgat-gggccgttgctca 358
Qy 241 ATCCGGTTCAGCTATTTCACCAACCATATGCCCTGGTGTGATTGCTGCTTCTTACCGCGA 300
Db 359 atccggttcagcta-tttccaaccatcatg-cctgggttgattcgtcttcttgtagccgga 416
Qy 301 AGACCAACAGGTGAGGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCACCGGTG 360
Db 417 agaccaaacaaggtgaaaggagcagcgaaagcactccgcaatctcatcaagtcacaggtg 476
Qy 361 CCTGTGATCATGTTGGCGGAGAGGCTGATCGGAGCCATCTGATCCGCCATCAAGGT 420
|||||

Db 477 cctctgatcaagtcattgpgcgagagagcgtgatgcgagccattgatccgccatgaaggt 536
Qy 421 CATCTGACCGTATATCTGTTGGAGAACACACACTTTCGCCCAAGGACCGCGAGGTGGCACTG 480
|||||
Db 537 catctgaccgtatatctcgcggagaaagcactctcccaaggaccgcggaggttcggaaactg 596
Qy 481 CGGCGTCTCAACAGGTGTTTCGCACGCAGATCCTACGCGCGATGCGTTCGGGATTTTCGAT 540
|||||
Db 597 cggcgtctcaacgcgtgttcgcacgcagatcctcagcgcgatgcttcgaggattcgtat 656
Qy 541 CCGAACTTGTGCGCATCGCTTTACCAAGGGCATTTATTAGAAAGAACCGGTACACAGATT 600
|||||
Db 657 ccgaacttgcgcgatgcgtttaccaaaggcattctctatagaagaagacgggtcacacgatt 716
Qy 601 AATCGCAAGGGCTCGTCAACCTCTTGTTCGGCGTTCCTATCGCGCAACGGTGGCGCAATT 660
|||||
Db 717 aatcgcgaaggcgtcgtgacccctcttcttcggcgcttcttcgcggaacggttcggaattc 776
Qy 661 GTATCTGCGCGTGTCAATCGGCTTTGAGACTGAAGGTAGGGCGCTTTAAAGGCATTTACAACC 720
|||||
Db 777 gtatctgcgctgtcatcgcgtcttgagactgaaggtagggcgtctaaaggcattacaacc 836
Qy 721 ACGAACGGCTTCTGCGCGTTCATCCACGGTTCGCGAGCGCGGCGCACACTCGAAATCA 780
|||||
Db 837 acgaacggcgttctggccgttgatgcagcgggttgctgcagcggcgccacactcgaatca 896
Qy 781 CTTGCTAAATTCGTTAGGCGATGACATCCGCTCGATACCGAACGTGGATATCATATCGTC 840
|||||
Db 897 ctctgtaattcgtctagcgatgacatccgcctcgtatccgaacgcyggtatcatatcgtcc 956
Qy 841 ATCGGAATTCGGAGAGCGCTCCACGCATTCGACGACCGCATGCGTCAGGAAATTCATC 900
Db 957 atcgcgaatccggaagccgcctccacgcattccgacgaccgatgcgtcaggaaaaattcatg 1016
Qy 901 CGGACACATATGGAATGGGGCTTCGCGTTCGGGGTACGGTTGAGTTTCGTCGGGCTCACA 960
Db 1017 gcgacacataggaaatgggcttcgcgtggcgggtacgggttgagttcgtcgggtcaca 1076
Qy 961 CGCGTCTCTAACTGGAACGTTGCGCATGCTCTATACGACGCTCGAAACTTCTTCCA 1020
|||||
Db 1077 gcgcctcctaactggaaaacgtgcgcatgtctctatacgcacgctcggaaactcttcca 1136
Qy 1021 GCCCTCGCGCTGCGAGTTCCTGAAGAACGATATTCCTCAATGGATGGGTTCGCGCCGAGC 1080
Db 1137 gccctcgcgctgcgagttcttgaaagaacgatattccaaatggatgggttcgcggcgcagc 1196
Qy 1081 ATCCCGGATTCGCTCCCGCTGATTCGCGCGGCAACCCCGACACCGATATCTATGCT 1140
Db 1197 atcccggaattcgtctcccgctgattggccgggcaaccccgacacgtaattctatgct 1256
Qy 1141 TTCGCCACCGTCAATCTCGGATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1200
Db 1257 ttcggcaatggtcatctcgtcgtatgacaggggcgcgagtcgacgaaacgtcgtctccagag 1316
Qy 1201 CTCTTCGAGCGGCAAAAGACCTCAATCGACATTTGCGCCCTTCGCAACCAACCGCTTGGT 1260
Db 1317 ctctcgcgagcgaaaagacctcaatcgacatttcgccttcgcacccaacccgcttgggt 1376
Qy 1261 ATTGCAAAATCCAACCAACCGGTCGCGCAAGTTAA 1296
|||||
Db 1377 attgcaaatccaagcaaacgggtcccgcaagtttaa 1412

RESULT 4
Q20834
ID Q20834 standard; DNA; 1321 BP.
XX
AC Q20834;
XX
DT 01-MAY-1992 (first entry)
XX
DE Modified glyphosate oxidoreductase gene.
XX

Db	1261	attggtaagtcacgaactggtccctgcatcctaa	1296	
RESULT	6			
X57309	ID	X57309 standard; DNA; 8418 BP.		
XX	AC	X57309;		
XX	DT	26-JUL-1999 (first entry)		
XX	DE	Sugar beet T-DNA containing cp4/epsps #2.		
XX	KW	Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;		
XX	KW	5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;		
XX	KW	tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.		
XX	OS	Beta vulgaris.		
XX	PN	WO9923232-A1.		
XX	PD	14-MAY-1999.		
XX	PD			
XX	PF	29-OCT-1998; 98WO-EP06859.		
XX	PR	31-OCT-1997; 97US-0112003.		
XX	PA	(NOVS) NOVARTIS AG.		
XX	PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX	PI	Mannerloef M, Steen P, Tenning PP;		
XX	DR	WPI; 1999-313347/26.		
XX	PT	Glyphosate resistant transgenic sugar beet plants		
XX	PS	ClaIm 15; Page 36-41; 55pp; English.		
XX	CC	This invention describes a novel sugar beet plant, including its		
XX	CC	descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase		
XX	CC	(cp4/epsps) enzyme activity which is obtainable by Agrobacterium		
XX	CC	mediated transformation with a gene allowing expression of cp4/epsps		
XX	CC	in plants, where the plant lacks both right and left T-DNA border		
XX	CC	sequences. The transgenic sugar beet plants of the invention are capable		
XX	CC	of tolerating herbicide treatment with glyphosate (also known as		
XX	CC	N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.		
XX	Sequence	8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;		
Query Match	74.2%;	Score 961.6; DB 20; Length 8418;		
Best Local Similarity	83.9%;	Prod. No. 9.5e-297;		
Matches 1087;	Conservative	0; Mismatches 209; Indels 0; Gaps 0;		
Qy	1	ATGGCTGAGAACCCACAAAAAGTAGGCATCGCTGGAGCCGGAAATCGTCGGCGTATGCACG	60	
Db	7095	atggctgagaaccacagaagtggtatcgctggagctgaatcgttgggtttgcact	7154	
Qy	61	GCCTGATGCTTCAGCCGCGGATTCAAAGTCACCTTGATTGACCCGAAACCCCTCGTGGC	120	
Db	7155	gccttgatgctcaacgctggatcaaggtacccttgattgatccaaacccaccagggt	7214	
Qy	121	GAAGTGCATCGTTTGGGAATCGCGGATGCTTCAACGCTCATCCGTCGTCCTATGTC	180	
Db	7215	gaaggtgctcttcttcg9gtaacgcgtgctcaacggttccctcgctgttccaatgtcc	7274	
Qy	181	ATGCCGGAAACTTGACGAGCGTGCAGAGTGGCTTCCTTGACCCGATGGGCGCTGTGCA	240	
Db	7275	atgccaggaacttgactagcgttccaaagtgccttcttgacccaatgg9gtccattgtcc	7334	
Qy	241	ATCCGGTTACGCTATTTCCTCAACCATCATCCCTGGTTGATTCCCTTCTCTGTAGCCGGA	300	

ID T85664 standard: DNA; 1631 BP.
AC T85664;
XX
XX
XX 21-NOV-1997 (first entry)
XX
XX CPT1-GOX gene fusion.
DE
XX
XX expression cassette; inducible promoter; alca; alcR; alda; regulator;
KW alcohol dehydrogenase; herbicide resistance gene; glyphosate;
KW N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EPSPS;
KW 5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1;
KW Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
XX
XX Chimeric Arabidopsis.
OS
OS Synthetic.
XX
XX W09706269-A1.
PN
XX
XX 20-FEB-1997.
XX
XX 02-AUG-1996; 96WO-GB01883.
XX
XX 03-AUG-1995; 95GB-0015941.
PR
XX
XX (ZENE) ZENECA LTD.
PA
XX
XX Jepson I;
XX
XX WPI; 1997-154273/14.
DR
XX
XX Chemically inducible cassette for expressing herbicide resistance
PT gene in plants - and derived plants, partic. for resistance to
PT glyphosate, avoids constitutive expression and minimises development
PT of herbicide tolerant weeds
XX
XX Example 3; Fig 7; 59pp; English.
PS
XX
XX A chemically inducible plant gene expression cassette which comprises an
CC inducible promoter linked to a gene (I) that confers resistance to a
CC herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-
CC glycine (glyphosate) or its salts, but may also be a gene for resistance
CC to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolones,
CC etc. The inducible promoter (e.g. alcA, alcR, alda or other alcR-induced,
CC gene promoter) is operatively linked to an alcR regulator sequence.
CC Induced expression of (I) avoids the risk that constitutive expression
CC may interfere with plant development; allows volunteer plants to be
CC controlled by herbicide applied without inducer and minimises the chance
CC that herbicide-resistant strains of weeds will arise. The expression
CC cassette is strictly controlled and suitable for general use in plants
CC (both mono- and dicotyledons). The alcA/alcR gene switch was exemplified
CC with genes conferring resistance to glyphosate. The switch was used to
CC drive inducible expression of glyphosate oxidase (GOX) in plants.
CC Switchable GOX was expressed alone or in conjunction with constitutive
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs
CC were optimised for expression in mono- and dicotyledonous crop species.
CC The present sequence comprises a fusion of the GOX gene fused to the
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This
CC sequence was ligated into pMUB1 (see T85666) and used in construction of
CC dicot vectors.
XX
XX Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match 67.8%; Score 878.8; DB 18; Length 1631;
Best Local Similarity 80.2%; Pred. No. 1.2e-270;
Matches 1079; Conservative 0; Mismatches 217; Indels 50; Gaps 2;
QY 1 ATGGCTGAGAACACAAAAAGTAGGATCGCTGGAGCCCGGAATGTCGGGTATGCACG 60
DB 1 ATGGCTGAGAACACAAAAAGTAGGATCGCTGGAGCCCGGAATGTCGGGTATGCACG 60
DB 274 atggtctgagaaccacaagaaggttgatcgtcgtgagtggaatcgttggttgcact 333
QY 61 CGCTGTATGCTTCAGCGCCCGCGGATTCAAAGTCACCTTGATTGACCCGAAACCTTCCTGGC 120

Db 334 gctttgatgtcttaacgctcgtggattcaagggttaccttgattgattccaaaccccaaggt 393
QY 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCGCTGCCCTATGATGCC 180
Db 394 gaaggtgctctcttcgtaacgctggttgcttcaacggttctcctcgttgttccaaatgtcc 453
QY 181 ATGCCGGGAACATTGACGAGCGTCCCGAAGTGGCTCTTGACC----- 223
Db 454 atgcaggaaacttgactagcgttccaaagtggcttcttggtactcgttgtaattcaagc 513
QY 224 -----CGATGGGGCGCTTGTCAATCCGGTTCAGCTATTTTCCAACCATCATGCCCTG 275
Db 514 ttacggatccaatgggtccatgctccatcgtttcagctactttcccaaccatcatgctctg 573
QY 276 GTTGATTGCTTCTGTTAGCGGGAAGCAACAAAGTGAAGGAGGAGGGAAGGCACT 335
Db 574 gttgatcgtttcttctgctggaagacaaagagtgaggaagcaagcaaggaagcact 633
QY 336 CCGCAATCTCATCAAGTCCACGGTCCCTCTGATCAAGTTCATTGGCGGAGGAGGTGATGC 395
Db 634 cgttaacctcatcaagtcactgtgecttgatcaagtccttgctgaggaagctgctgc 693
QY 396 GAGCATCTGATCCGCCATGAAGTTCATCTACCGTATATCGTGGAGAAGCAGACTTTCGC 455
Db 694 tagccaccttatccgtcacgaaggtcaccttaccgtgtaccgttgaggaagcagacttcgc 753
QY 456 CAAGGACCGCGAGGTTGGGAACCTGCGCGCTCTCAACGGTGTTCGACGCAAGATCTTCAG 515
Db 754 caaggacgctggaagttggaaccttcgtcctcaacggtgctcgtactctctctcctcag 813
QY 516 CGCGATCGCTTGGCGGATTTTCGATCCGAACTTGTGCATGCGTTCATACCAAGGCATTC 575
Db 814 cgtcgtcgtatcgtgattcgtactccttaacttgctcagcctttaccgaagggaatcct 873
QY 576 TATAGAGAGAACCGTTCACAGCATTAATCCGCAAGGCGCTGTGACCCCTCTTGTTCGCGC 635
Db 874 tatcgaagagaacggttcacaccatacaacccacaaggttcgtgactctctcttctcgtc 933
QY 636 TTTTATCGCAACCGTGGCGAATTTGTATCTGCGCTGTCATCGGCTTTGAGACTGAAGG 695
Db 934 ttcatcgtcaacgctggaagattcgtcgtcgtcgtgtatcgtgattcgaagactgaagg 993
QY 696 TAGGCGCTTAAAGGATTTACAACACGACGCGGTTCTTGGCCGTTGATGACGAGC----- 750
Db 994 tctgctcctcaaggttatcaccaccacaacggtgttcttctgctgctgctgctgctgct 1053
QY 751 -----GTTCTCGACGCGCGGCGACACTCGAATTCATTCCTTAAT 790
Db 1054 gtgaattcaagcttaactgcagttgttcagctggtgcacactccaagctctcttctgaact 1113
QY 791 CGCTAGCGCATGACATCCCGCTCGATACCGAACGTGGATATCATATGTCATCGGAATC 850
Db 1114 cccttggtgatgaactcccatggtgataccgaacggtgataccacacatcgtatgccaaac 1173
QY 851 CGGAAGCGCTTCCACGATTTCCGACGACCGATGCGTTCAGGAAATTCATCCGACACTA 910
Db 1174 cagaagctgtctccacgtatttccaaactaccggtcttcttggaagttcatcgtactactcta 1233
QY 911 TGGAAATGGGCTTTCGGTGGCGGTACGGTTGAGTTTCGCTGGGCTCACACCCGCTCCTA 970
Db 1234 tggagatgggtctctcgttctgctggaacggttgagttcgtctcactgctcactcactcta 1293
QY 971 ACTGGAACCGTTCGCATGCTCTATACGACGCTCGAATAATCTTCTCCAGCCCTCGCGC 1030
Db 1294 actggaagctgctcagcttctctacactcgtcgtcgttaagtgtcttccagctcgtc 1353
QY 1031 CTGCGAGTTTGAAGAAGCATATTTCCAATAAGTGGGTTCCCGCGGAGCATCCCGGATT 1090
Db 1354 ctgcagttctgagaagacgttactccaagtggatgggtttccgtccaagcatcccaagatt 1413
QY 1091 CGCTCCCGTATTTGGCGGGCAACCCGACCGAGGTAATCTATGCTTTCGGCCACG 1150


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FT /note= "homologous to the Tnp gene"  
FT 428292...429623  
FT /*tag= h  
FT /standard_name= "ORF K8"  
FT /product= "glutamate dehydrogenase-like protein"  
FT /note= "homologous to the GlUD1 gene"  
FT complement (430538...431284)  
FT /*tag= i  
FT /standard_name= "ORF K9"  
FT /product= "transposase homologue"  
FT complement (431296...432840)  
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FT /standard_name= "ORF K10"  
FT /product= "transposase homologue"  
FT /note= "homologous to the Tnp gene"  
FT complement (433880...434110)  
FT /*tag= k  
FT /standard_name= "ORF K11"  
FT /product= "protein of unknown function"  
FT /note= "homologous to the FixU gene"  
FT complement (434107...434433)  
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FT /standard_name= "ORF K12"  
FT /product= "protein of unknown function"  
FT complement (434517...434711)  
FT /*tag= m  
FT /standard_name= "ORF K13"  
FT /product= "ferrodoxin/ferrodoxin-like protein"  
FT /note= "homologous to the FdxN gene"  
FT complement (434753...436234)  
FT /*tag= n  
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FT /gene= "nifB"  
FT /product= "protein involved in Femo co-factor  
FT biosynthesis"  
FT complement (436460...438130)  
FT /*tag= o  
FT /standard_name= "ORF K15"  
FT /gene= "nifA"  
FT /product= "positive regulator of nif, fix and other  
FT genes"  
FT complement (438297...438590)  
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FT /gene= "fixX"  
FT /product= "protein required for nitrogenase activity"  
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FT complement (439923...441032)  
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FT /gene= "fixA"  
FT /product= "protein required for nitrogenase activity"  
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FT /standard_name= "ORF K22"
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FT /gene= "dctA"  
FT /product= "C4-dicarboxylate transport protein"  
FT /note= "homologous to the DctAI gene"  
FT 446599...447843  
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FT /note= "homologous to the CamC gene"  
FT 447844...448500  
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FT protein"  
FT /note= "homologous to the LinA gene"  
FT 448497...450203  
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FT /standard_name= "ORF L3"  
FT /product= "putative protein with degradative function"  
FT 450341...451396  
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FT /product= "luciferase alpha-subunit-like protein"  
FT /note= "homologous to the LuxA gene"  
FT 452980...454494  
FT /*tag= ab  
FT /standard_name= "ORF L6"  
FT /gene= "nifD"  
FT /product= "alpha-subunit of Femo protein of nitrogenase"  
FT 454590...456131  
FT /*tag= ac  
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FT /gene= "nifK"  
FT /product= "beta-subunit of Femo protein of nitrogenase"  
FT 456187...457677  
FT /*tag= ad  
FT /standard_name= "ORF L8"  
FT /product= "protein involved in Femo co-factor  
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FT /note= "homologous to the NifB gene"  
FT 457687...459096  
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FT biosynthesis"  
FT /note= "homologous to the FixF gene"  
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FT /note= "homologous to the NifX gene"  
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FT /product= "protein of unknown function"  
FT 460501...460920  
FT /*tag= ah  
FT /standard_name= "ORF L12"  
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FT of nitrogenase"  
FT /note= "homologous to the NifH gene"  
FT 461228...461545  
FT /*tag= ai  
FT /standard_name= "ORF L13"  
FT /product= "protein of unknown function"  
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FT		/product= "processing protease-like protein"
FT		/note= "homologous to the PP gene"
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Best Local Similarity 51.3%; Pred. No. 1.8;		
Matches 136; Conservative 0; Mismatches 125; Indels 4; Gaps 2;		
QY	997	ACGCACGCTCGAAACTTCTTC-CAGCCCTCGCGCTCGAGTTCGAGAAGCATATTC 1055
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QY	1056	CAAAATGGATGGGTTCGCGCGGAGCATCCGGATTCTGCTCCCGTATTGGCGGGCAAC 1115
Db	395408	CTATTGGTCGGGTCTCGGCCCAATGACCGCGGACGCCCGTTCATCGGCC---CAAC 395352
QY	1116	CGGGACACCCGACGTAATCTATGCTTTTCCGCCACGCTCATCTCGGCATGACAGGGCGCC 1175
Db	395351	GAAGATCGCGGTCTCTTCTTAACACCGGCGACGCGCTTGGCTGGACGATGAGCTC 395292
QY	1176	GATGACCGCAACGCTCGTCTCAGAGCTCTCGCAGCGGAAAGACCTCAATCGACATTTTC 1235
Db	395291	CGGCTCTGCGCGGTCTCATTCGCGACCTGGTATCTGCGCGGAAGCCGAGATCGACGCCAC 395232
QY	1236	GCCCTTCGCACCAACCGCTTTTGGT 1260
Db	395231	CGACCTCGCGTTCAGCGCTACGCT 395207
RESULT 11		
ID	V30459/C	
XX	AC	V30459 standard; DNA: 536165 BP.
XX	AC	
DT	06-JUL-1999	(first entry)
DE	Rhizobium species symbiotic plasmid pNGR234.	
XX		
KW	Symbiosis; open reading frame; ORF; plasmid; vector; transportation;	
KW	degradation; metabolism; host range; nitrogen fixation; nodulation;	
KW	legume; plant; ds.	
XX		
OS	Rhizobium sp.	
XX		
PN	W09802560-A2.	
XX		
PD	22-JAN-1998.	
XX		
PF	10-JUL-1997; 97WO-IB00950.	
XX		
PR	20-MAY-1997; 97GB-0010395.	
XX		
PR	12-JUL-1996; 96EP-0730001.	
XX		
PA	(MOLE-) INST MOLECULAR BIOTECHNOLOGY.	
PA	(BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.	
XX		
PI	Broughton WJ, Freiberg CB, Perret XP, Rosenthal A;	
XX		
XX	WPI; 1998-110606/10.	
XX		
PT	New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to	
PT	develop products for modifying plant characteristics, e.g. nitrogen	
PT	fixation, synthesis of compounds and stress response	
XX		
PS	Claim 1; Fig 3; 228pp; English.	
XX		
CC	This is the nucleotide sequence of the plasmid pNGR234a isolated from	
CC	Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the	

(2010) / GEN HOSPITAL CONF:

३८

३८

PI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
PI Rahme LG, Tan M, Tsongalis J;
XX WPI: 1999-357851/30.

XX Virulence factors useful in developing disease treatments

XX Disclosure; Fig 3; 228pp; English.

XX The present sequence represents a *Pseudomonas aeruginosa* nucleic acid
CC sequence. *P. aeruginosa* is an opportunistic human pathogen present in
CC soil water and plants. The specification describes virulence polypeptides
CC and nucleic acid sequence encoding such polypeptides. These sequences
CC can be used to identify a compound which is capable of decreasing the
CC expression of a pathogenic virulence factor. Compounds that inhibit
CC the expression or activity of virulence factor polypeptides can be
CC used to treat pathogenic infections, especially where the infection
CC is a *P. aeruginosa* infection.
CC note: the sequences given in the specification were poorly legible, and
CC in some instances assumptions were made as to the identity of the base;
CC it is therefore possible that the sequence given below is not entirely
CC correct.

XX Sequence 603 BP; 119 A; 219 C; 171 G; 94 T; 0 other;
SQ

Query Match 2.6%; Score 34; DB 20; Length 603;
Best Local Similarity 52.9%; Pred. No. 0.54;
Matches 73; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 16 AAAAAATAGGCAATCGGTGGAGCGGGAATCGTGGCGCTATGCACGGCGCTGATCGTTTCAG 75

Db 453 AGAGATGATAGTGTGTAGCGGTGGCGCTATCGCGCTGTGTACCGCCGCGGAGCTGGCG 394

QY 76 CGCGCGGATTCAAAGTCAACCTGATTGACCGGAACCTCTCGCGAAGTGCATCGTTT 135

Db 393 CTCCCCGGACTGGCGGTGACCCCTGGTGGAGCGGGCGAGAGTGGCGCTGAGGCATCCTGG 334

QY 136 GGGAAATCCGGATGCTTC 153

Db 333 GCGGAGCGGGATCGTC 316

RESULT 15

VI5073/c

ID VI5073 standard; DNA: 922 BP.

XX AC VI5073;

XX VI5073;

DT 19-MAY-1998 (first entry)

XX Hybrid DNA comprising a family 45 cellulase core region.

DE Cellulase core region; isolation; microorganism; identification;

XX Cellulase core region; isolation; microorganism; identification;

KW hybrid DNA; ss.

XX Chimeric - *Cylindrocarpum* sp.

OS Chimeric - *Humicola insolens*.

XX Key Location/Qualifiers

FT CDS 2..922

FT /*tag= a

FT /product= "hybrid gene construct"

XX WO9743409-A2.

XX 20-NOV-1997.

XX 12-MAY-1997; 97WO-DK00216.

XX 10-MAY-1996; 96DK-0000562.

XX (NOVO) NOVO-NORDISK AS.

PA

XX

PI

XX

DR

DR

XX

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 922 BP; 166 A; 325 C; 257 G; 174 T; 0 other;

XX

Query Match 2.6%; Score 34; DB 19; Length 922;

Best Local Similarity 47.2%; Pred. No. 0.67;

Matches 103; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 553 CATCGTTTACCAAGGCGATTCTTATAGAGAGAACGCTACACGATTAATCCCAAGGG 612

Db 373 CTTCCTCCCTTACGCGGCGCAGTCGTAAGAGTGAGAGCGTAGCAACACACAGCAGCTGGA 314

QY 613 CTCTGTGACCTCTTTTTCGCGGCTTTTATCGCGAACGCTGGCGAATTTGTATCTCGCGCT 672

Db 313 CTGCGAGCCTCCAGAGAGCTTGTAGCGGCAAGCCATAGCGAGGTTGTCTGTGACAGC 254

QY 673 GTCATCGGCTTTGAGACTGAAGGTAGGCGGCTTAAAGGCATTTACAACACACGAGCGGTT 732

Db 253 CCACGGGGAGTTGTTGTCTGAGGTGTAGGAAGTCCCGCGCTTGAACGCGCTCACCGGCTT 194

QY 733 CTGCGCGTTGATGCAGCGGTTGTGCGAGCGGCGCACA 770

Db 193 GCGCTCGAGATGGGTTGTCTGTCTGCGAGCTCA 156

Search completed: January 1, 2001, 03:42:34

Job time: 20162 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:17:38 ; Search time 157.96 Seconds
(without alignments)
1240.873 Million cell updates/sec

Title: US-08-484-274-6
Perfect score: 1296
Sequence: 1 ATGGGTGAGAACACAAAA.....AAACGGTCCGCCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/PCFUS_COMB.seq.*
7: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1296	100.0	1296	2	US-08-484-274A-6
3	1291.2	99.6	1692	2	US-08-484-274A-3
4	1255.2	96.9	1293	1	US-08-391-339-4
5	1255.2	96.9	1293	2	US-08-484-274A-4
6	1255.2	96.9	1689	1	US-08-391-339-3
7	1201.6	92.7	1296	1	US-08-391-339-7
8	1201.6	92.7	1296	2	US-08-484-274A-7
9	961.6	74.2	1296	1	US-08-391-339-8
10	961.6	74.2	1296	2	US-08-484-274A-8
11	958.4	74.0	1296	1	US-08-391-339-17
12	958.4	74.0	1296	2	US-08-484-274A-17
13	56.2	4.3	69	1	US-08-391-339-30
14	56.2	4.3	69	1	US-08-391-339-33
15	56.2	4.3	69	2	US-08-484-274A-30
16	56.2	4.3	69	2	US-08-484-274A-33
17	50.6	3.9	65	1	US-08-391-339-28
18	50.6	3.9	65	2	US-08-484-274A-28
19	48.2	3.7	61	1	US-08-391-339-31
20	48.2	3.7	61	2	US-08-484-274A-31
21	47.6	3.7	62	1	US-08-391-339-27
22	47.6	3.7	62	2	US-08-484-274A-27
23	47.2	3.6	68	1	US-08-391-339-32
24	47.2	3.6	68	2	US-08-484-274A-32
25	33	2.5	41	1	US-08-391-339-29
26	33	2.5	41	2	US-08-484-274A-29

27	33	2.5	423	1	US-08-470-179-144	Sequence 144, Appl
c 28	32.4	2.5	1209	1	US-08-314-309A-5	Sequence 5, Appl
c 29	32.4	2.5	1513	1	US-08-314-309A-2	Sequence 2, Appl
c 30	32.4	2.5	1546	1	US-08-314-309A-3	Sequence 3, Appl
c 31	32.4	2.5	1722	1	US-08-314-309A-1	Sequence 1, Appl
c 32	31.4	2.4	2241	5	US-09-144-759-17	Sequence 17, Appl
c 33	31.4	2.4	2295	5	US-09-144-759-19	Sequence 19, Appl
c 34	31.4	2.4	2301	5	US-09-144-759-21	Sequence 21, Appl
c 35	31.2	2.4	3358	3	US-08-469-537A-104	Sequence 104, Appl
36	31	2.4	1531	2	US-08-449-986-1	Sequence 1, Appl
37	31	2.4	1531	3	US-08-756-855-1	Sequence 1, Appl
c 38	30.2	2.3	2880	1	US-08-462-484-3	Sequence 3, Appl
c 39	30.2	2.3	2880	2	US-08-441-147-3	Sequence 3, Appl
c 40	30.2	2.3	2880	6	PCT-US95-07536-3	Sequence 3, Appl
c 41	29.8	2.3	2970	6	PCT-US92-06391-1	Sequence 1, Appl
c 42	29.6	2.3	1300	4	US-08-440-845D-8	Sequence 8, Appl
c 43	29	2.2	1296	1	US-08-391-339-7	Sequence 7, Appl
c 44	29	2.2	1296	2	US-08-484-274A-7	Sequence 7, Appl
c 45	29	2.2	8931	5	US-09-028-934-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-391-339-6
; Sequence 6, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-391-339-6

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Best Local Similarity 100.0%; Pred. No. 0;

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QY	121	GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC	180
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Db	241	ATCCGCTTCAGCTATTCTTCCAAACCATCATGCCCTGGTTGATTTCGCTTCTAGCCCGA	300
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Db	361	CCTCTGATCAAGTCAATGGCGGAGAGCTGATCGGAGCCATCTGATCCGCCATGAAGGT	420
QY	421	CATCTGACCGTATATCTGGAGAGCAGACTTCGCCAAGGACCGCGGAGGTTGGAACTG	480
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QY	481	CGGCGTCTCAACCGTGTTCGCACCGATCCTCAGCGCCGATGGCTTGGCGGATTTCCAT	540
Db	481	CGGCGTCTCAACCGTGTTCGCACCGATCCTCAGCGCCGATGGCTTGGCGGATTTCCAT	540
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QY	601	AATCCGCAAGGCTCGTGACCCCTCTCTCTTTCGGCGTATTCGCGAACGCTGGCGAATTT	660
Db	601	AATCCGCAAGGCTCGTGACCCCTCTCTCTTTCGGCGTATTCGCGAACGCTGGCGAATTT	660
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QY	841	ATCGCGAATCCGGAAGCGCTCCACCGCATTCGACGACCGATGCGTCAGGAAAATTCATC	900
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QY	901	GCACACCTATGGAATGGGGCTTCGGGTGGCGGTACGGTTGAGTTCGCTGGGCTCACA	960
Db	901	GCACACCTATGGAATGGGGCTTCGGGTGGCGGTACGGTTGAGTTCGCTGGGCTCACA	960
QY	961	GCCGCTCCTAATCGAAACCTGGCATGTCTCTATACGCAACGCTCGAAACCTCTTCCA	1020
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Db	1021	GCCCTCGCGCTCGGATTCGTAAGAACGATATTCGAAATGGATGGGTTCCGCGCCGAGC	1080

QY	1081	ATCCCGGATTTCGCTCCCGTGGTGGCGGCAACCCGACACCCGACCTAAATCTATGCT	1140
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QY	1141	TTCCGCCACCGTTCATCTCGGCATGACAGGGGGCGGATGACCGCAACGCTGCTCAGAG	1200
Db	1141	TTCCGCCACCGTTCATCTCGGCATGACAGGGGGCGGATGACCGCAACGCTGCTCAGAG	1200
QY	1201	CTCCTCGGAGGCAAGACCTCAATCGACATTCGCCCTTCGCCACCAACCGCTTGGT	1260
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QY	1261	ATTGCCAATCCAAACCAACGGTCCGGCAAGTTAA	1296
Db	1261	ATTGCCAATCCAAACCAACGGTCCGGCAAGTTAA	1296
RESULT 2			
US-08-484-274A-6			
: Sequence 6, Application US/08484274A			
: Patent No. 5776760			
: GENERAL INFORMATION:			
: APPLICANT: Kishore, Ganesh M.			
: APPLICANT: Barry, Gerard F.			
: TITLE OF INVENTION: Glyphosate Tolerant Plants			
: NUMBER OF SEQUENCES: 33			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Arnold, White & Durkee			
: STREET: P.O. Box 4433			
: CITY: Houston			
: STATE: Texas			
: COUNTRY: USA			
: ZIP: 77210-4433			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/484,274A			
: FILING DATE: 07 June 1996			
: CLASSIFICATION: 435			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Patterson, Melinda L.			
: REGISTRATION NUMBER: 33,062			
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (713)789-2679			
: INFORMATION FOR SEQ ID NO: 6:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1296 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: double			
: TOPOLOGY: linear			
: MOLECULE TYPE: DNA (recombinant)			
us-08-484-274A-6			

Query Match	100.0%;	Score 1296;	DB 2;	Length 1296;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1296;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY	61	GCCTGTATGCTTCAGCGCCCGCGGATTCAAAGTCAACCTTGAATGACCGCAACCTCTCTGGC	120
Db	61	GCCTGTATGCTTCAGCGCCCGCGGATTCAAAGTCAACCTTGAATGACCGCAACCTCTCTGGC	120
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Db 121 GAAGGTGCATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCCCTATGTCC 180
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Db 301 AGACAAACAAGGTGAAGGACGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
Qy 361 CTTCTGATCAAGTCAATTCGGCGAGGAGCTGATCGAGCCCATCTCATCCGCCATGAAGGT 420
Db 361 CTTCTGATCAAGTCAATTCGGCGAGGAGCTGATCGAGCCCATCTCATCCGCCATGAAGGT 420
Qy 421 CATCTGACCGTATATCTGTGGAGAAGCAGACTTCGCCAAGGACCGGGAGGTGGGAACGT 480
Db 421 CATCTGACCGTATATCTGTGGAGAAGCAGACTTCGCCAAGGACCGGGAGGTGGGAACGT 480
Qy 481 CGGCTCTCAACGGTGTTCGCACGCGAGATCTCTACGCGCGATGCTTCGGGGATTTTCGAT 540
Db 481 CGGCTCTCAACGGTGTTCGCACGCGAGATCTCTACGCGCGATGCTTCGGGGATTTTCGAT 540
Qy 541 CCGAACTTGTCCGATCGCTTTACCAAGGGCATTTCTATAGAAGAAACGGTCCACAGATT 600
Db 541 CCGAACTTGTCCGATCGCTTTACCAAGGGCATTTCTATAGAAGAAACGGTCCACAGATT 600
Qy 601 AATCGGAAGGGCTCGTGACCCCTTTGTTTCGGGGTTTTTATCGGAACGGTGGGAATTT 660
Db 601 AATCGGAAGGGCTCGTGACCCCTTTGTTTCGGGGTTTTTATCGGAACGGTGGGAATTT 660
Qy 661 GTATCTCGCGCTGTCAATCGGCTTTGAGACTGAAGTACGGCGCTTAAAGGATTAACAAC 720
Db 661 GTATCTCGCGCTGTCAATCGGCTTTGAGACTGAAGTACGGCGCTTAAAGGATTAACAAC 720
Qy 721 ACGAACGCGCTTCTGGCGCTTCATCGACGCGTGTTCGAGCGCGCGCACACTCGAAATCA 780
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Qy 781 CTTGCTAATTCGTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATCGTC 840
Db 781 CTTGCTAATTCGTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATCGTC 840
Qy 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGACGACCGATGCGTCAAGGAAATTCATC 900
Db 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGACGACCGATGCGTCAAGGAAATTCATC 900
Qy 901 CGCACACTATGGAATGGGCTTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTACA 960
Db 901 CGCACACTATGGAATGGGCTTTCGCGTGGCGGTACGGTTGAGTTTCGCTGGGCTACA 960
Qy 961 CGCGCTCTACTGGAACGTCGCGATGTGCTCTATAGGACGCTCGAANAATCTTCTCCA 1020
Db 961 CGCGCTCTACTGGAACGTCGCGATGTGCTCTATAGGACGCTCGAANAATCTTCTCCA 1020
Qy 1021 GCCCTCGCGCTCGGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCCGGCCGAGC 1080
Db 1021 GCCCTCGCGCTCGGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCCGGCCGAGC 1080
Qy 1081 ATCCCGGATTCGCTCCCGGTGATTTGGCGGCAACCCGACACCCGACGATATCTATGCT 1140
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Qy 1141 TTCGGCCACGGTCTATCTCGGCGATGACAGGGGGCGGATGACCGCAACGCTCGTCTCAG 1200
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Qy 1201 CTCTTCGAGCGGAAAGACCTCAATCCACATTTCCGCCCTTCGCACCAACCCGCTTTGGT 1260
Db 1201 CTCTTCGAGCGGAAAGACCTCAATCCACATTTTCGCCCTTCGCACCAACCCGCTTTGGT 1260

Qy 1261 ATTGCAAAATCAAGCAAAACGGGTCCGCCAAAGTTAA 1296
Db 1261 ATTGCAAAATCAAGCAAAACGGGTCCGCCAAAGTTAA 1296
RESULT 3
US-08-484-274A-3
: Sequence 3, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 3:
: LENGTH: 1692 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-484-274A-3

Query Match 99.6%; Score 1291.2; DB 2; Length 1692;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGCGTGAAGAACCAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
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Qy 241 ATCCGGTTCAGCTATTTTCCCAACCATCATGCCCTGGTGTGATTCGCTTCTGTAGCCGGA 300
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Qy 421 CATCTGACCGTATATCGTGGAGAACAGACATTCGCGAAGGACCGGAGGTGTTGGAACTG 480
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Db 780 GTATCTGCGCGTGTATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGATTTACAAC 839
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Db 840 ACGAACCGCTTCTGCGCGTGTATCGAGCGGTGTCGAGCGGTGTCGAGCGCGGACACCTCGAAATCA 899
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Db 960 ATCCGGAATCCGGAAGCGGTCTCCAGCATTCGAGACCGATGCGTCAGGAAATTCATC 1019
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Db 1320 CTCTCTCGAGGGGAAAGACCTCAATCGACATTTGCGCCCTTCGCAACCAACCGCTTTGGT 1379
Qy 1261 ATTGGCAATCCAGCAACGGGTTCGGCAAGTTAA 1296
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RESULT 4

US-08-391-339-4
; Sequence 4, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B44F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
; US-08-391-339-4

Query Match 96.9%; Score 1255.2; DB 1; Length 1293;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 ATGCGTGAAGACCAACAAAGTAGGATCGCTGGAGCGGAAATCGTGGCGTATGCACG 60
Db 1 ATGCTGAGAACCAACAAAGTAGGATCGCTGGAGCGGAAATCGTGGCGTATGCACG 60
Qy 61 GCGCTGATGCTTACGCGCGCGGATTCAGAGTCACTTGATGACCCGAACTCTCTGGC 120
Db 61 GCGCTGATGCTTACGCGCGCGGATTCAGAGTCACTTGATGACCCGAACTCTCTGGC 120
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Db 298 AGACCAAAAGGTGAAGGAGGAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACCGTG 357
Qy 361 CCTCTGATCAAGTCATTCGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420

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Db 358 CCTCTGATCAAGTCATTCGGGAGGAGGCTGATCGAGGCAATCTATCGCCCATGAAGGT 417
Qy 421 CATCTGACCGTATATCGTGGAGAACAGACTTCGGCAAGGACCGGGAGGTTGGGAACGTG 480
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Qy 481 CGGCGTCTCAACGGTGTTCGGCAGCAGATTCCTCAGCGCGGATTCGTTGCGGGATTCGAT 540
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Qy 541 CGGAACCTTCGTCATCGCTTTACCAAGGCAATTCCTATAGAGAGAGAACGGTCACACGATT 600
Db 538 CGGAACCTTCGTCATCGCTTTACCAAGGCAATTCCTATAGAGAGAGAACGGTCACACGATT 597
Qy 601 AATCGCAAGGCTCGTACCGCTCTTGTTCGGCGCTTTTATCGGAACGGTGGCGGAATTT 660
Db 598 AATCGCAAGGCTCGTACCGCTCTTGTTCGGCGCTTTTATCGGAACGGTGGCGGAATTC 657
Qy 661 GTATCTGGCGGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTTAAAGGCAATTCACACC 720
Db 658 GTATCTGGCGGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTTAAAGGCAATTCACACC 717
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Db 718 ACGAAGCGGTTCTGGCGTTCATCGAGGCTTGTGCGAGCGCGCACACTCGAAATCA 777
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Qy 1201 CTCCTCGAGGCGAAAGACCTCAATCGACATTCGCCCTTCGACCAACCGCTTTGGT 1260
Db 1198 CTCCTCGAGGCGAAAGACCTCAATCGACATTCGCCCTTCGACCAACCGCTTTGGT 1257
Qy 1261 ATTGCAAAATCCAAAGCAACGGTTCGGCAAGTTAA 1296
Db 1258 ATTGCAAAATCCAAAGCAACGGTTCGGCAAGTTAA 1293
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RESULT 5
US-08-484-274A-4
; Sequence 4, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
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```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Mellinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
; US-08-484-274A-4
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Query Match 96.9%; Score 1255.2; DB 2; Length 1293;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGAACACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60
Db 1 ATGCTGAGAACACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGGTATGCACG 60
Qy 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGAACCTCTCTGCG 120
Db 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGAACCTCTCTGCG 120
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATCGTTCAACGGCTCATCGTTCCTATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCCGGATCGTTCAACGGCTCATCGTTCCTATGTCC 180
Qy 181 ATGCGGGGAAACTTGACGAGCGTGCGGAAGTGGCTCCTTGACCCGATGGGCGGTTGTCA 240
Db 181 ATGCGGGGAAACTTGACGAGCGTGCGGAAGTGGCTCCTTGACCCGAT-GGGCGGTTGTCA 239
Qy 241 ATCCGCTTCAGCTATTTTCCAAACCATCATGCGCTGGTGGTGGTTCGTTTCGTTAGCCGA 300
Db 240 ATCCGCTTCAGCTA-TTTCCAAACCATCATG-CCTGGTTGATTGCGTTTCTGTAGCCGA 297
Qy 301 AGACCAAAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 298 AGACCAAAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Qy 361 CCTCTGATCAAGTTCATTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 358 CCTCTGATCAAGTTCATTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
Qy 421 CATCTGACCGTATATCGTGGAGAACAGACTTCGCGCAAGGACCGCGGAGGAGGTTGGGAAC 480
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Qy 481 GCGCGTCTCAACGGTGTTCGGCAGCAGATTCCTCAGCGCGGATTCGTTGCGGGATTCGAT 540
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Db	478	CGCGCTCTCAACGGTGTTCGACGCAGATCTCTACGCCGCGATGCGTTCTCGGGGATTTTCGAT	537
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Db	1138	TTCCGGCATGTGTCATCTCGGCATGACAGGGGGCGCGATGACCGCAACGCTCGTCTCAGAG	1197
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RESULT

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RESUL 0
US-08-391-339-3
; Sequence 3, Application US/08391339
; Patent No. 5463175
;
; GENERAL INFORMATION:
;
; APPLICANT: Kishore, Ganesh M.
;
; APPLICANT: Barry, Gerard F.
;
; TITLE OF INVENTION: Glyphosate Tolerant Plants
;
; NUMBER OF SEQUENCES: 33
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dennis R. Hoerner, Jr.,
;
; ADDRESS: Monsanto Co. BBAF
;
; STREET: 700 Chesterfield Village Parkway
;
; CITY: St. Louis
;
; STATE: Missouri
;
; COUNTRY: USA
;
; ZIP: 63198
;
; COMPUTER READABLE FORM:

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Db 1077 GCGGCTCCTAAGTGAAGGTCGGATGCTCTATACGACGCTCGAAACCTTCTTCCA 1136
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Db 1137 GCGCTCGCGCTCGGAGTTCTCAAGAACGATATCCAAATGATGGGTTCCGGCGGAGC 1196
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Db 1197 ATCCCGGATTCGCTCCCGTGTATGGCGGGCAACCGGACACCGAGCTAATCTATGCT 1256
QY 1141 TTCGGCCAGGTCATCTCGGATGACAGGGGCGCGATGACCGGAACGCTGCTCAGAG 1200
Db 1257 TTCGGCCAGGTCATCTCGGATGACAGGGGCGCGATGACCGGAACGCTGCTCAGAG 1316
QY 1201 CTCCTCGGAGGGAAGACCTCAATCGACATTTCCGCCCTTCGCCACCAACCGCTTTGGT 1260
Db 1317 CTCCTCGGAGGGAAGACCTCAATCGACATTTCCGCCCTTCGCCACCAACCGCTTTGGT 1376
QY 1261 ATTTGCAATCAACGAACGGGTCGGCAAGTTAA 1296
Db 1377 ATTTGCAATCAACGAACGGGTCGGCAAGTTAA 1412

RESULT 7
US-08-391-339-7
: Sequence 7, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. B4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391.339

: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156.968
: FILING DATE:
: APPLICATION NUMBER: US/07/117.370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
US-08-391-339-7

Query Match 92.7%; Score 1201.6; DB 1; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAAG 60
Db 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
QY 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTCACTTTGATTGACCCGAACCTCCTGGC 120
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Db 541 CCGAACTTCTCGCATCGCTTTTACCAAGGCGATTTATAGAGAGAGACCGGTACACGATT 600
QY 601 AATCCGAAGGCTCGTGACCTCTTGTTCGGCGTTTATCCGGAACGGTGGCGAATTT 660
Db 601 AATCCGAAGGCTCGTGACCTCTTGTTCGGCGTTTATCCGGAACGGTGGCGAATTT 660
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661	Db	GTATCTCGCGGTCTATCGGTTTGTGAGACTGAGGTCTGCTCTCAAAGGCAATTACAACC	720
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721	Db	ACTAACGGTGTCTGSGCTGTTGATGCAGCTGTGTGTGTCAGCTGGTGACACTCTAAATCA	780
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841	Qy	ATCCGGAATTCGGAGCGCTCCACGCATTCGACGACCGATGCTCAGGAAATTCATC	900
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901	Db	GCACACCTATCGAAATGGGTCTTCGTGTCTGCTGCTACTGTTGAGTTGCTGGTCTCAC	960
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1021	Db		1080
1021	Db	GCCTTCGCGCTCGCAGTTCTCGAAGACGATATTCCAANTGGATGGGTTCGTCCTAGC	1080
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1141	Db	TTTGTGTCACGGTCACTCTCGGTATGACAGGTGCTCCAATGACTCGCAACTCTCGTCTCAGAG	1200
1201	Qy	CTCCTCCGACGGCGAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGTTTGGT	1260
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1201	Db	CTCCTCCGACGGCGAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGTTTGGT	1260
1261	Qy	ATTGGCAATTCACGAACACGGGTCCGGCAAGTTAA	1296
1261	Db		1296
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RESULTS

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US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
;
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Mellinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MB0T130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:

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Db 841 ATCCGAAATCCGAAGCGCTCCACCGCATTCGACGACGGATGCGTCAGGAAAAATTCATC 900
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Qy 961 GCGGCTCTTAAGTGAAGCGTCCGATGTCTATAGCAGCGCTCGAAAACCTTCCTTCCA 1020
Db 961 GCTGCTCTTAAGTGAAGCGTCCGATGTCTATAGCAGCGCTCGAAAACCTTCCTTCCA 1020
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Qy 1081 ATCCGGGATTCGCTCCCGCTGATTCGGCGGCAACCCGACACCGAGTAACTATGCT 1140
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Qy 1141 TTCGCCACGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGCTCTCAGAG 1200
Db 1141 TTGGTACGGTCACTCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCTCTCAGAG 1200
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Db 1201 CTCCTCGGAGGGAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCGCTTTGGT 1260
Qy 1261 ATTGCAATCCAGCAACGCGGTCGGCAAGTTAA 1296
Db 1261 ATTGCAATCCAGCAACGCGGTCGGCAAGTTAA 1296

RESULT 9

US-08-391-339-8
; Sequence 8, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-8

Query Match 74.2%; Score 961.6; DB 1; Length 1296;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGCTATGTCAGC 60
Db 1 ATGGCTGAGAACCAAGAAGTTGGTATCGCTGAGCTGGGAATCGTTGGTGTTCGACT 60
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Qy 121 GAAGGTGCAATCGTTTGGGAATCCCGGATCGCTTCAAGGCTCATCGTTCGTCCTATGTGCC 180
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Qy 181 ATCCCGGGAAGACTTCACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGCGGCTGTGTCA 240
Db 181 ATCCCGGGAAGACTTCACGAGCGTGCAGAGTGGCTCCTTGACCCGATGGCTGTGTGTCC 240
Qy 241 ATCCCGTTTCAAGTATTTTCCAAACCATCATGTCCTTGGTTGATTTGCTTTCCTGTAGCCGGA 300
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Db 301 AGACCAACAAGGTGAAGGAGCAGGGAAGACACATCCGCAATCATCAAGTCCACCGGTG 360
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Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420
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Db 421 CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAAGGAGCGGAGGTTTGGGAATTC 480
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Db 901 GCTACTCTATGGAGATGGGTCTCTCGTTGCTGGAACGGTTGAGTTGCTGGTCTGCTCACT 960

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Qy 1081 ATCCCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGCTAATCTATGCT 1140
Dy 1081 ATCCCGGATTCGCTCCCGGTGATTTGGCGGGCAACCCGGACACCCGACGCTAATCTATGCT 1140
Qy 1141 TTCCGGCAGCGTATCTCGCGCATGACAGGGCGCGGATGACCGAAGCGTCTGCTCAGAG 1200
Dy 1141 TTCCGGTACGCTACCTCGGTATGACTGCTTCCAAATGACCGAAGCGTCTGCTCAGAG 1200
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Dy 1201 CTCTCCGAGTGAAGACCTCTATGCATCTCTCCATTCGCAACCAACCGGTTTCGGT 1260
Qy 1261 ATTGGCAATCCAAAGCAACCGGTCGCGCAAGTTAA 1296
Dy 1261 ATTGGTAAGTCCAAAGCAACCGTGGTCTGCATCTAA 1296

RESULT 10

US-08-484-274A-8
; Sequence 8, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-8

Query Match 74.2%; Score 961.6; DB 2; Length 1296;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAAAAAGTAGGATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
Dy 1 ATGGCTGAGAACCAACAGAGGTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGCACT 60

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Dy 361 CCTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGNAAGGT 420
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Dy 541 CTTAACTTGTCTACGCTTTTACCAAGGAATCCTATCGAAGAGAACGGTCACACCATC 600
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Dy 721 ACCAAGGCTTCTGCTGTGATGACAGCTGTTTGCAGCTGTGACACACTCCAAAGTCT 780
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Qy 841 ATCCGGAATCCGGAGCGCTCCAGCATTCGAGACGACCGATGCGTCAGGAAATTCATC 900
Dy 841 ATCGCAACCCAGAGCTGCTCCACGTAATCCAACTACCGATGCTTCTGGAAGTTCATC 900
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Dy 961 GCTGCTCCTAAGTGAAGACGTCGCTACGTTCTCTACACTCACGCTCGTAAAGTTCCTCCA 1020
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Dy 1021 GCTCTCGCTCTGCCAGTTCTGAAGAACGTTACTTCCAAAGTGGATGGGTTTCGCTCAAGC 1080
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Dy 1081 ATCCAGATTCCTTCAGCATGATGGTGTGCTACCCGTACTCCAGACGTTATCTACGCT 1140

Qy	1141	TTGGGCGCAGGTCATCTCGGCATGACAGGGGCGGATGACCGCAACGCTGCTCTCAGAG	1200
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Qy	1201	CTCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTTTCGCACCAAAACCGGTTTGGT	1260
Db	1201	TT	1260
Qy	1261	ATTGGCAAAATCCAAGCAAAACGGGTCCGGCAAGTTAA	1296
Db	1261	TT	1296
Qy	1261	ATTGGTAAGTCCAAGCAAACTGGTCTGCATCCITAA	1296
Db	1261	TT	1296
RESULT 11			
US-08-391-339-17			
: Sequence 17, Application US/08391339			
: Patent No. 5463175			
: GENERAL INFORMATION:			
: APPLICANT: Kishore, Ganesh M.			
: APPLICANT: Barry, Gerard F.			
: TITLE OF INVENTION: Glyphosate Tolerant Plants			
: NUMBER OF SEQUENCES: 33			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Dennis R. Hoerner, Jr.,			
: ADDRESSEE: Monsanto Co. B4f			
: STREET: 700 Chesterfield Village Parkway			
: CITY: St. Louis			
: STATE: Missouri			
: COUNTRY: USA			
: ZIP: 63198			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/391.339			
: FILING DATE:			
: CLASSIFICATION: 800			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US/08/156.968			
: FILING DATE:			
: APPLICATION NUMBER: US/07/17.370			
: FILING DATE:			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Hoerner, Dennis R., Jr.			
: REGISTRATION NUMBER: 30,914			
: REFERENCE/DOCKET NUMBER: 38-21(10533)			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (314)537-6099			
: INFORMATION FOR SEQ ID NO: 17:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1296 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: double			
: TOPOLOGY: linear			
: MOLECULE TYPE: DNA (recombinant)			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: 1..1296			
: US-08-391-339-17			
Query Match 74.0%; Score 958.4; DB 1; Length 1296;			
Best Local Similarity 83.7%; Pred. No. 0;			
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps			
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Db	61	GCGCATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGACCGCAACCCCTCTGGC	120

Qy 1201 CTCCTCGAGCGGAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGGTTTGGT 1260
Dd 1201 CTCCTCGAGGTGAGAACCTCTATCGACATCTCCATTCGCAACAAACCGGTTTCGGT 1260
Qy 1261 ATTGGCAATCCAGCAAAACCGGTCGCGCAAGTTAA 1296
Dd 1261 ATTGGTAAGTCCAGCAAAACCGGTCGCAATCCCTAA 1296

RESULT 12

US-08-484-274A-17
: Sequence 17, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESS: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1296
US-08-484-274A-17

Query Match 74.08; Score 958.4; DB 2; Length 1296;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Qy 1 ATGGCTCAGAACCAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGGGATGACG 60
Dd 1 ATGGCTGAGAACCAACAAAGATTGGTATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT 60
Qy 61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTGATGACCCGGAACCCCTCCCTGGC 120
Dd 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
Qy 121 GAAGGTGCATGTTGGGAATGCGGGATGCTTCAACGGCTCATCCGTCGTCCTCATGTCC 180
Dd 121 GAAGGTGCCCTTTTCGGTAAACGCTGGTTCGCTTCAACGGTTCCCTCCGTTGTTCCAAATGTCC 180
Qy 181 ATGCCCGGAAACTTGACGAGTGCCTGAGTGGCTCTTGACCCGATGGGCGCGTGTGCA 240
Dd 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCCAATGGGTCCATTGTCC 240

```
RESULT 13
US-08-391-339-30
; Sequence 30, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-391-339-30

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 714 TACAACCAACGACGGCTTCTGGCGTTGATGCAGCGGTGTCGCGACGCGGCACACTC 773
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Db 1 TACAACCACTAACCGTCTTCTGGCTGTGATGCAGCTGTTCCAGCTGTTCCAGCTGTCGACACTC 60
|||||
QY 774 GAATCACT 782
|||||
Db 61 TAATCACT 69

RESULT 14
US-08-391-339-33
; Sequence 33, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-391-339-30

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 714 TACAACCAACGACGGCTTCTGGCGTTGATGCAGCGGTGTCGCGACGCGGCACACTC 773
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Db 1 TACAACCACTAACCGTCTTCTGGCTGTGATGCAGCTGTTCCAGCTGTTCCAGCTGTCGACACTC 60
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QY 774 GAATCACT 782
|||||
Db 61 TAATCACT 69

RESULT 15
US-08-484-274A-30
; Sequence 30, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435

STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-391-339-33

Query Match 4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1128 CGTAATCTATGCTTTCGGCCACGGTCATCTCGGATGACAGGGCGCGGATGACGCGCAAC 1187
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CGTAATCTATGCTTTCGGTCACGGTCATCTCGGATGACAGGGCGCGGATGACGCGCAAC 60
|||||
QY 1188 GCTCGTCTC 1196
|||||
Db 61 TCTCGTCTC 69
```

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-30

Query Match 4.3%; Score 56.2; DB 2; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 714 TACAACACGAGCGGTTCTGGCCGTTGATGCAGCGGTTGTGCGACGCGGCGCACACTC 773
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TACAACCACTAAGCGTGTCTGGCTGTGATGCAGCTGTGTTGCAGCTGGTGCACACTC 60
QY 774 GAAATCACT 782
|||||||
Db 61 TAAATCACT 69

Search completed: January 1, 2001, 03:17:58
Job time: 29302 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:42 ; Search time 3327.86 Seconds
(without alignments)
2407.829 Million cell updates/sec

Title: US-08-484-274-6
Perfect score: 1296
Sequence: 1 ATCGGTGAGACCAACAAAA.....AAACGGTCCGCCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1.*
2: gb_est2.*
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6: gb_est6.*
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8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*
12: gb_est12.*
13: gb_est13.*
14: gb_est14.*
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123: gb_gss23:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	44.4	3.4	434	124	P149R	AL160534 Leishmania
C 2	37.4	2.9	702	96	AQ328054	AQ328054 nbxb0042I
C 3	36.8	2.8	922	121	CNS015Y8	AL106058 Drosophil
C 4	36	2.8	380	22	AW500960	AW500960 UI-HF-BP0
C 5	36	2.8	389	22	AW501280	AW501280 UI-HF-BP0
C 6	36	2.8	895	123	CNS04UDT	AL307658 Tetraodon
C 7	35.6	2.7	614	21	AW254765	AW254765 ML105 pep
C 8	35	2.7	360	16	AV190084	AV190084 AV190084
C 9	35	2.7	382	36	C47876	C47876 C47876 Yuj1
C 10	35	2.7	517	17	AV386799	AV386799 AV386799
C 11	34.8	2.7	171	17	AV316270	AV316270 AV316270
C 12	34.8	2.7	494	14	AL387587	AL387587 MtBC43E07
C 13	34.8	2.7	634	19	AW097371	AW097371 ts43a11.y
C 14	34.6	2.7	676	34	BE248875	BE248875 NF023D11D
C 15	34.6	2.7	205	18	AV413471	AV413471 AV413471
C 16	34.6	2.7	251	18	AV418303	AV418303 AV418303
C 17	34.6	2.7	271	24	AW719954	AW719954 LjNEST12e
C 18	34.6	2.7	273	18	AV427698	AV427698 AV427698
C 19	34.6	2.7	300	18	AV406977	AV406977 AV406977
C 20	34.6	2.7	349	18	AV412853	AV412853 AV412853
C 21	34.6	2.7	416	18	AV425451	AV425451 AV425451
C 22	34.6	2.7	423	18	AV407852	AV407852 AV407852
C 23	34.6	2.7	429	18	AV408636	AV408636 AV408636
C 24	34.6	2.7	429	18	AV415123	AV415123 AV415123
C 25	34.6	2.7	452	18	AV423367	AV423367 AV423367
C 26	34.4	2.7	460	35	BE357122	BE357122 DGL_146.B
C 27	34.4	2.7	474	25	AW925090	AW925090 WS1_75.CO
C 28	34.4	2.7	586	35	BE357121	BE357121 DGL_146.B
C 29	34.4	2.7	652	35	BE362682	BE362682 DGL_88.H0
C 30	34.4	2.7	974	121	CNS002K5	AL097775 Drosophil
C 31	34.2	2.6	699	118	B07704	B07704 318H1F05706
C 32	34.2	2.6	1009	123	CNS03ZOP	AL267874 Tetraodon
C 33	34	2.6	258	39	W09527	W09527 ma01b07.r1
C 34	34	2.6	261	36	D40242	D40242 RICS2075A.R
C 35	34	2.6	425	7	AA071231	AA071231 vq32g02.r
C 36	34	2.6	433	4	AA542047	AA542047 vk43d01.r
C 37	34	2.6	636	97	AQ447252	AQ447252 mgxb00006C
C 38	33.8	2.6	222	19	AV536254	AV536254 AV536254
C 39	33.8	2.6	226	5	AA644181	AA644181 ab63a02.s
C 40	33.8	2.6	360	36	C41677	C41677 C41677 Yuj1
C 41	33.8	2.6	935	123	CNS03IPN	AL245876 Tetraodon
C 42	33.6	2.6	409	35	BE411304	BE411304 ISC004.B1
C 43	33.6	2.6	452	35	BE356986	BE356986 DGL_146.B
C 44	33.6	2.6	460	15	AU088715	AU088715 AU088715
C 45	33.6	2.6	500	36	BE517838	BE517838 WHE08003.C

ALIGNMENTS

RESULT 1
P149R/c

LOCUS DEFINITION	P149R	434 bp	DNA	GSS	16-MAR-2000
Leishmania major Friedlin PAC P149 right end-sequence, genomic survey sequence.					
ACCESSION	AL160534				
VERSION	AL160534.1	GI:7258935			
KEYWORDS	GSS.				
SOURCE	Leishmania major.				
ORGANISM	Leishmania major.				
REFERENCE	1 (bases 1 to 434)				
AUTHORS	Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.				
TITLE	A physical map of the Leishmania major Friedlin genome				
MEDLINE	Genome Res. 8 (2), 135-145 (1998)				
REFERENCE	2 (bases 1 to 41)				
AUTHORS	Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicats@sanger.ac.uk				
COMMENT	see http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/Lmajor/ The primer sequence can be obtained from alicats@sanger.ac.uk.				
FEATURES	Location/Qualifiers				
source	1..434				
	/organism="Leishmania major"				
	/strain="Friedlin"				
	/db_xref="taxon:5664"				
	/clone="PAC P149"				
BASE COUNT	76 a 131 c 157 g 70 t				
ORIGIN					
Query Match	3.4%;	Score 44.4;	DB 124;	Length 434;	
Best Local Similarity	54.2%;	Pred. No. 0.022;			
Matches	90;	Conservative	0;	Mismatches	76;
				Indels	0;
				Gaps	0;
QY	34	GGAGCGGAATCGTCGGGTATGACGGCGCTGATGCTTCAGCGCGCGGATTCAAAGTC	93		
Db	357	GGCGCGGCAATTCGGTGTGTCAGCACCAGCTGCGCCATCGCGGCACCGAGTC	298		
QY	94	ACCTTGATTGACCGAACCCTCTCGGGAAGGTGCATCGTTGGGAATCGCGATGCTTC	153		
Db	297	GTTCCTGTGATCGCGCGCGGCGGACCGAGACCTCTATGGCAACGGCGGCTTCATC	238		
QY	154	ACGGGCTCATCGTCCTCCCTATGTCATGTCATGCGCGGAACTTGACGA	199		
Db	237	CAGCGCGAGGCGGTGCGAGCGGTATGCTTCCCGCGGACTTGAAGA	192		
RESULT 2					
AQ328054/c					
LOCUS	AQ328054	702 bp	DNA	GSS	08-JAN-1999
DEFINITION	nbxb0042I02f CUGI Rice BAC Library Oryza sativa genomic clone				
ACCESSION	nbxb0042I02f				
VERSION	nbxb0042I02f.1	GI:4119904			
KEYWORDS	GSS.				
SOURCE	AQ328054.1				
ORGANISM	Oryza sativa.				
REFERENCE	1 (bases 1 to 702)				
AUTHORS	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.				
TITLE	Wing,R.A. and Dean,R.A.				
JOURNAL	A BAC End Sequencing Framework to Sequence the Rice Genome				
COMMENT	Unpublished (1998)				
	Contact: Wing RA				
	Clemson University Genomics Institute				

Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwling@ciemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 365.

FEATURES

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i. 7702
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nxb00042102f"
/clone_lib="CGUI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="F. coli DH10B"

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/root/note-2: col on 108
/note=vector: col on 108
HindIII: Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

RESULT 3
CNS015V8/C

CNS01518/C	LOCUS	922 bp	DNA	GSS	26-JUL-1999
	DEFINITION	Drosophila melanogaster genome survey sequence sp6 end of BAC BACN15P08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			

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FEATURES
source
Seq primer: M13 Forward.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3073464"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      62 a 115 c 133 g 70 t
ORIGIN
Query Match      2.8%; Score 36; DB 22; Length 380;
Best Local Similarity 50.0%; Pred. No. 6.6;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 364 CTGATCAAGTCATTGGCGGAGGAGGTGATGCGAGGCATCTGATCGCCCATGAAGTTCAT 423
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 CGGGTGCATGCCCTCCGACCGGACGAGGATCGATCGGATGAATGCCGCGAGGAGTG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 CTGACCGTATATCGTGAGAGCAGACTTCGCCAAGACCGCGGAGGTTGGGAACTCGGG 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GCGATCGACACCGCGCGGAGGCGGAACCTGCCAAGCTCGGCTGTGATCGCGATCCTGCAC 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 CGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATCGTGTGGGGATTTCGATCCG 543
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CGCAAGAACAACATGATCGCGGCGCTTCATCGCGGCCCATTCGCTGCAGGACGACGACG 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 5
AWS01280/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1. .389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3073186"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
FEATURES
source
Seq primer: M13 Forward.
Location/Qualifiers
1. .380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3073464"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      65 a 115 c 137 g 72 t
ORIGIN
Query Match      2.8%; Score 36; DB 22; Length 389;
Best Local Similarity 50.0%; Pred. No. 6.7;
Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 364 CTGATCAAGTCATTGGCGGAGGAGGTGATGCGAGGCATCTGATCGCCCATGAAGTTCAT 423
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Db 378 CGGGTGCATGCCCTTCGCGACCGGACGAGGATCGATCGGATGAATGCCGCGAGGAGTG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 CTGACCGTATATCGTGAGAGCAGACTTCGCCAAGACCGCGGAGGTTGGGAACTCGGG 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GCGATCGACACCGCGCGGAGGCGGAACCTGCCAAGCTCGGCTGTGATCGCGATCCTGCAC 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 CGTCTCAACGGTGTTCGACGCGAGATCCTCAGCGCGGATCGTGTGGGGATTTCGATCCG 543
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CGCAAGAACAACATGATCGCGGCGCTTCATCGCGGCCCATTCGCTGCAGGACGACGACG 199
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RESULT 6
CNS040UDT
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. .895
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="027A06"
/clone_lib="B"
/note="Genoscope sequence ID : C0A027BA03B2-end : SP6"
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Qy	443	AACGAGACTTCGCCAAGAGACCCCGGAGGTTGGGAACTCGGGCGTCTCAACGGTGTTCCGA	502
Db	435	AATCGGAATATCCCAAGGGCGGAAGGCTTCCTTCAGANTCTTCTCGANTGTTCTTCGAG	376
Qy	503	CGCAGATCCTCAGCGCCGATCGTTGGGGGATTTCCGATCCGAACCTTTCGCGATGGGTTTA	562
Db	375	ATCAGCCCGGCGCAGCTCTTTGAGGAGGTGGAAAGTTGAGGCCACCTCCCGGAGGTGGCG	316
Qy	563	CCAAAGGCGATTCTTATAGAAGAGAACGCTACACGATTAAATCCGCAAGGGTCTCGTGACCC	622
Db	315	TCGATGCGGTGATGTTAGGGTTCTCCTTCAGGTACTCTCCGTCAAATGCATGTACCTT	256
Qy	623	TCATTGTTTCGGCGTTTATATCCCGAACGGTGGCGAATTTGTATCTGCG	669
Db	255	TTCTTTATCATCGATTCTCTGCACATGGCGTTGAATTTCTCTTTGAG	209

REFERENCE
AUTHORS

C47876
C47876.1 CI:2384129
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodirinae; Caenorhabditis.
1 (bases 1 to 382)
Kohara.Y., Mochizashi.T., Tabara.H., Watanabe.H., Sugimoto.A., Sano
M., Miyata.A. and Nishizaki.A.

TITLE JOURNAL COMMENT

Expression map of the C.elegans genome
Unpublished (1996)
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES

Source
1..382
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk453a5"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
110 a 112 c 116 g 43 t 1 others

BASE COUNT
ORIGIN

Query Match 2.7%; Score 35; DB 36; Length 382;

Best Local Similarity 53.2%; Pred. No. 13;
Matches 74; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1113 AACCCGACACCGCAGCTATCTGCTTCGCGCCAGCGTCTCGGCATGACAGGGC 1172
DB 174 AGCTCGCTCAGAGGCTATAGCTTCAGTGGCGCCAGAGCCAGTCTGGAGGCCAGAC 233
QY 1173 GCGCATGACCGCAACGCTCGTCTCAGAGCTCTCGCAGGCGAAAGACCTCAATCGACAT 1232
DB 234 GACCGAGGTTCCCTGCTGCGTGAAGAGCCCGCCGCGAGAGAGCGCGCTCACCAT 293
QY 1233 TTCCGCTTCCGACCAAC 1251
DB 294 CTCAATCCAAGAGCCCGCAGC 312

RESULT 10
AV386799

LOCUS AV386799 517 bp mRNA EST 21-JAN-2000
DEFINITION AV386799 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
cDNA clone CM007a05_r, mRNA sequence.
ACCESSION AV386799
VERSION AV386799.1 GI:6541015
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 517)
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A Large Scale Structural Analysis of cDNAs in a Unicellular Green
Alga, Chlamydomonas reinhardtii. I. Generation of 3433
Non-redundant Expressed Sequence Tags
DNA Res. 6, 369-373 (1999)
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

JOURNAL
COMMENT

FEATURES
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/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="CM007a05_r"
/clone_lib="Chlamydomonas reinhardtii C9"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 102 a 148 c 185 g 82 t
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Query Match 2.7%; Score 35; DB 18; Length 517;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 107; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 321 GCAGGCGAAAGCACTCGCAATCTCATCAAGTCCACGGTGCTCTGATCAAGTCATTGGC 380
DB 175 GCTGACGAGCGTCTGCGGAGATCATCAAGCCGAGGCGCCCGACGACAACTCAAGCG 234
QY 381 GGAGAGGCTGATCGGAGCCATCTGATCCGCATGAAGGTCACTGACCGTATATCTGG 440
DB 235 CATGGGACGAACGACCTTCCGAGACCAACGAGGAGGGTGCACGACGATGA 294
QY 441 AGAAGCAGACTTCGCCAAGACCCGAGGTTGGGAACTGGGGCTCTCAACGGGTTCG 500
DB 295 CGACGAGGAGGAGGAGGAGGCCAAAGTAAACGGCATCGTTGCCTACTCGCGGTACTTG 354
QY 501 CACGCAGATCTCAGCGCCGATGCTGCGGATTTTCGATCCGAAC 547
DB 355 GGGACACGACAGAGCGGGCTAAGCTGCGGGTTGTTGGTGGGACT 401

RESULT 11
AV316270/c

LOCUS AV316270 171 bp mRNA EST 08-NOV-1999
DEFINITION AV316270 RIKEN full-length enriched, adult male thymus Mus musculus
cDNA clone 5830435F07 3', mRNA sequence.

ACCESSION AV316270
VERSION AV316270.1 GI:6281688
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 171)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,E.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
Suzuki,H., Takahashi,F., Tateo,M., Tomimaga,N., Tsunoda,Y.,
Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@tc.riken.go.jp,
URL: <http://genome.rtc.riken.go.jp/>
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
Y.

TITLE
JOURNAL
COMMENT

Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

[illegible]

```

Location/Qualifiers
1. .171
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5830435P07"
/clone_lib="RIKEN full-length enriched, adult male thymus"
/sex="male"
/tissue_type="thymus"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Site.1: Salt; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGACCTCTTTTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGATTATTTATTTATTCCTCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

```

BASE COUNT	45 a	41 c	33 g	51 t	1 others
ORIGIN					

	Query Match	2.78	Score 34.8	DB 17	Length 171
	Best Local Similarity	65.4%	Pred. No. 12		
	Matches 51	Conservative	0	Mismatches 27	Indels 0
	Gaps				
Qy	888	AGGAAATTCATCCGCACACCTATGGAATYGGGGCTTCGCGTGGCGGGGTACGGTTGAGTT	947		
Db	84	AGGATTTTTCAGAAAATCAATGGAATGGGGCAGTGTCTGTGGGTCCAGTTGATTT	25		
Qy	948	CGCTGGGCTCACGCCGC	965		
Db	24	CTCAGGTCGCCCTTCTGC	7		

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
<http://sequence.toulouse.inra.fr/Mtruncatula.html>).

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
5. <i>Other</i>	
6. <i>Other</i>	
7. <i>Other</i>	
8. <i>Other</i>	
9. <i>Other</i>	
10. <i>Other</i>	
11. <i>Other</i>	
12. <i>Other</i>	
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16. <i>Other</i>	
17. <i>Other</i>	
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19. <i>Other</i>	
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80. <i>Other</i>	
81. <i>Other</i>	
82. <i>Other</i>	
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95. <i>Other</i>	
96. <i>Other</i>	
97. <i>Other</i>	
98. <i>Other</i>	
99. <i>Other</i>	
100. <i>Other</i>	

Location/Qualifiers

1. .494

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db_xref="taxon:3880"

/clone="MBC43E07"

/tissue_lib="MtBC"

/tissue_type="arbuscular mycorrhiza"

/dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"

/note="vector: pBluescript PSK; Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epilobes soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Strategene and packaged using Gigapack XL packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAasht helper phage and propagated in SOUR cells. Clone ordering and sequencing was performed by the Centre National de Sequençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT	131 a	97 c	128 g	138 t
ORIGIN				

	Query Match	2.7%	Score 34.8;	DB 14;	Length 494;
	Best Local Similarity	54.8%;	Pred. No. 16;		
	Matches	69;	Conservative	0;	Mismatches 57; Indels 0; Gaps 0;
Qy	623	TCTTGTTTCGGCGT	TTATCGCGAACGGTGC	GCGAATTTGTATCTGCGCGTGCATCGGCT	682
Db	359	TCATGTGGCGTCTG	CGAAGAGGGTGGC	ACAGATTTTGTATTGGGGTGCCAACTGCT	418
Qy	683	TTGACACTGAAGGT	AGGGCGGTTAAAGG	GCATTACAACACGACGCGGTTCTGGCCCGTTG	742
Db	419	ATGAGAGGCAACTG	TAGCCAGTCAGAGAT	ATAAATTCAGGCACGCGCTTCTCTCCCGTG	478
Qy	743	ATGCAG	748		
Db	479	ATGGAG	484		

RESULT 13

LOCUS	AW097371	634 bp	mrna	EST	19-OCT-1999
DEFINITION	rs43a11.y1 Sommer <i>Pristionchus pristionchus pacificus</i> cDNA 5', similar to WP:Y61A9LA_74.D CE22688 ;, mRNA sequence.				
ACCESSION	AW097371				
VERSION	AW097371.1	GI:6067682			
KEYWORDS	EST.				
SOURCE	<i>Pristionchus pacificus</i> .				
ORGANISM	<i>Pristionchus pacificus</i>				
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; <i>Pristionchus</i> .				
AUTHORS	McCarte,J., Clifton,S., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Paper,D., Harvey,N., Schurk,R., Richter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.				
TITLE	The Washington Univ. Nematode EST Project, 1999				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: McCarter Jp				

AW097371 634 bp mRNA EST 19-OCT-1999
rs43all.y1 Sommer *Pristionchus pristionchus* pacificus cDNA 5',
similar to WP.Y61A9LA_74.D CE23688 ;, mRNA sequence.
AW097371
AW097371.1 GI:6067682
EST
Pristionchus pacificus.
Pristionchus pacificus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; *Pristionchus*.
1 (bases 1 to 634)
McCartter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen,
M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Paper, D., Harvey,
N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas,
M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCartney JP

sequence.
AL387587.
AL387587.1 GI:9687338
EST.
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae
Magnoliophyta; eudicotyledons; core eudicots; Rosi-
fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 494)
Journet,E.P., Crespeau,H., van-Tulnen,D., Gouzy,J.
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gla-
v., and Gamas,P.
Medicago truncatula
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope-
contact : Pascal Gamas and Etienne-Pascal Journet,
Biologie Molculaire des Relations Plantes-Microor-


```
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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XhoI; Isolate=Miyakojima MG-20"

BASE COUNT
ORIGIN

49 a	67 c	33 g	56 t
------	------	------	------

BASE CO
ORIGIN

		Query Match	2.7%	Score 34.6;	DB 18;	Length 205;	
		Best Local Similarity	59.8%;	Pred.	No. 15;	Mismatches	0;
		Matches	58;	Conservative	0;	Mismatches	39; Indels 0; Gaps 0;
Qy	9	CACCCACAAAAAGTAGGCATCGCTGGAGCCGGAATCOTCGGGGTATGCCAGCGCGCTCAT	68				
Db	98	GCACGACAAGAATTCTGTTCACGGCGGTGCCGGTCTCATCGCACTCACACGGTGTTCA	157				
Qy	69	GCTTCAGCGCCCGGATTCAAAGTCACCCTTCATTGAC	105				
Db	158	GCTTCTCCATGACGGCTTCCATGTCCTCCATCATGCAC	194				

Query Match 2.7%; Score 34.6; DB 18; Length 205;

Best Local Similarity	59.88;	pred. No. 15;
Matches	58: Conservative	0: Mismatches
		39: Indels
		0: Cans

QY 9 GAACCACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCGCTGAT 68

98 GCAGCAGACATCTGCTACCGCCCTTCATCCGACCTCACCGCTCTTA 157

Qy 69 GCTTCAGCGCCGGATTCAAAGTCACCTTCATTGAC 105

158 C C T T C C A T C A C C C C T T T C A T C C A T C C A C 194

Search completed: January 1, 2001, 01:12:46
Job time: 25785 sec

Job time: 25785 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:15:19 ; Search time 7299.04 Seconds
(without alignments)
775.497 Million cell updates/sec

Title: us-08-484-274-7
Perfect score: 1296
Sequence: 1 ATGGCTGAGAACACANAAAA.....AAACGGGTCCGGCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.:

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_om.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl1.*
- 8: gb_pl2.*
- 9: gb_pr1.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: em_fun.*
- 13: em_hum1.*
- 14: em_hum2.*
- 15: em_in.*
- 16: em_om.*
- 17: em_or.*
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- 19: em_pat.*
- 20: em_ph.*
- 21: em_pl.*
- 22: em_ro.*
- 23: em_sts.*
- 24: em_sy.*
- 25: em_un.*
- 26: em_vi.*
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- 31: em_ba1.*
- 32: em_ba2.*
- 33: em_hum3.*
- 34: em_hum4.*
- 35: gb_pr4.*
- 36: gb_htg3.*
- 37: gb_htg4.*
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- 39: gb_htg6.*
- 40: gb_htg7.*
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- 43: em_htg3.*

- 44: em_hum5.*
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- 48: gb_htg9.*
- 49: gb_htg10.*
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- 89: gb_sts1.*
- 90: gb_sts2.*
- 91: gb_sy.*
- 92: gb_un.*
- 93: gb_vil.*
- 94: gb_vil2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1296	100.0	1296	5	AR016594	AR016594 Sequence
2	1296	100.0	1296	5	I15327	I15327 Sequence 7
3	1201.6	92.7	1296	5	AR016593	AR016593 Sequence
4	1201.6	92.7	1296	5	I15326	I15326 Sequence 6
5	1196.8	92.3	1692	5	AR016591	AR016591 Sequence
6	1160.8	89.6	1293	5	AR016592	AR016592 Sequence 4
7	1160.8	89.6	1293	5	I15325	I15325 Sequence 4
8	1160.8	89.6	1689	5	I15324	I15324 Sequence 3
9	1011.2	78.0	1296	5	AR016595	AR016595 Sequence
10	1011.2	78.0	1296	5	I15328	I15328 Sequence 8
11	1006.4	77.7	1296	5	AR016604	AR016604 Sequence
12	1006.4	77.7	1296	5	I15337	I15337 Sequence 17

13	926.8	71.5	1631	5	A59869	A59869 Sequence 1
14	87.4	6.7	3430	2	PSEAKSD	M69158 Pseudomonas
15	69.2	5.3	2289	2	PSEKSDA	M69159 Pseudomonas
16	69	5.3	69	5	AR016616	AR016616 Sequence
17	69	5.3	69	5	AR016619	AR016619 Sequence
18	69	5.3	69	5	I15349	I15349 Sequence 30
19	69	5.3	69	5	I15352	I15352 Sequence 33
20	68	5.2	68	5	AR016618	AR016618 Sequence
21	68	5.2	68	5	I15351	I15351 Sequence 32
22	63.4	4.9	65	5	AR016614	AR016614 Sequence
23	63.4	4.9	65	5	I15347	I15347 Sequence 28
24	62	4.8	62	5	AR016613	AR016613 Sequence
25	62	4.8	62	5	I15346	I15346 Sequence 27
26	61	4.7	61	5	AR016617	AR016617 Sequence
27	61	4.7	61	5	I15350	I15350 Sequence 31
28	42.8	3.3	196999	57	AC073946	AC073946 Mus muscu
29	42.6	3.3	1586	88	MMU70653	U70653 Mus muscu
30	42.6	3.3	1598	88	MMU70654	U70654 Mus muscu
31	42	3.2	31202	37	AC013022	AC013022 Drosophil
32	42	3.2	302357	29	AE003443	AE003443 Drosophil
33	41	3.2	41	5	AR016615	AR016615 Sequence
34	41	3.2	41	5	I15348	I15348 Sequence 29
35	40.4	3.1	186935	48	AC022322	AC022322 Homo sapi
36	40.2	3.1	840	89	CNS01EDB	AL140400 Anopheles
37	40.2	3.1	38914	2	MSG8937CS	L78820 Mycobacteri
38	40.2	3.1	179553	49	AC024253	AC024253 Homo sapi
39	39.8	3.1	223469	56	AC069019	AC069019 Mus muscu
40	39.4	3.0	767	54	ETIMAX	M30933 E.Tenella a
41	39.4	3.0	1612	88	MMU70652	U70652 Mus muscu
42	39.2	3.0	47268	40	AC020414	AC020414 Drosophil
43	39	3.0	34220	38	AC014160	AC014160 Drosophil
44	39	3.0	235414	29	AE003708	AE003708 Drosophil
45	38.8	3.0	1558	88	MMU70646	U70646 Mus muscu

ALIGNMENTS

RESULT 1						
AR016594	AR016594	1296 bp	DNA	PAT	05-DEC-1998	
LOCUS	Sequence 7 from patent US 5776760.					
DEFINITION	AR016594					
ACCESSION	AR016594					
VERSION	AR016594.1	GI:3972871				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1296)					
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.					
TITLE	Glyphosate tolerant plants					
JOURNAL	Patent: US 5776760-A 7 07-JUL-1998;					
FEATURES	Location/Qualifiers					
source	1..1296					
BASE COUNT	287 a	344 c	332 g	333 t		
ORIGIN						
	Query Match 100.0%; Score 1296; DB 5; Length 1296;					
	Best Local Similarity 100.0%; Pred. No. 0;					
	Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
yy	1	ATGGCTGAGAACACAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60			
bb	1	ATGGCTGAGAACACACAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60			
yy	61	GCTTTGATGCTTCAACGCTCGTGGATTCAAAAGTCACCTTGATTGACCCGCAACCCCTCCTGGC	120			
bb	61	GCTTTGATGCTTCAACGCTCGTGGATTCAAAAGTCACCTTGATTGACCCGCAACCCCTCCTGGC	120			
yy	121	CAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGGCTCATCGCTGCTCCCTATGTCTC	180			

Db	121	GAAGGTGCATCGTTTGGGAATGCGCGAATGCTTCAACGGCTCATCCCGCTGCTCCCTATGTCC	180			
QY	181	ATGCCGGAAACTTGACGAGCGTCCGCAAGTGGCTCTTGACCGGATGGGCGCTTCTCA	240			
Db	181	ATGCCGGAAACTTGACGAGCGTCCGCAAGTGGCTCTTGACCGGATGGGCGCTTCTCA	240			
QY	241	ATCCGGTTCAGCTATTCTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTTAGCCGA	300			
Db	241	ATCCGGTTCAGCTATTCTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTTAGCCGA	300			
QY	301	AGACCAACAAGGTGAAGGAGCAGGCGCAAGACCTCGGCAATCTCATCAAGTCACGGTG	360			
Db	301	AGACCAACAAGGTGAAGGAGCAGGCGCAAGACCTCGGCAATCTCATCAAGTCACGGTG	360			
QY	361	CCCTGTATCAAGTCATTGGCGGAGGAGGCTGATGCGAGGACCTGTGATCGGCCCATGAAGGT	420			
Db	361	CCCTGTATCAAGTCATTGGCGGAGGAGGCTGATGCGAGGACCTGTGATCGGCCCATGAAGGT	420			
QY	421	CATCTGACCGTATATCGTGAGAGCAGACTTCCCAAGGACCGCGGAGGTTGGGAAC	480			
Db	421	CATCTGACCGTATATCGTGAGAGCAGACTTCCCAAGGACCGCGGAGGTTGGGAAC	480			
QY	481	CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTCCAT	540			
Db	481	CGCGCTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTCCAT	540			
QY	541	CTTAACCTGTGCGATGCTTTTACCAAGGCGATCTTATAGAAGAACACGCTCACACGATT	600			
Db	541	CTTAACCTGTGCGATGCTTTTACCAAGGCGATCTTATAGAAGAACACGCTCACACGATT	600			
QY	601	AATCCGGAAGGGTCGTGACCCCTCTTGTTCGGCGTCTTATCGCAACGCTGGCGAATTT	660			
Db	601	AATCCGGAAGGGTCGTGACCCCTCTTGTTCGGCGTCTTATCGCAACGCTGGCGAATTT	660			
QY	661	GTATCTCGCGCTCTCATCGGTTTTGAGACTGAAGGTGCTGCTCTCAAGGCAATTCACACC	720			
Db	661	GTATCTCGCGCTCTCATCGGTTTTGAGACTGAAGGTGCTGCTCTCAAGGCAATTCACACC	720			
QY	721	ACTAAGGCTGTTCTGGCTGTTGATGCAAGCTGTTGTTGCAGCTGCTGCACACTCTAAATCA	780			
Db	721	ACTAAGGCTGTTCTGGCTGTTGATGCAAGCTGTTGTTGCAGCTGCTGCACACTCTAAATCA	780			
QY	781	CTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	840			
Db	781	CTTGCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC	840			
QY	841	ATCGGAATCCGGAAGCGCTCCAGCATTCGCGACGACCGATCGGTCAGGAAATTCATC	900			
Db	841	ATCGGAATCCGGAAGCGCTCCAGCATTCGCGACGACCGATCGGTCAGGAAATTCATC	900			
QY	901	GCACACCTATGGAATGGGCTTTCGTTGCTGGTACTGTTGAGTTTGTGCTCTCACAC	960			
Db	901	GCACACCTATGGAATGGGCTTTCGTTGCTGGTACTGTTGAGTTTGTGCTCTCACAC	960			
QY	961	GCTGCTCTAACTGGAACCGTGGCATGTGCTCTATACGCAACGCTCGAAACCTTCCTCCA	1020			
Db	961	GCTGCTCTAACTGGAACCGTGGCATGTGCTCTATACGCAACGCTCGAAACCTTCCTCCA	1020			
QY	1021	GCCTCGCGCTCGGATGTTCTGAAGAACGATATTCACAAATGGATGGGTTTTCTCTAGC	1080			
Db	1021	GCCTCGCGCTCGGATGTTCTGAAGAACGATATTCACAAATGGATGGGTTTTCTCTAGC	1080			
QY	1081	ATTCTGATTTCTTCCAGTATTGGTGTGCAACTCGTACACCCGACGTAATCTATGCT	1140			
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QY	1141	TTTGGTCACGGTCAATCGGATATGACAGTGTCTCAATGACTGCAACTCTCGTCTCAGAG	1200			
Db	1141	TTTGGTCACGGTCAATCGGATATGACAGTGTCTCAATGACTGCAACTCTCGTCTCAGAG	1200			
QY	1201	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCCGCTTTGGT	1260			
Db	1201	CTCCTCGCAGGCGAAAGACCTCAATCGACATTTCCGCCCTTCGCACCAACCCGCTTTGGT	1260			

QY 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACCT 60

Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
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Db 61 GCGCTGATGCTTCAGCGCCGGGATTCAAAAGTCAACCTTGATTGACCCGAACCCCTCTCTGGC 120
QY 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTCC 180
QY 181 ATCCGGGAACCTGAGAGCGTGGCGAAGTGGCTCTTTCAGCCGATGGGGCGCTGTCTCA 240
Db 181 ATCCGGGAACCTGAGAGCGTGGCGAAGTGGCTCTTTCAGCCGATGGGGCGCTGTCTCA 240
QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTCTGTTAGCCGGA 300
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTCTGTTAGCCGGA 300
QY 301 AGACCAACAAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCAAGTCCACGGTG 360
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QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420
Db 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420
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Db 421 CATCTGACCCGTATATCTGTGAGAGCAGACTTCCGCAAGGACCGCGAGGTTGGGAACCTG 480
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QY 601 AATCCGCAAGCGCTCGTGACCCCTTGTTCGGCGTTTATCGCGAACGGTGGCGAATTT 660
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DEFINITION Sequence 6 from patent US 5463175.
ACCESSION I15326
VERSION I15326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;
FEATURES Location/Qualifiers
source
1. .1296
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN
Query Match 92.7%; Score 1201.6; DB 5; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGAATCGTTGGTGTATGCAC 60
Db 1 ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGCGTATGCACG 60
QY 61 GCTTTGATGCTTCAACCTCGTGGATTCAAAAGTCAACCTTGATTGACCCGAACCCCTCTCTGGC 120
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RESULT 5
AR016591
LOCUS AR016591 1692 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776760.
ACCESSION AR016591
VERSION AR016591.1 GI:3972868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1692)
AUTHORS Barry.G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: us 5776760-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..1692
/organism="unknown"

BASE COUNT 381 a 480 c 469 g 361 t 1 others
ORIGIN
Query Match 92.3%; Score 1196.8; DB 5; Length 1692;
Best Local Similarity 95.2%; Pred. NO. 0;
Matches 1234; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 1 ATGGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTGTGGTGTATGCACT 60
Db 120 ATGTCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCCGAATCGTCGGGTATGCACG 179
Qy 61 GCTTTGATGCTTCAACGTCGTTGGAATCAAAAGTCACCTTGAATGACCCGAAACCTCTTCGC 120
Db 180 GCGTGTATGCTTCAAGCGCGCGGATTCAAAGTCACCTTGAATGACCCGAAACCTCTTCGC 239
Qy 121 GAAGTGCATGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTCC 180
Db 240 GAAGTGCATGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTCC 299
Qy 181 ATGCCGGGAAACTTTGACGAGCGTCCGAAAGTGGCTCTTGACCCGATGGGGCCGTGTGCA 240
Db 300 ATGCCGGGAAACTTTGACGAGCGTCCGAAAGTGGCTCTTGACCCGATGGGGCCGTGTGCA 359
Qy 241 ATCCGGTTCAAGTATATTTTCAACCATCATGCCCTTGGTGAATTCGCTTTCTGTTAGCCGGA 300
Db 360 ATCCGGTTCAAGTATATTTTCAACCATCATGCCCTTGGTGAATTCGCTTTCTGTTAGCCGGA 419
Qy 301 AGACCAACAGGTGAAGGACGAGCGGAAAGCACTCCGCAATCTCANTCAAGTCACAGGTG 360
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Qy 361 CCTCTGATCAAGTATATTTGGCGAGGAGCTGATCGAGCCCATCTGATCCGCCATGAAGGT 420
Db 480 CCTCTGATCAAGTATATTTGGCGAGGAGCTGATCGAGCCCATCTGATCCGCCATGAAGGT 539
Qy 421 CATCTGACCGTATATCTGTTGGAGAGACAGACTTCGCCAAGGACCGCGAGGTGGGAAGT 480
Db 540 CATCTGACCGTATATCTGTTGGAGAGACAGACTTCGCCAAGGACCGCGAGGTGGGAAGT 599
Qy 481 CGGGCTCTCAACGGTGTTCGCACGCAGATCCTCTCTGCTGATGCTTTTCGCTGATTTTCGAT 540
Db 600 CGGGCTCTCAACGGTGTTCGCACGCAGATCCTCTGAGCCCGATGCGTTGCGGGATTTTCGAT 659
Qy 541 CCTAATCTTGTGCGATGCTTTTACCAAGGGCATCTCTATAGAGAGAAAGCGGTACACAGATT 600
Db 660 CCGAATCTGCGATGCGTTTACCAAGGGCATCTCTATAGAGAGAAAGCGGTACACAGATT 719
Qy 601 AATCCGAAGGGTCTGACCGCTCTTGTTCGGGGTTCCTTATCGGGAATTTATCGGGAATTT 660
Db 720 AATCCGAAGGGTCTGACCGCTCTTGTTCGGGGTTCCTTATCGGGAATTTATCGGGAATTT 779
Qy 661 GTATCTCGCGTCTCATCGGTTTTCAGACTGAAGGTCTGCTCTCAAAGGATTTACAAACC 720
Db 780 GTATCTCGCGTCTCATCGGTTTTCAGACTGAAGGTCTGCTCTCAAAGGATTTACAAACC 839
Qy 721 ACTAAGGTTCTTGGGCTGTGTGATGCGAGCTGTGTGAGTGGTGCACACTCTAAATCA 780
Db 840 ACGAAGCGGTTCTGCGGCTGTGTGATGCGAGCGTGTGCGAGCCGCGCACACTCGAATCA 899
Qy 781 CTTGCTTAATTCGCTAGGCGATGACATCCCGTTCGATACCGAAGCTGGATATCATATCGTC 840
Db 900 CTTGCTTAATTCGCTAGGCGATGACATCCCGTTCGATACCGAAGCTGGATATCATATCGTC 959
Qy 841 ATCCGGAATCCGGAAGCGGCTCCACCGATTCGAGACCGGATGCTGTCAGGAAATTCATC 900
Db 960 ATCCGGAATCCGGAAGCGGCTCCACCGATTCGAGACCGGATGCTGTCAGGAAATTCATC 1019
Qy 901 CGGACACTATGGAATGGGTTCTGCTGTGCTGCTACTGTTGAGTTTGTGCTCTCACA 960
Db 1020 CGGACACTATGGAATGGGTTCTGCTGTGCTGCTACTGTTGAGTTTGTGCTCTCACA 1079
Qy 961 GCTGCTCTTAATCGGAACGTCGCGATGCTCTATACGACAGCTTCGAAACTTCTTTCCA 1020

Db	1080	GCCTGCTTAACTGGAACGTGGCATGTGCTCTATACGCACGCTCGAAACTTCTTCCA	1139
QY	1021	GCCTTCGCGCTCGGAGTCTTGAAGAACGATATTCCAAATGGATGGGTTTTCGTCTTAGC	1080
Db	1140	GCCTTCGCGCTCGGAGTCTTGAAGAACGATATTCCAAATGGATGGGTTTCGCGCCGAGC	1199
QY	1081	ATTCTGATTTCTTCCAGTGATTTGGTCTGTCGCAACTCGTACACCCGACGTAATCTATGCT	1140
Db	1200	ATCCGGATTCGTTCCTCGTTCCTCGTTCCTCGTTCCTCGTTCCTCGTTCCTCGTTCCT	1259
QY	1141	TTTGGTACGGTTCATCTCGGTATGACAGGTGCTCCAAATGACTCGAAGTCTCGTCTCAGAG	1200
Db	1260	TTCCGGCATGGTTCATCTCGGCATGACAGGGCGCCGATGACCAAGCTCGTCTCAGAG	1319
QY	1201	CTCCTCGCAGCGCAAGAACCTCAATCGACATTTCCGCCCTTCGCACCAAAACCGCTTTGGT	1260
Db	1320	CTCCTCGCAGCGCAAGAACCTCAATCGACATTTCCGCCCTTCGCACCAAAACCGCTTTGGT	1379
QY	1261	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1296
Db	1380	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1415
RESULT	6		
LOCUS	AR016592	1293 bp	DNA
DEFINITION	Sequence 4 from patent US 5776760.		PAT 05-DEC-1998
ACCESSION	AR016592		
VERSION	AR016592.1	GI:3972869	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1293)		
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5776760-A 4 07-JUL-1998;		
FEATURES	Location/Qualifiers		
source	1..1293		
BASE COUNT	286 a 367 c 359 g 281 t		
ORIGIN			
Query Match	89.6%;	Score 1160.8;	DB 5; Length 1293;
Best Local Similarity	95.0%;	Pred. No. 0;	
Matches 1231; Conservative	0;	Mismatches 62;	Indels 3; Gaps 3;
QY	1	ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60
Db	1	ATCTCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGCGTATGCACG	60
QY	61	GCCTTGTATGCTTCAAGCTCGTGATTTCAAGTCAACCTGATTTGACCCGAAACCTCTCGC	120
Db	61	GCCTTGTATGCTTCAAGCTCGTGATTTCAAGTCAACCTGATTTGACCCGAAACCTCTCGC	120
QY	121	GAAGTCCATCGTTGGGAATCGCGGATGCTTCAAGCGGTTCATCCGCTGCTCCCTATGTCC	180
Db	121	GAAGTGCATCGTTGGGAATCGCGGATGCTTCAAGCGGTTCATCCGCTGCTCCCTATGTCC	180
QY	181	ATGCCGGGAAACTTGACGAGCGTGCAGAAAGTGGCTCTCTTGACCCGATGGGGCGGTTGTCA	240
Db	181	ATGCCGGGAAACTTGACGAGCGTGCAGAAAGTGGCTCTCTTGACCCGATGGGGCGGTTGTCA	239
QY	241	ATCCGGTTTCAAGTATTTTCCAAACCATCATGCTGCTGTTGATTCGCTTTCTGTTAGCCGA	300
Db	240	ATCCGGTTTCAAGTATTTTCCAAACCATCATGCTGCTGTTGATTCGCTTTCTGTTAGCCGA	297
QY	301	AGACCAAAACAGCTGAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360
Db	298	AGACCAAAACAGCTGAGGAGCAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	357

QY	361	CTCTGTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	420
Db	358	CTCTGTGATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	417
QY	421	CATCTGACCGTATATCGTGGAGAGACAGACTTCCGCCAAGGACCCCGAGGTTGGGAAGT	480
Db	418	CATCTGACCGTATATCGTGGAGAGACAGACTTCCGCCAAGGACCCCGAGGTTGGGAAGT	477
QY	481	CGCGCTCTCAACGGTGTTCGACGCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	540
Db	478	CGCGCTCTCAACGGTGTTCGACGCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	537
QY	541	CCTAACCTGTTCGATGCTTTTACCAAGGGATCTTATAGAAGAGAACGGTTCACACGATT	600
Db	538	CCGAACCTGTTCGATGCTTTTACCAAGGGATCTTATAGAAGAGAACGGTTCACACGATT	597
QY	601	AATCCGCAAGGGTCTGTGACCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	660
Db	598	AATCCGCAAGGGTCTGTGACCCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	657
QY	661	GATCTGCGGTGTCTATCGGTCTTGTAGACCTGAAGGTGCTGCTCTCTCTCTCTCTCTCTCTCT	720
Db	658	GATCTGCGGTGTCTATCGGTCTTGTAGACCTGAAGGTGCTGCTCTCTCTCTCTCTCTCTCTCT	717
QY	721	ACTAACGGTGTCTGCGTGTGATGACGCTGTTGTTGACGCTGTTGTTGACGCTGTTGTTGACGCT	780
Db	718	ACCAACGGGCTTCTGGCGGTTGATGACGCGTTCGTCGACGCGGCGCACACTCGAAATCA	777
QY	781	CTTGTCTAAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGCT	840
Db	778	CTTGTCTAAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGCT	837
QY	841	ATCCGAATCCGGAAGCGCTCCACGCAATTCGACGACCGATGCGTCCAGGAAATTCATC	900
Db	838	ATCCGAATCCGGAAGCGCTCCACGCAATTCGACGACCGATGCGTCCAGGAAATTCATC	897
QY	901	GCACACCTATGGAATGGGTCTTGGTGTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	960
Db	898	GCACACCTATGGAATGGGTCTTGGTGTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	957
QY	961	GCTGCTCTTAATTCGGAACGCTGGCATGCTCTATACGACCGCTCGAAACCTTCTTCCA	1020
Db	958	GCGGCTCTTAATTCGGAACGCTGGCATGCTCTATACGACCGCTCGAAACCTTCTTCCA	1017
QY	1021	GCCTTCGCGCTCGGATCTGGAAGACGATATTCCTAAATGGATGGGTTTTCGTCTTAGC	1080
Db	1018	GCCTTCGCGCTCGGATCTGGAAGACGATATTCCTAAATGGATGGGTTTTCGCGCCGAGC	1077
QY	1081	ATTCTGTATTTCTTCTCAGTGATTTGGTGTGCAACTCGTACACCCGACGTAATCTATGCT	1140
Db	1078	ATCCCGATTTCTGCTTCCCGTGAATGGCGGCAACCCGACACCCGACGTAATCTATGCT	1137
QY	1141	TTTGGTTCACGGTTCATCTCGGTATGACAGGTGCTTCCAAATGACTGCAACTCTCGTCTCAG	1200
Db	1138	TTCCGGCATGGTTCATCTCGGCATGACAGGGGCGCCGATGACCGCAACGCTCTCAGAG	1197
QY	1201	CTCTCTCGCAGGCAAAAGACCTCAATCGACATTTTCGCGCTTTCGCAACCAACCGCTTTGGT	1260
Db	1198	CTCTCTCGCAGGCAAAAGACCTCAATCGACATTTTCGCGCTTTCGCAACCAACCGCTTTGGT	1257
QY	1261	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1296
Db	1258	ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA	1293
RESULT	7		
LOCUS	I15325	1293 bp	DNA
DEFINITION	Sequence 4 from patent US 5463175.		PAT 02-APR-1996
ACCESSION	I15325		
VERSION	I15325.1	GI:1250233	
KEYWORDS	Unknown.		
SOURCE	Unknown.		

QY 241 ATCCGGTTCAGCTATTCTTCCAAACCATCATGCTCCCTGGTGTGATTCGCTTTCTGTTAGCCGGA 300
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Db 359 ATCCGGTTCAGCTA-TTTTCCAAACCATCATG-CCTGGTGTGATTCGCTTTCTGTTAGCCGGA 416
QY 301 AGACCAACAAGGTGAAGGAGCAGCGGAAGAGCACTCCGCAATCTCATCAAGTCCACCGTG 360
Db 417 AGACCAACAAGGTGAAGGAGCAGCGGAAGAGCACTCCGCAATCTCATCAAGTCCACCGTG 476
QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
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Db 477 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 536
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAAGT 480
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Db 537 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAAGT 596
QY 481 CGCGCTCAACGGTGTTCGACGCGCAGATCCTCTCTGCTGATGCTTTGGCTGATTTCCGAT 540
Db 597 CGCGCTCAACGGTGTTCGACGCGCAGATCCTCAGCGCGATGCGTTGCGGGATTTCCGAT 656
QY 541 CCTAACTTGTGCGATGCTTTTACCAGGGCATCTTATAGAAGAACGCTCAACGATT 600
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Db 657 CCGAACTTGTGCGATGCGTTTACCAAGGGCATTTCTATAGAAGAACGCTCAACGATT 716
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTTTTCGGCGTTTATCCGGAACGGTGGCGAAATTT 660
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Db 717 AATCCGCAAGGGCTCGTGACCCCTCTTTTTCGGCGTTTATCCGGAACGGTGGCGAAATTC 776
QY 661 GTATCTCGCGGTGATCGGTGTTGAGACHTGAAGGTGCTGCTCTCAAGGCAATTCACACC 720
Db 777 GTATCTCGCGGTGATCGGTGTTGAGACHTGAAGGTGAGGCGCTTAAAGGCATTTACAAAC 836
QY 721 ACTAAACGGTGTCTGGCGTGTGATGAGCTGTTGTTGACGCTGGTGACACTCTAAATCA 780
Db 837 ACGAACGGCTGTCTGGCGTGTGATGAGCGGTGTTGCGACCGCGGCGACACTCGAAATCA 896
QY 781 CTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATCGTC 840
Db 897 CTTCCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCGTGGATATCATATCGTC 956
QY 841 ATCCGGAATCCGAAGCGCTCCACCATTTCCGACGACCGATGGTCAAGGCAATTCATC 900
Db 957 ATCCGGAATCCGAAGCGCTCCACCGATTTCCGACGACCGATGGTCAAGGCAATTCATC 1016
QY 901 GCGACACCTATGGAATGGGTCTTCGCTGTTGCTGGTACTGTTGAGTTTGTGCTCTCACA 960
Db 1017 GCGACACCTATGGAATGGGTCTTCGCTGTTGCTGGTACTGTTGAGTTTGTGCTCTCACA 1076
QY 961 GCTGCTCCTAACTGGAAACGTGGCGATGTGCTCTATACGACGCTCGAAACTCTTTCCA 1020
Db 1077 GCGGCTCCTAACTGGAAACGTGGCGATGTGCTCTATACGACGCTCGAAACTCTTTCCA 1136
QY 1021 GCCTTCGCGCTCGAGTCTGAAGAACGATATTCAAATGGATGGTTCGTCCTAGC 1080
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QY 1081 ATTCCTGATTCTCTCCAGTGTGTTGGTGGCAACTCGTACACCCGACGTAATCTATGCT 1140
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QY 1141 TTTTGGTACAGGTCAATCTCGGTATGACAGTGTCTTCAATGACTGCAACTCTCTGCTCAGAG 1200
Db 1257 TTCGGCATGGTCAATCTCGGCATGACAGGGGCGCGGATGACCGCAACGCTCTCAGAG 1316
QY 1201 CTCTTCGACGGCCAAAGACCTCAATCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT 1260
Db 1317 CTCTTCGACGGCCAAAGACCTCAATCGACATTTTCGCCCTTCGCCACCAACCGCTTTGGT 1376
QY 1261 ATTTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
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Db 1377 ATTTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1412

RESULT 9
AR016595
LOCUS AR016595 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5776760.
ACCESSION AR016595
VERSION AR016595.1 GI:3972872
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1296)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 8 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..1296
BASE COUNT 271 a 359 c 305 g 361 t
ORIGIN

Query Match 78.0%; Score 1011.2; DB 5; Length 1296;
Best Local Similarity 86.3%; Pred. No. 2.8e-277;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 1 ATGGCTCAGAACCAACAAAAGTAGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
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Db 1 ATGGCTCAGAACCAACAAAAGTAGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
QY 61 GCTTTGATGCTTCAACGTCTGGATTCAAAAGTCACTTTGATTGACCCGAACCCCTCTGGC 120
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Db 61 GCTTTGATGCTTCAACGTCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
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Db 121 GAAGGTGCTTCTTTCGGTAAACGCTGGTTGCTTCAACGGTTCTCCGTGTGTCCAAATGTC 180
QY 181 ATGCGCGGAAACTTGACGAGCGTCCGAAGTGGCTCTTGACCGGATGGGGCCGTTGTGCA 240
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Db 181 ATGCCAGGAACTTGACTAGGCTTCCAAGTGGCTTCTGACCCAAATGGGTCCATTTGTC 240
QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCTTGGTGTGATTCGCTTTCTGTTAGCCGGA 300
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Db 481 CGTCTGCTCAACGGTGTTCGTAATACTTCACTCAAACTCTCAGCGCTGATGCAATTCGCTGAT 540
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATCTTATAGAAGAACGCTCAACGATT 600
Db 541 CCTTAATTTGCTCACGCTTTTACCAAGGGAATCCTTATCGAAGAACGCTCAACGATC 600
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTCTTTCGGCGTTTATTCGCGCAACGGTGGCGAAATTT 660
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QY 661 GTATCTCGCGGTGCTATCGGTGTTGAGACTGAAGGTGCTGCTCTCAAGGCAATTCACACC 720
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Qy	721	ACTAACGGTGTTCTTGCTGTTTGATGCAGCTGTTGTTGCAGCTGGTGACACTCTAAATCA	780
Db	721	ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGACACTCCAAGTCT	780
Qy	781	CTTGCTAAATTCGTAGCGCATGACATCCGCTCGATACCGAAGCTGGATATCATATCGTC	840
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATGGATACCGAAGCTGGATACCATCGTG	840
Qy	841	ATCGGAATTCGGAAGCCGCTCCAGCGATTCGAGCAGCCGATGGCTCAGGAAAATTCATC	900
Db	841	ATCGCAACCCAGAAGCTGCTCCAGTATTCCAACTACCGATGCTTCGGAAAGTTGATC	900
Qy	901	GCACACCTATGGAATVGGGTCTTCGTGTGCTGGTACTGTTGAGTTGTGGTCTCACCA	960
Db	901	GCTACTCTATGGAGATGGGTCTTCGTGTTCGTGGAACCGTTGAGTTTCGCTGGTCTCACT	960
Qy	961	GCTGCTCTTAAGCTGGAAGCTGGCATGTGCTCTATACGCAGCTCGAAGAACTTCCTCCA	1020
Db	961	GCTGCTCTTAAGCTGGAAGCGTCTCAGGTCTCTACACTCAGCTCGTAAGTTGCTTCCA	1020
Qy	1021	GCCTTCGCGCTCCGAGTTCTGAAGAAGCATATTCCAAATGGATGGGTTCGTCTCCTAGC	1080
Db	1021	GCTCTCGCTCCGCAAGTTCTGAAGACGTTACTCCAAGTGGATGGGTTCCTCGTCCAAGC	1080
Qy	1081	ATTCTGATTCTCTTCCAGTAGATTGGTCGTGCAACTCTGTACCCGACGTAAATCTATGCT	1140
Db	1081	ATCCAGATTCCCTTCACGTGATTGGTCGTACCCGTACTCCAGACGTTATCTACGCT	1140
Qy	1141	TTTGGTCACGGTCATCTCCGGTAGACAGGTGCTCAATGACTGCACACTCTGCTCTCAGAG	1200
Db	1141	TTCCGGTCACGGTCACCTCCGGTAGACTGGTGCTCCAATGACCGCAACCCCTCGTTCTGAG	1200
Qy	1201	CTCTTCGACGGCGAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAACCCGCTTGGT	1260
Db	1201	CTCTTCGACGGTGGAAGACCTCTATCGACATCTCTCCATTCGCACCAACCCGTTTCGGT	1260
Qy	1261	ATTGGCAATTCGAAGCAACCGGTCCGGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCCAAGCAAACTGGTCTGCATCTAA	1296
RESULT 10			
I15328			
LOCUS			
DEFINITION	Sequence 8 from patent US 5463175.		
ACCESSION	I15328		
VERSION	I15328.1		
KEYWORDS	GI:1250236		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1296)		
TITLE	Barry, G.F. and Kishore, G.M.		
JOURNAL	Glyphosate tolerant plants		
FEATURES	Patent: US 5463175-A 31-OCT-1995;		
source	Location/Qualifiers		
	1..1296		
BASE COUNT	/organism="unknown"		
ORIGIN	271 a 359 c 305 g 361 t		
Query Match 78.0%; Score 1011.2; DB 5; Length 1296;			
Best Local Similarity 86.3%; Pred. No. 2.8e-277;			
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps			
Qy	1	ATGGCTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60
Db	1	ATGGCTGAGAACACAAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60
Qy	61	GCTTGTATGCTTCAAGCTCGTGGATTCAAGTCACTTGATTGACCCGGAACCCCTCTGGC	120

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QY 1201 CTCTCCAGCGGAAAGACCTCAATCGACATTTGCGCCCTTCGCACCAAAACCGCTTTGGT 1260
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Db 1201 CTCTCCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGCTTCGGT 1260

QY 1261 ATTGGCAAAATCCAGCAAAACGGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGTAAGTCCAAGCAAAACGGTTCCTGCATCCTAA 1296

RESULT 11
AR016604
LOCUS AR016604 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 17 from patent US 5776760.
ACCESSION AR016604
VERSION AR016604.1 GI:3972881
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barty,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5776760-A 17 07-JUL-1998;
FEATURES
    source
        location/Qualifiers
            1..1296
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN

Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
Best Local Similarity 86.0%; Pred. No. 6.6e-276;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACACAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCAT 60
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Db 1 ATGGCTGAGAACACAAAGAGGTGGTATCGCTCGAGCTGGAATCGTTGGTGTATGCAT 60

QY 61 GCTTTGATGCTTCAAGCTCGTGGAATCAAAAGTCAACCTTGATTGACCCGAACCCCTCTCGG 120
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Db 61 GCTTTGATGCTTCAAGCTCGTGGAATCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120

QY 121 GAAGGTGCATCGTTTGGGAATCCGGAATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
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Db 121 GAAGGTGCCTCTTTTCGTAACGCTGTTGCTTCAACGGTTCCTCCGTTGTTCCAAATGTCC 180

QY 181 ATCCCGGGAACCTTGACGAGCTGCGGAAGTGGCTCGTTGACCCGATGGGGCCGTTGTCA 240
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Db 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCCTTGACCCAAATGGGTCCATTTGTC 240

QY 241 ATCCGGTTCAGCTATTTTTCCAACCATCATCCCTCGTGTGATTGCTTCTGTTAGCGGA 300
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Db 241 ATCCGTTTCGGCTACTTTTCCAACCATCATCGCTTGGTGTGATTGCTTCTGTTGCTTGGGA 300

QY 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
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Db 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACTCATCAAGTCCACTGTG 360

QY 361 CCTCTCATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420
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Db 361 CPTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGCTCACGAAGGT 420

QY 421 CATCTGACCGCTATATGCTGGAGAACGAGACTTCGCCAAAGGACCGCGAGGTTGGGAACCTG 480
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Db 421 CACCTTACCGTGTACCGTGGAGAACGAGACTTCGCCAGGAGCCGCTGAGAGTTGGGAACCT 480

QY 481 CGCGCTCTCAACGGTGTTCGACGACGAGTCCCTCTCTGCTGATGCTTTGGCTGATTTTCGAT 540
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Db 481 CGTCGCTCAACGGTGTTCGTAATACTCAATCCTCAGCGCTGATGCATTTGGTGATTTTCGAT 540

QY 541 CCTAACTTTGTCGATCGTTTACCAGGGGCAATCTTTATAGAAGAACGGTTCACACGATT 600
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Db 541 CCTAACTTTGTCACGCGCTTTTACCAAGGAATCCTTATCGAAGAGAACGGTTCACACCATC 600
QY 601 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGGGTTTTTATCGGAAACGGTGGCGAATTT 660
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AACCACAAGGTCTCGTACTCTCTTGTTCGTCGTTTATCGCTAACGGTGGAGAGTTC 660
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 GTATCTCGCGTGTATCATCGGTTTTGAGACTGAAGTCTGCTCTCAAGAGGCATTTACAACC 720
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 GTGTCCTGCTGTTATCGGATTTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 ACTAACGGTGTTCGGCTGTTGATGAGCTGTTGTCAGCTGTGACACTCTAAATCA 780
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 ACCAACGGTGTTCCTGCTGTTGATGAGCTGTTGTCAGCTGTGTCAGCTTCCAAGTCT 780
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 CTTGCTAATTCGGTAGCGATGACATCCGCTCATACCGAACGTGATATCATATCGTC 840
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 781 CTTGCTAATTCCTTGGTGATGACATCCATTTGATACCGAACGTGATACCATCGTG 840
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QY 841 ATCCGGAATCCGAAGCCGCTCCACGCATTTCCGACGACCGATGCTCAGGAAAAATTCATC 900
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Db 841 ATCCGCAACCCAGAAGCTGCTCCACGTAATCCAACTACCGATGCTTCTGGAAGTTTCATC 900
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 GCGACACCTATGGAATGGGCTCTTCGTTGCTGGTACTGTTGAGTTTGTGGTCTCACA 960
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Db 901 GCTACTCCTATGGAGATGGGCTCTTCGTTGCTGGAACCGTTGAGTTTCGCTGGTCTCACT 960
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 GCTGCTCCTAACTGGAACCGTGCGCATGTCTATACGCACGCTCGAAAACTTCTTCCA 1020
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Db 961 GCTGCTCCTAACTGGAAGCGTGCTCAGCTTCTTACACTCGCGCTCGTAAGTTGCTTCCA 1020
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 GCCTCCGCGCTCGAGTTCTGAAGAACGATATTTCCAAATGGATGGGTTTTTCGTCCTAGC 1080
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1081 ATTCTGCTATCTCTCCAGTATGTTGGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1140
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QY 1201 CTCTCCAGCGGAAAAAGACCTCAATCGACATTTTCGCCCTTTCGCCACCAAAACCGCTTTGGT 1260
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QY 1261 ATTGGCAAAATCCAGCAAAACGGGTCCGGCAAGTTAA 1296
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Db 1261 ATTGGTAAGTCCAAGCAAAACGGTTCCTGCATCCTAA 1296
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RESULT 12
I15337
LOCUS I15337 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 17 from patent US 5463175.
ACCESSION I15337
VERSION I15337.1 GI:1250245
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barty,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants.
JOURNAL Patent: US 5463175-A 17 31-OCT-1995;
FEATURES
    source
        location/Qualifiers
            1..1296
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN

Query Match 77.7%; Score 1006.4; DB 5; Length 1296;
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Best Local Similarity 86.08; Pred. No. 6.6e-276; Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;			
Qy	1	ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT	60
Db	1	ATGGCTGAGAACCAAAAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTGCACT	60
Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCAACCTTGATTTGACCCGAAACCCCTCGGC	120
Db	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCAACCTTGATTTGATTCACCAACCCACAGGT	120
Qy	121	GAAGTGTCATCGTTTGGGAATCGCGGATGCTTCAACGCTCATCGCTCGTCCCTATGTC	180
Db	121	GAAGTGTCCTTTCGGTAACGCTGGTTGCTTCAACGCTTCTCGTGGTTTCCCAATGTC	180
Qy	181	ATGCCGGGAAACTTGCACGAGCTGCCGAAGTGGCTTCCCTTGACCCGATGGGCCGTTGCA	240
Db	181	ATGCCAGGAACCTTGACTAGCTGCCAAGTGGCTTCTTGACCCCAATGGGTCCATGTCC	240
Qy	241	ATCCGGTTCAGCTATTTTCAACCAATCATGCCCTGGTTGATTCGGTTCCTGTAGCCGGA	300
Db	241	ATCCGCTTTCGGCTACTTTTCAACCAATCATGCTTGGTTGATTCGTTTCTTGTGCTGA	300
Qy	301	AGACCAACAAGGTGAAGGACGCGGAAGCACTCCCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAACAAGGTGAAGGACGCGTAAGGCACTCCGTAACCTCATCAAGTCCCACTGTG	360
Qy	361	CCTCTGATCAAGTCAATTCGCGGAGGAGCTGATGCGAGCCATCTCATCCGCCATCAAGGT	420
Db	361	CCTTTGATCAAGTCTTGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCACGAAGT	420
Qy	421	CATCTGACCGTATATCTGGGAGAAGCAGACTTCGCCAAGGACCGCGGAGTTGGGAATG	480
Db	421	CACCTTACCCTGTACCGTGGAGAAGCAGACTTCGCCAGGACCGTGGAGTTGGGAAT	480
Qy	481	CGGCTCTCAACGGTGTTCGACGACGATCTCTCTGCTGATGCTTTCGGTGTATTCGAT	540
Db	481	CGTCTCTCAACGGTGTTCGTAATCTCAATCTCAAGCTGATGCTATCGGTGATTCGAT	540
Qy	541	CCTAACTTCTCGCATGCTTTTACCAAGGCAATCTTATAGAGAACGCGTCACACGATT	600
Db	541	CCTAACTTCTCAGCCCTTTTACCAAGGCAATCTTATAGAGAACGCGTCACACCATC	600
Qy	601	AATCGCAAGGCTCGTGACCCCTCTTGTTCGGCGTTTTTATCGGAACGGTGGGGAATTT	660
Db	601	AACCCACAAGTCTCGTGACTCTCTTGTTCGTCTGCTTTTATCGCTTAACGGTGGAGATT	660
Qy	661	GTATCTGCGCTGTCATCGGTTTTCAGACTGAAGTCTGCTCTCAAGGCAATACAC	720
Db	661	GTGCTGCTGCTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGCTATCACACC	720
Qy	721	ACTAACGCTGTTCTGGCTGTTGATGCACTGTTGTTGACGCTGTTGCACTCTTAAATCA	780
Db	721	ACCAACGCTGTTCTGCTGTTGATGCACTGTTGTTGACGCTGTTGCACTCTTAAATCA	780
Qy	781	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCAAGCTGGATATCATATGTC	840
Db	781	CTTGCTAATTCCTTGGTGTATGACATCCCAATTTGGATACCAAGCTGGATACCAATGTC	840
Qy	841	ATCGGAATCCGGAAGCCGCTCCAGCATTCGAGACCGATGCGTGAGGAATTCATC	900
Db	841	ATCGCAACCCAGAGCTGCTCCAGCATTCCAACTACCGATGCTTCTGGAAGTTTATC	900
Qy	901	CGCACACCTATGGAATGGCTTTCGCTGTTGCTGCTGTTGCTGCTGCTGCTGCTACA	960
Db	901	GCTACTCTATGAGATGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT	960
Qy	961	GCTGCTCTAACTGGAACGTCGCGATGCTCTATAGCAGCTCGGAATCTTCTTCCA	1020
Db	961	GCTGCTCTAACTGGAACGTCGCTGCTCTCTACACTCGCGCTCGTAAGTTGCTTCCA	1020
Qy	1021	GCCCTCGCCCTCGGATTTCTGAGAAGCATATTCCAATGGATGGGTTTTTCGCTCTGA	1080

Db	1021	GCTCTCGCTCTGCGAGTTCTTGAGAAGAGTTACTCCAAAGTGGATGGGTTTCCGTCCAAGC	1080
Qy	1081	ATTCTCTGATTTCTTCCAGTGAATTTGGTCTGTGCAACTCGTACACCGAGTAAATCTATGCT	1140
Db	1081	ATCCCGGATTTCCCTTCCAGTGAATTTGGTCTGTGCAACTCGTACACCGAGTAAATCTACGCT	1140
Qy	1141	TTTGGTCAAGGTCTATCTCGGTATGACAGGTGCTTCAATGACTGCAACTCTCTGCTCTCAG	1200
Db	1141	TTCTGCTACGGTCACTCTCGGTATGACTGGTGTCTCAATGACCGCAACCTCGTTTCTGAG	1200
Qy	1201	CTCTCGCAGCGGAAAGACCTCAATCCACATTTCCGCTTTCGCACCAACCGCTTTGGT	1260
Db	1201	CTCTCGCAGGTGAGACCTCTATCGACATCTCTCCATTCGCACCAACCGTTTTCGCT	1260
Qy	1261	ATTGCCAATCCAAAGCAACGGTCCGCGCAAGTTAA	1296
Db	1261	ATTGSTAAGTCCAAGCAACCTGGTCTCTCATCTTAA	1296
RESULT 13			
A59869 LOCUS A59869 1631 bp DNA PAT 06-MAR-1998			
DEFINITION Sequence 1 from Patent WO9706269.			
ACCESSION A59869			
VERSION A59869.1 GI:3715060			
KEYWORDS			
SOURCE Arabidopsis sp.			
ORGANISM Arabidopsis sp.			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.			
REFERENCE Jenson, I.			
AUTHORS TITLE INDUCIBLE HERBICIDE RESISTANCE			
JOURNAL Patent: WO 9706269-A 1 20-FEB-1997;			
ZENEC LTD (GB)			
FEATURES Location/Qualifiers			
source 1..1631			
BASE COUNT 342 a 454 c 381 g 454 t			
ORIGIN			
Query Match 71.5%; Score 926.8; DB 5; Length 1631;			
Best Local Similarity 82.4%; Pred. No. 3.4e-253;			
Matches 1109; Conservative 0; Mismatches 187; Indels 50; Gaps 2;			
Qy	1	ATGGCTGAGAACCACAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT	60
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Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACTTGTGATTCACCCGAAACCCCTCGGC	120
Db	334	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACTTGTGATTCACCCGAAACCCAGGT	393
Qy	121	GAAGTGTCATCGTTTGGGAATGCCGATGCTTCAACGCTCATCGCTGCTCTCATATGTC	180
Db	394	GAAGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTCTCTCGCTGTTTCCAATGTC	453
Qy	181	ATGCCGGGAAACTTGACGAGCGTGGCGAAGTGGCTCTCTTGACC-----	223
Db	454	ATGCCAGCAAACTTGACTAGGCTTCCAAAGTGGCTTCTGGATCTGTGTGAATTCAGC	513
Qy	224	-----CGATGGGCGCTTGTCAATCCGGTTGAGCTATTTTCCAAACATCATCCCTG	275
Db	514	TTACGGATCCAATGGGTCCATGTCATCCGTTTACGTAAGTCTTCCCAACCATCATCCCTG	573
Qy	276	GTTGATTCGCTTCTTGTAGCGGAAGACCAAAAGGTGAAGGAGGAGGAGGAAAGCACT	335
Db	574	GTTGATTCGCTTCTTGTAGCGGAAGACCAAAAGGTGAAGGAGGAGGAGGAAAGCACT	633
Qy	336	CCGCAATCTCATCAAGTCCAGGTCCTCTGATCAAGTCTTGGCGGAGGAGGCTGATGC	395

Db	2627	CCTGAGTCACGCCAGGCACCTGGAGCGGTTGGCACCCGCATCGCAACACGACGCGGTGCCG	2686
Qy	502	ACGCAGATCCCTCTCTGCTGATGCTTTGGCTGATTTTCGATCTTAACCTTTGCTCGCATGCTTTT	561
Db	2687	GTGGACGCTCTGCTGGCGGCAACCGCTGGCGAGGCGAGCGCGCACTGAGCCCGTCACTG	2746
Qy	562	ACCAAGGCACTCTTATAGAGAGACGGTCAACAGGATTAATCCCAAGGCGTCTGTGACC	621
Db	2747	CTGGCGGGTGTCTTTTCCCGCGCACCGCGGACITTCATCGACCCCTTACCGGGTTGTGTGC	2806
Qy	622	CTCTTGTTCGGCGTTTATCGGAAACGCTGCGGAATTTGTATCTGCGCGTGTCTATCGST	681
Db	2807	GAACCTGTTGGAAGCGGCCAAGCCAGCGCGTGGCTTTGTTGAGGCGCAGG---TCGAT	2863
Qy	682	TTTGAGACTGAAGTCTGCTCTCAAAAGGCATTTACAACCACTTAACGGTGTCTTGCTGCTTT	741
Db	2864	GGCGGGCAATTGCACAGCGCGGGGTGAGCCTGGCCAGCGACCAAGGACGCTCAATGCC	2923
Qy	742	GATGAGCTGTTGTTGAGCTGGTGACACACTCTAANTCACTTGTCTAATTCGCTA---GGC	798
Db	2924	CCCCAGTGTCTGATCAGCTGTGCTGCCATTTCTCGGAAACTGACCGCGCGCTGACGGGC	2983
Qy	799	GATGACATCCCGCTCGATACCGAAGTGGATATCATATATCGTCATCGCGCAATCCGGAAGCC	858
Db	2984	AMCGGGTACCGCTGGACACAGACGCGGTTACCACCTGATGTTGCCGGGTGAGCACCAAG	3043
Qy	859	GCTCACGCAATCCGACGACCGCATCGCTCAGGAAATTTTCATCGGCACACCTATGCAAAATG	918
Db	3044	CGCCTGCCGTTTGCAATGCTGCTGGAGCGCAAGTTTCATCATGACGCCCATGCCCCAA	3103
Qy	919	GGTCTCTGTTGCTGGTGTGTTGTTGAGTTTCTGTGCTCTACAGTGTCTCTAACTGGA	978
Db	3104	GCT-TGCCCTCGCGCGCACGTGGAGTTTCGCGCGCTGGAGGACCGCCCAAGCATGCAA	3162
Qy	979	CGTGC 983	
Db	3163	CGGC 3167	
RESULT	15		
PSEKSDA			
LOCUS	PSEKSDA	2289 bp	DNA
DEFINITION	Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase		BCT 26-APR-1993
ACCESSION	gene, complete cds.		
VERSION	M69159.1	GI:151317	
KEYWORDS	ketoglutarate semialdehyde dehydrogenase.		
SOURCE	Pseudomonas putida (strain ATCC 12633) DNA.		
ORGANISM	Pseudomonas putida		
REFERENCE	Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.		
AUTHORS	1 (bases 1 to 2289)		
TITLE	Burlingame,R.P., Maruya,A., Ally,A.H., Ally,D. and Backman,K.C.		
	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas putida		
JOURNAL	Unpublished (1991)		
FEATURES	Location/Qualifiers		
source	1..2289		
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	/strain="ATCC 12633"		
	/db_xref="taxon:303"		
	133..1749		
gene	/gene="ketoglutarate semialdehyde dehydrogenase"		
CDS	133..1749		
	/gene="ketoglutarate semialdehyde dehydrogenase"		
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	/db_xref="GI:151318"		
	/translation="MTLTGNMLIQQAITGRREAIRAINPATDLPLEPAYLGSDGEHV		

EQACALAWAAPDRYRSTSLATRAEFLEETIAAEIALGDELIDRAVETGLPRARILGE
RGRTCCQLRFTFARTVRAGCWLVDVDAALPERQPLPRADLRQRIALGPAVFGASNF
PLAFSVAGDITASALAAGCCPVVKHAHAPCTSELVGRVARARVQKSAIPGVFSLLP
GSGREVIALVSDPRIKAVGTGSRSGMALINAAOARLEPIPVYAMSSINPVLLPP
AALFARGEALAOQFVASITOGAGOFCTNPGILVMAOQGPALDAFIKAANLVQRSPAOT
MLTPGIFSAVENGVELTAENHTAQTVAVGRAAKREPVGTPVRIPGGSGFCECALQAE
MFGAASLIVOCASDDEIRQVTEHLEQLTATLHDDADLESARLALLPVLERRAGRLIV
NGMPTGVEVEDAMVHGPFPTSDARTTSVGTAAILRLRPVCYQDFPDFTLLPALQH
GNPIQLRLRLDGRPRPTCTPNLPPTATT"
BASE COUNT 378 a 766 c 734 g 411 t
ORIGIN

Query Match 5.3%; Score 69.2; DB 2: Length 2289;
Best Local Similarity 52.4%; Pred. No. 1.3e-08;
Matches 152; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
Qy 4 GCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAANTCGTTGGTGTATGCACACTGCT 63
Db 1728 GCCAACAAATCGCCAGCACATAACCGTCTATCGCGCGGGAATCATCGCGCTGCGCTG 1787
Qy 64 TTGATGCTTCAACGTCGTGGATTCAAAGTCAACCTTGTATTGACCCCAACCCCTCCTGCCGAA 123
Db 1788 CTGCNACTGGCGCGCTGGGCTGGGGTGGGCTGCTGACACGAGAGCCCGCCCAT 1847
Qy 124 GGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGCTGCTCCCTATGTCCATG 183
Db 1848 GGTGCTCTGTTCCGCAATGCCGGCATCTGGCGACCGAGCAGGTGTTTCCCATCCGGAT 1907
Qy 184 CCGGAAACTTGCAGAGCGTCCGGAAGTGGCTCTTGACCCGATGGGCGCGTGTGTCATC 243
Db 1908 TTGTCGATCCTGAAACGCTTGCTTGCCTGCCATGCTCATGGACCGCATGGGCGCGT 1967
Qy 244 CGGTTACGCTATTTCACCAACCATCATGCCCTGGTTGATTCCGCTTTCTGTT 293
Db 1968 GACTGGAAGTACATGCCGCGCCCTGCCGTGGTTTGGCCGCGCTACTGTT 2017

Search completed: January 1, 2001, 03:15:47
Job time: 29231 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:42:34 ; Search time 263.11 Seconds
(without alignments)
1850.400 Million cell updates/sec

Title: US-08-484-274-7
Perfect score: 1296
Sequence: 1 ATGGCTGAGACACAAAAA.....AACGGGTCCGCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1294.4	99.9	1321	13 Q20834	Modified glyphosat
2	1200	92.6	1321	13 Q20833	Manipulated glypho
3	1193.6	92.1	1692	13 Q22705	Glyphosate oxidore
4	1157.6	89.3	1689	13 Q20832	Glyphosate oxidore
5	1011.2	78.0	1296	13 Q20835	Synthetic glyphosa
6	1011.2	78.0	8418	20 X57309	Sugar beet T-DNA c
7	926.8	71.5	1631	18 T85664	CPT1-COX gene fusi
8	703	54.2	8798	20 X57308	Sugar beet T-DNA c
9	701.8	54.2	8012	20 X57305	Sugar beet T-DNA c
10	37.4	2.9	3292	14 Q46544	Yeast SSRP DNA seq
11	37.4	2.9	3292	19 V09625	S. cerevisiae SSRP
12	35.8	2.8	6558	21 Z45602	cDNA sequence of a

13	35.6	2.7	5460	17	T16508	Vector pAC3A1 cont
14	35.4	2.7	501	6	N50025	Sequence encoding
15	35.2	2.7	501	6	N50023	Sequence encoding
16	35	2.7	38734	20	Z32020	Human MTH1 relate
17	34.4	2.7	32207	20	V73805	KSHV LUR DNA (nucl
18	34.4	2.7	137507	19	V1941	KSHV LUR DNA (nucl
19	34	2.6	1209	12	Q12569	Protease2 open rea
20	34	2.6	1513	12	Q12567	Alkaline protease
21	33.8	2.6	1220	18	V75229	Staphylococcus aur
22	33.8	2.6	3690	13	Q30849	Type III procollag
23	33.6	2.6	501	6	N50030	Sequence encoding
24	33.6	2.6	501	6	N50031	Sequence encoding
25	33.6	2.6	501	6	N50032	Sequence encoding
26	33.6	2.6	10266	17	T33007	Mouse SRY-related
27	33.4	2.6	2516	15	Q56832	Small round virus
28	33.2	2.6	1694	17	T15232	Tumor necrosis fac
29	33.2	2.6	1694	18	T94635	TNF-RI-1D ligand p
30	33.2	2.6	2442	20	X59335	SEQ ID 10 from WO9
31	33.2	2.6	2442	20	X31981	Sulfated fucose-co
32	33	2.5	423	18	T80725	Type II topoisomer
33	33	2.5	2800	20	X57965	S. pneumoniae Orni
34	33	2.5	2800	20	X57966	S. pneumoniae Orni
35	33	2.5	2800	20	X29247	S. pneumoniae hist
36	33	2.5	2800	20	X29248	S. pneumoniae resp
37	33	2.5	2800	20	V82065	Streptococcus pneu
38	33	2.5	2800	20	V82066	Streptococcus pneu
39	33	2.5	2800	20	V82058	Streptococcus pneu
40	33	2.5	2800	20	V82059	Streptococcus pneu
41	33	2.5	5059	20	X84332	Streptococcus pneu
42	32.8	2.5	543	13	Q23092	Antigen tc-7a gene
43	32.8	2.5	922	19	V15073	hybrid DNA compris
44	32.8	2.5	1526	20	Z42235	human normal bladd
45	32.8	2.5	2455	21	Z45836	cDNA of intestinal

ALIGNMENTS

RESULT 1	
Q20834	
ID Q20834 standard; DNA; 1321 BP.	
XX Q20834;	
AC Q20834;	
DT 01-MAY-1992 (first entry)	
DE Modified glyphosate oxidoreductase gene.	
XX Recombinant; GOR; resistance; ss.	
XX Bacterial isolate LBAA.	
OS	
XX Key Location/Qualifiers	
FT CDS 9..1304	
FT /*tag= a	
FT /note= "encodes wild type glyphosate oxidoreductase"	
XX	
PN W09200377-A.	
XX	
PD 09-JAN-1992.	
XX	
PF 24-JUN-1991; 91WO-US04514.	
XX	
PR 24-JUN-1991; 91US-0717370.	
PR 25-JUN-1990; 90US-0543236.	
XX	
PA (MONS) MONSANTO CO.	
XX	
PI Kishore GM, Barry GF;	
XX	
DR WPI; 1992-041559/05.	
DR P-PSDB; R20642.	
XX	

PT Gene encoding glyphosate oxido-reductase enzyme - used to
PT transform plants to produce plants tolerant to glyphosate
XX herbicide
XS
PS
XX Claim 1; Page 102; 142pp; English.

XX The sequence is that of the gene encoding a glyphosate oxidoreductase
CC (GOR) enzyme which has been modified using mutagenic primers. The
CC gene sequence was redesigned to eliminate as much as possible the
CC following sequences or sequence features (while avoiding the
CC introduction of unnecessary restriction sites), stretches of G's
CC and C's of 5 or more; A + T rich regions (predominantly) that could
CC function as polyadenylation sites or potential RNA destabilisation
CC regions, and codons not frequently found in plant genes. The G + C %
CC of the GOR gene was reduced from 56% in the manipulated version
CC (Q20833) to 52% in the modified version. However it still encodes
CC the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA.
CC It is used to transform plants such that they express the enzyme
CC sufficiently to enhance the glyphosate tolerance of the plant.
CC Transformed plants resistant to glyphosate can be obtd. so that
CC weeds can be selectively controlled in fields contg. crops.
CC See also Q20832-Q20841 and Q22705.

XX Sequence 1321 BP; 293 A; 349 C; 339 G; 340 T; 0 other;

Query Match 99.9%; Score 1294.4; DB 13; Length 1321;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACCT 60
DB 9 atggctgagaaacacacaaaaglaggcacgcctggagcctggaatcgttgggtgatgcact 68
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAAGTCAACCTGATTGACCCGACCCCTCTGGC 120
DB 69 gctttgatgcttcaacgctcggtgatcaaaagtcaccttgattgacccgaacctctcggc 128
QY 121 GAAGGTCATCGTTTGGGAATGCGGATGCTTCAAGCGCTCATCCGTCGTCCTATGTCC 180
DB 129 gaaggctcatcgtttgggaatgcggatgcttcaacggctcatccgctcgtccctatgtcc 188
QY 181 ATGCCGGGAACATTGACGACGGTGGCAAGTGGCTCTCTTGAACCCGATGGGGCCGTTGTCA 240
DB 189 atgccgggaacattgacgacggtgcccgaagtggctctcttgaaccgcatggggccgttgca 248
QY 241 ATCCGCTTACGCTATTCTTCAACCATCATCGCTGGTGGTGGTCTTCTGTTAGCCGGA 300
DB 249 atccgcttcagctatttcccaaccatcatcgctggtgattcgcttctctttagccgga 308
QY 301 AGACCAAAACAGGTGAAGGAGCAGGCAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
DB 309 agaccaaacaagtgaaaggacgagcgaaagacactccgcaatctcatcaagtcacaggtg 368
QY 361 CTTCTGATCAAGTCATTGGCCGAGGAGGCTGTATGCGAGCCATCTGATCCGCCATGAAGGT 420
DB 369 cctctgatcaagtcatctggcggaggaggtgatcgagccatctgatccgccatgaaggt 428
QY 421 CATCTGACCGTATATCGTGAGAGAGAGACTTCCCAAGGACCGCGAGGTTGGGAACCTG 480
DB 429 catctgaccgcta catcgtggagagcagactctcccaaggacccgagaggttggcaactg 488
QY 481 CGCGCTCTCAACGGTGTCCGACGACAGATCCTCTGCTGATGCTTTGGCTGATTTTCGAT 540
DB 489 cggcgtctcaacggtgttcgacgacgagatcctctcgtgatgcttcttgatattcgat 548
QY 541 CTTAACTTTTCGGCATCGTTTACCAGCGCATTTCTATAGAAAGAACGGTTCACAGATT 600
DB 549 cctaactgtcgcatacgtctttaaaggagcattcttatagaagagaacggttcacacgatt 608
QY 601 AATCCGCAAGGGCTCGTGACCCCTTGTGTTGGCGGTTTATCCGAACGGTGGCGAATTT 660
DB 609 aatccgcgaaggctcgtgacccctcttcttccggcgttttatccgcgaacggtggcgaaatt 668

QY 661 GTATCTCGCGCTGTATCGGTTTGTAGACTGAAGTCTGTCTCTCAAAGGCATTACAAAC 720
DB 669 gtatctcgcgcgtgtcatcgcgtttttgagactgaagtcgctctcacaaggcattacaacc 728
QY 721 ACTAACCGTGTTCGTGCTTGTATGACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 729 actaacggtgtctcgtgtgtgtatgcagctgtgtgtgcagctgtgtgtgcacactctaaatca 788
QY 781 CTTCGCTAACTTTCGTAGCGGATGACATCCCGCTCGATACCGACCGTGGATATCATATCGTC 840
DB 789 ctctgctaactcgcgtagcgatgacatcccgctcgatcaccgaacgtggatcatcctcgtc 848
QY 841 ATCGCGAATCCGGAAGCGCTCCACGCTTCGAGACGACCGATGCTCAGGAAAAATTCATC 900
DB 849 atcgcgaatccggaagcgcgtccacgcattccgacgaccgatgcgtcaggaaaaattcatc 908
QY 901 GCGACACTATGGAATGGGTCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 909 gcgacacctatggaaatgggtctctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtcaca 968
QY 961 GCTGCTCTTAACCTGGAACCGTGGCATGTGCTCTATAGCGACGCTCGAAAAACTTCCTCCA 1020
DB 969 gctgctcttaactggaaacgctgcgcattgtctctatcgcacgctcgaaaaactctctcca 1028
QY 1021 GCCTCTCGCGCTCGAGTCTTCTGAAGAACGATATTTCCAAATGGATGGTGTTCGTCTCTAGC 1080
DB 1029 gcctcgcgcgtcgcagttcttgaagaacgatattccaaaatggatgggtttctcgtcctcagc 1088
QY 1081 ATTCTCTGATTTCTTTCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1089 attctctgattctctcctcagtgattggctcgtgcgaactcgtacacccgcagcgaatctatgct 1148
QY 1141 TTTGGTCAACGCTCATCTCGGTATGACAGGTGCTCCCAATGACTGCAACTCTGCTCTCAGAG 1200
DB 1149 ttgggtcacaggtcatctcgtgtatgcagaggtgctccaatgactgcaactcctcgtctcagag 1208
QY 1201 CTCTCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAAAACCGGTTTGGT 1260
DB 1209 ctctcgcagcgcaaaagacctcaatcgacattctcgccttcgcacccaacacggttttgggt 1268
QY 1261 ATTGGGCAAAATCCAAGCAAAACGGGTCCGGCAAGTTAA 1296
DB 1269 attggcaaatcccaagcaaacgggtccgggcaagttaa 1304

RESULT 2
Q20833 ID Q20833 standard; DNA; 1321 BP.
XX AC Q20833;
XX AC Q20833;
DT 01-MAY-1992 (first entry)
XX DE Manipulated glyphosate oxidoreductase gene.
XX KW Recombinant; GOR; resistance; ss.
XX OS Bacterial isolate LBAA.
XX FH Key Location/Qualifiers
CDS 9..1304
FT /*tag= a
FT /note= "encodes wild type glyphosate oxidoreductase"
XX PN W09200377-A.
XX XX 09-JAN-1992.
XX XX 24-JUN-1991; 91WO-US04514.
XX XX 24-JUN-1991; 91US-071370.
PR 25-JUN-1990; 90US-0543236.

ID T85664 standard; DNA; 1631 BP.
AC T85664;
XX
XX 21-NOV-1997 (first entry)
DT XX
XX
XX CPT1-GOX gene fusion.
DE
XX expression cassette; inducible promoter; alca; alcr; aida; regulator;
KW alcohol dehydrogenase; herbicide resistance gene; glyphosate;
KW N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EPSPS;
KW 5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1;
KW Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
XX
XX Chimeric Arabidopsis.
OS Synthetic.
XX
XX W09706269-A1.
PN
XX
XX 20-FEB-1997.
PD
XX 02-AUG-1996; 96WO-GB01883.
XX
XX 03-AUG-1995; 95GB-0015941.
PR
XX (ZENE) ZENECA LTD.
PA
XX
XX Jepson I;
PI
XX
XX WPI; 1997-154273/14.
DR
XX
XX Chemically inducible cassette for expressing herbicide resistance
PT gene in plants - and derived plants, partic. for resistance to
PT glyphosate, avoids constitutive expression and minimises development
PT of herbicide tolerant weeds
XX
XX Example 3; Fig 7; 59pp; English.
PS
XX
XX A chemically inducible plant gene expression cassette which comprises an
CC inducible promoter linked to a gene (I) that confers resistance to a
CC herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-
CC glycine (glyphosate) or its salts, but may also be a gene for resistance
CC to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolinones,
CC etc. The inducible promoter (e.g. alca, alcr, aida or other alcr-induced
CC gene promoter) is operatively linked to an alcr regulator sequence.
CC Induced expression of (I) avoids the risk that constitutive expression
CC may interfere with plant development; allows volunteer plants to be
CC controlled by herbicide applied without inducer and minimises the chance
CC that herbicide-resistant strains of weeds will arise. The expression
CC cassette is strictly controlled and suitable for general use in plants
CC (both mono- and dicotyledons). The alca/alcr gene switch was exemplified
CC with genes conferring resistance to glyphosate. The switch was used to
CC drive inducible expression of glyphosate oxidase (GOX) in plants.
CC Switchable GOX was expressed alone or in conjunction with constitutive
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs
CC were optimised for expression in mono- and dicotyledonous crop species.
CC The present sequence comprises a fusion of the GOX gene fused to the
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This
CC sequence was ligated into pMUB1 (see T85666) and used in construction of
CC dicot vectors.
XX
XX Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match 71.5%; Score 926.8; DB 18; Length 1631;
Best Local Similarity 82.4%; Pred. No. 1.9e-284;
Matches 1109; Conservative 0; Mismatches 187; Indels 50; Gaps 2;

QY 1 ATCGCTGAGAACACAAAAAGTAGCGCTGGAGCTGGAATCGTTGGTGTGCACT 60
|||||
DB 274 atggctgagaccacagaagggttgatcgctggagctggaatcggtgtgtgacct 333
|||||

QY 61 GCCTTTGATGCTTCAACGTCGTGATTCAAAAGTCACCTTGTATTGACCCGACCTCTCTGGC 120

Db 334 gctttgatgcttcaacgctcgtggattcaaggttaccttgattgattccaaacccaccaggt 393
QY 121 GAAGTGTCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCGCTCGTCCCTATGTC 180
|||||
Db 394 gaaggtgctctcttcttcggaacgctggttgcctcaacggttctctccgttgttccaaatgccc 453
QY 181 ATGCGGGAACCTTGACGAGCGTGCAGAGTGGCTCTCTTGACC----- 223
|||||
Db 454 atgcaggaactgactagcttccaaagtggcttctggatcctgttggtaattcaagc 513
QY 224 -----CGATGGGCGGTGTCATCGGTTTCCAACTTTCACCACTATGTCCTG 275
|||||
Db 514 ttacggatccaaatgggtccatgtccatccgtttcagctactttccaaacctatgccttg 573
QY 276 GTTGATTCGGTTTCTGTAGCCGGAAGCAACCAAGTGAAGGAGGAGCGGAGCAAGCACT 335
|||||
Db 574 gttgattcgtttcttctgtctggaagaccacaaagtgaaagagcaagtaaggacct 633
QY 336 CCGCAATCTCATCAAGTCCAGCGTCCCTCTGATCAAGTCAATTGGCGGAGGAGGCTGATGC 395
|||||
Db 634 ccgtaacctcatcaagtccactgtgcttgcataagtccttggctgaggaagctgatgc 693
QY 396 GAGCCATCTGATCGCCCATGAAGTTCATCTGACCGTATATCGTGGAGAGCAGACTTTCGC 455
|||||
Db 694 tagccacttatccgtcacgaaggtcaccttaccgtgtaccgtggaagcagacttcgc 753
QY 456 CAAGGACCGGAGGTTGGAACTCGCGGCTCTCAACGGTCTTCGCCACGAGATCCCTCTC 515
|||||
Db 754 caagggaccgtggaaggttgggaactctgctctcaacgggtgtctgactcaaaacctccag 813
QY 516 TGCTGATGCTTTGCGTGATTTCGATCTCACTTGTCTGCATGCTTTTACCAAGGCACTTCT 575
|||||
Db 814 cgtgtatgcatgctgatttgcataactgtctcagcctttaccagaaggaatcct 873
QY 576 TATAGAGAGAACGGTCACAGGATTATTCGCAAGGGCTGCTGACCCCTCTTGTGTTCCGGC 635
|||||
Db 874 taccgaagagaacggtcacaccatcaaccacaaaggtctcgtgactcctctgttctgcgc 933
QY 636 TTTTATCGCAAGCGTGGCAATTTGTATCTGCGCGTGTATCGGTTTTCGAGACTGAAGG 695
|||||
Db 934 ttcatcgtctaaacgggtggaagattcgtctgctcgtgttatcggaatcgaagactgaag 993
QY 696 TCCTGCTCTCAAAAGCATTAACACCACTAACGGTGTGCTGGCTGTTGATG----- 745
|||||
Db 994 tcgtgctctcaaggggtatcaccaccacaaacgggtgtctctgctgtgatgctcagtggt 1053
QY 746 -----CAGCTGTTGTTGTCAGCTGGTGACACTCTTAAATCACTTGTCTTAAT 790
|||||
Db 1054 gtgaattcaagcttactgacgttgtgcagctggtgcacactccaagctctctgtctaact 1113
QY 791 CGTGTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATATATGTCATCCGGAATC 850
|||||
Db 1114 cctcttgatgatactccattgtatccgaacgtggataccacacatcgtagcgaacc 1173
QY 851 CGGAAGCGCTCCACGCAATTCGACGACCGATCGTGCAGGAAATTCATCGGACACACTA 910
|||||
Db 1174 cagaagctgtccacgtatttcccaactaccgactcttctggaagattcatcgtactacta 1233
QY 911 TGAATATGGTCTCTGTTGTTGCTGGTACTGTTGAGTTGCTGCTGCACAGCTGCTCCTA 970
|||||
Db 1234 tggagatgggtctctgctgtgtggaacgttgaagtcgctggtctcactgctgctcta 1293
QY 971 ACTGGAAACGTGCGCATGTGCTCTATACGACACGCTCGAAACCTCTTTCACAGCCCTCCGCG 1030
|||||
Db 1294 actgggaagcgtgctcactctcttctcactcgtgctcgaagttgcttccagctctcgtc 1353
QY 1031 CTGCGAGTTCTGAAGAACGATATTTCCAAATGGATGGGTTTTCCTCTAGCATTCCTGATT 1090
|||||
Db 1354 ctgccagttctgaagaacgttactccaagtggatgggtttctcccaagcatccccagatt 1413
QY 1091 CTCTTCCAGTGTGCTGCTGGCAACTCGTACACCGCACTAATCTATGCTTTGTTGTCAGC 1150
|||||

Db	1414	cccttcacagtattgctgctgtacctccgctactctccagacgcttatactatcgtcttcggtcacg	1473
Qy	1151	GTCACTCTCGGTATGACAGAGTGTCCCAANTGACTGCAACTCTCGTCTCAGAGCTCTCCGCGAG	1210
Db	1474	gtcacttcggtatgactggtgtgtcccaatgacgcgaacctcgcttctgagctccctcgca	1533
Qy	1211	GCGAAAGACCTCAANTCGACATTTCCGCCCTTTCGCACCAACCGCTTTCGTTATTTGGCAAT	1270
Db	1534	gtgagaagacctctatcgacatctccatctccattcgacacaaacctgttcggtattggttaagt	1593
Qy	1271	CCAAGCAACGGTCCGCGCAAGTTAA	1296
Db	1594	ccaaagcaaacctggcctcgatcctaa	1619
RESULT	8		
X57308	ID	X57308 standard; DNA; 8798 BP.	
XX	AC	X57308;	
XX	DT	26-JUL-1999 (first entry)	
XX	DE	Sugar beet T-DNA containing cp4/epsps.	
XX	DE		
XX	KW	Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;	
XX	KW	5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;	
XX	KW	tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.	
XX	OS	Beta vulgaris.	
XX	PN	W09923232-AL.	
XX	PD	14-MAY-1999.	
XX	PF	29-OCT-1998; 98WO-EP06859.	
XX	PR	31-OCT-1997; 97US-0112003.	
XX	PA	(NOVS) NOVARTIS AG.	
XX	PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.	
XX	PI	Mannerloef M, Steen P, Tenning PP;	
XX	DR	WPI; 1999-313347/26.	
XX	PT	Glyphosate resistant transgenic sugar beet plants	
XX	PS	Claim 11; Page 31-36; 55pp; English.	
XX	CC	This invention describes a novel sugar beet plant, including its	
XX	CC	descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase	
XX	CC	(cp4/epsps) enzyme activity which is obtainable by Agrobacterium	
XX	CC	mediated transformation with a gene allowing expression of cp4/epsps	
XX	CC	in plants, where the plant lacks both right and left T-DNA border	
XX	CC	sequences. The transgenic sugar beet plants of the invention are capable	
XX	CC	of tolerating herbicide treatment with glyphosate (also known as	
XX	CC	N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.	
XX	SQ	Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;	
Query Match	54.2%;	Score 703; DB 20; Length 8798;	
Best Local Similarity	85.3%;	Pred. No. 6.9e-213;	
Matches 784; Conservative	0; Mismatches 135; Indels	0; Gaps	
Qy	1	ATGCGCTCAGAACACAAAAAGATGATCGCTGGAGCTGGAATCGTTGGTGTATGCACT	60
Db	7205	atggctgagaaccacaaagaaggttgatcgtcgagctggaatcgttggtgttgact	7264
Qy	61	GCITTTGATGCTTCAAGCTGTGATTCAAAGTCACCTTGATTGACCCGCAACCTCTCTGCG	120
Db	7265	gctttgatcttcaacgctggtgattcaccgttaccgttgattgatccaaaccccgagct	7324

XX WO9923232-A1.
XX 14-MAY-1999.
XX 29-OCT-1998; 98WO-EP06859.
XX 31-OCT-1997; 97US-0112003.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Mannerloef M, Steen P, Tenning PP;
XX WPI; 1999-313347/26.
XX Glyphosate resistant transgenic sugar beet plants
XX Claim 8; Page 24-29; 55pp; English.
XX This invention describes a novel sugar beet plant, including its
XX descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
XX (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
XX mediated transformation with a gene allowing expression of cp4/epsps
XX in plants, where the plant lacks both right and left r-DNA border
XX sequences. The transgenic sugar beet plants of the invention are capable
XX of tolerating herbicide treatment with glyphosate (also known as
XX N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
XX Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;
SQ

Query Match 54.2%; Score 701.8; DB 20; Length 8012;
Best Local Similarity 86.4%; Pred. No. 1.6e-212;
Matches 775; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACACAAAAAGTAGGATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
DB 7116 ATGGCTGAGAACACAAAAAGTAGGATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 7175

QY 61 GCTTTGATGCTTCAAGCTCGTGATTCACAAAGTCACCTGATTCAGCCGACCCCTCTCGC 120
DB 7176 GCTTTGATGCTTCAAGCTCGTGATTCACAAAGTCACCTGATTCAGCCGACCCCTCTCGC 7235

QY 121 GAAGGTGCATCGTTTGGGATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTC 180
DB 7236 GAAGGTGCATCGTTTGGGATGCGGATGCTTCAACGGCTCATCCGCTGCTCCCTATGTC 7295

QY 181 ATCCCGGAAACTTGACGAGCGTGCAGAGTGCGTCTTTCAGCCGATGGGCGCGTGTCA 240
DB 7296 ATCCCGGAAACTTGACGAGCGTGCAGAGTGCGTCTTTCAGCCGATGGGCGCGTGTCA 7355

QY 241 ATCCGCTTCAGCTATTTTCCAACTCATCGCTGCTGCTGCTTTCGCTTTCGCTAGCCGGA 300
DB 7356 ATCCGCTTCAGCTATTTTCCAACTCATCGCTGCTGCTGCTTTCGCTTTCGCTAGCCGGA 7415

QY 301 AGACAAACAAGGTGAAGGACGAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
DB 7416 AGACAAACAAGGTGAAGGACGAGGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 7475

QY 361 CCTCTCATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCCATGAAGGT 420
DB 7476 CCTCTCATCAAGTCATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCCATGAAGGT 7535

QY 421 CATCTCAGCTATATGCTGTGAGAGGACAGACTTCGCCAAGACCGCGGAGGTTGGGAAC 480
DB 7536 CATCTCAGCTATATGCTGTGAGAGGACAGACTTCGCCAAGACCGCGGAGGTTGGGAAC 7595

QY 481 CGCGCTTCAACGGTGTGCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTTCGAT 540
DB 7596 CGCGCTTCAACGGTGTGCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTTCGAT 7655

QY 541 CCTAACCTGTGCGATGCTTTTACCAAGGCGATTCCTTATAGAGAGAACGGTTCACACGATT 600

DB 7656 CCTAACTGTCTCAGCGCTTTACCAAGGGAATCCTTATCGAAGGAGCAACGGTCCACCATC 7715
QY 601 AATCCGCAAGGCTCGTGACCCCTTCTTTTCGGCGTTTATCGGAAACGGTGGGCAATTT 660
DB 7716 AACCCACAAGGTCTCGTGAATCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7775

QY 661 GTATCTCGCGCTGCTCATCTCGGTTTTCAGACTGAAGGTGCTGCTTCAAGAGCATTTACAAC 720
DB 7776 GTATCTCGCGCTGCTCATCTCGGTTTTCAGACTGAAGGTGCTGCTTCAAGAGCATTTACAAC 7835

QY 721 ACTAACGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 7836 ACTAACGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7895

QY 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGCAACGCTGATATCATATCGTC 840
DB 7896 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGCAACGCTGATATCATATCGTC 7955

QY 841 ATCCGCAATTCGGAAGCGCTCCACGCTTTCGACGACCGATGCTGCTGCTGCTGCTGCTGCT 897
DB 7956 ATCCGCAATTCGGAAGCGCTCCACGCTTTCGACGACCGATGCTGCTGCTGCTGCTGCTGCT 8012

RESULT 10
Q46544/c
ID Q46544 standard; DNA; 3292 BP.
XX
AC Q46544;
XX
DT 26-NOV-1993 (first entry)
XX
DE Yeast SSRP DNA sequence.
XX
KW Structure-specific recognition protein; SSRP; yeast; DM 3002;
KW library; open reading frame; highly charged domain; DM 1001; human;
KW high mobility group protein; polyadenylation signal; ss.
XX
OS Saccharomyces cerevisiae.
XX
FH Key Location/Qualifiers
FT CDS 1..1626
FT /tag= a
FT polyA_signal 1632..1637
FT /tag= b
XX
PN WO9313222-A.
XX
PD 08-JUL-1993.
XX
PF 18-DEC-1992; 92WO-US11107.
XX
PX 26-DEC-1991; 91US-0814964.
XX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Brown SJ, Bruhn SL, Donahue BA, Essigmann JM, Kellett PJ;
PI Lippard SJ, Pili PM, Toney JH;
XX
DR WPI; 1993-227336/28.
DR P-PSDB; R38746.
XX
PT Identifying c-DNA encoding eukaryotic DNA structure-specific
PT recognition protein - by screening expression prods. of library
PT using labelled oligo-nucleotide probe then detecting prod.
PT selectively binding to probe
XX
PS Claim 24; Page 103-06; 142pp; English.
XX
CC This sequence represents the yeast derived sequence encoding a
CC structure-specific recognition protein (YSSRP). This sequence was
CC isolated from a combination of three subcloned EcoRI fragments
CC derived from the YSSRP clone lambda-ypt, to yield a sequence of 3292

PT New modified human beta interferon polypeptide(s) - prepd. by
PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
XX
XX
PS Claim 28; Chart 2c, page 34; 71pp; English.
XX
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
XX
SQ Sequence 501 BP; 112 A; 30 C; 69 G; 85 T; 205 other;

Query Match 2.7%; Score 35.4; DB 6; Length 501;
Best Local Similarity 28.9%; Pred. No. 0.24;
Matches 69; Conservative 50; Mismatches 120; Indels 0; Gaps 0;
Qy 505 CAGATCCCTCTCGTGGTAACTTCGATCCTAACTTCGATCCTTTTACC 564
|| : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 351 CATVARYTTNCCHCKNGTAAATCTCTCTTCVARYTTTCVARNACNGTIVTVAR 292
Qy 565 AAGGCATTCTTATAGAGAAGAGCGTCACAGGATTATCCGCAAGCGCTCGTGACCCCTC 624
: : : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 291 RTGRTTDATYTGRTGTANACRTTNGCVARVARTTYTCNACDATNGTTCCTCCANCC 232
Qy 625 TTGTTTCGGCGTTTATCCGAACGGTGGCAATTTGTATCTGCGCGTGTATCGGTTT 684
: : : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 231 NGTNWNNWNRVTCYTGHCRAADATNGCRAADATRTTATGVARCATYTCRTADATNGT 172
Qy 685 GAGACTGAAGTCTGCTCTCAAAGGCATTACAAACCACTAACGGTGTTCTCGCTGTGCA 743
: : : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 171 VARNGCNGCRTCYTCYTYTGRAAYTGRNTNCCRTCAAATCYTCATGNGGDATRTGCA 113

RESULT 15
N50023/c
ID N50023 standard; DNA; 501 BP.
XX
AC N50023;
XX
DT 04-SEP-1991 (first entry)
XX
DE Sequence encoding new modified human beta interferon polypeptides
DE IFN α 416.
XX
KW Antiviral; cell growth regulator; Immune system regulator;
KW antiproliferative; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
XX
PN EP163993-A.
XX
PD 11-DEC-1985.
XX
PF 17-MAY-1985; 85EP-0105750.
XX
PR 17-MAY-1984; 84GB-0012564.
XX
PA (SEAR) SEARLE G D & CO.
XX
PI Bell LD, Boseley PG, Porter AG;
XX
DR WPI; 1985-311944/50.
DR P-PSDB; P50022.
XX
PT New modified human beta interferon polypeptide(s) - prepd. by

PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
XX
XX
PS Claim 28; Chart 2a, page 32; 71pp; English.
XX
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
XX
SQ Sequence 501 BP; 107 A; 31 C; 69 G; 80 T; 214 other;

Query Match 2.7%; Score 35.2; DB 6; Length 501;
Best Local Similarity 29.0%; Pred. No. 0.28;
Matches 63; Conservative 47; Mismatches 107; Indels 0; Gaps 0;
Qy 505 CAGATCCCTCTCGTGGTAACTTCGATCCTAACTTCGATCCTTTTACC 564
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Db 351 CATVARYTTNCCHCKNGTAAATCTCTCTTCVARYTTTCVARNACNGTIVTVAR 292
Qy 565 AAGGCATTCTTATAGAGAAGAGCGTCACAGGATTATCCGCAAGCGCTCGTGACCCCTC 624
: : : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 291 RTGRTTDATYTGRTGTANACRTTNGCVARVARTTYTCNACDATNGTTCCTCCANCC 232
Qy 625 TTGTTTCGGCGTTTATCCGAACGGTGGCAATTTGTATCTGCGCGTGTATCGGTTT 684
: : : : || : : || : : || : : || : : || : : || : : || : : || : :
Db 231 NGTNWNNWNRVTCYTGHCRAADATNGCRAADATRTTATGVARCATYTCRTADATNGT 172
Qy 685 GAGACTGAAGTCTGCTCTCAAAGGCATTACAAACCA 721
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Db 171 VARNGCNGCRTCYTCYTYTGRAAYTGRNTNCCRTCR 135

Search completed: January 1, 2001, 03:43:13
Job time: 20201 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:17:58 ; Search time 157.96 Seconds
(without alignments)
1240.873 Million cell updates/sec

Title: US-08-484-274-7
Perfect score: 1296
Sequence: 1 ATGGCTGACAAACAGNAAAA.....AAACGGTCCGCCAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1296	100.0	1296	1	US-08-391-339-7
2	1296	100.0	1296	2	US-08-484-274A-7
3	1201.6	92.7	1296	1	US-08-391-339-6
4	1201.6	92.7	1296	2	US-08-484-274A-6
5	1196.8	92.3	1692	2	US-08-484-274A-3
6	1160.8	89.6	1293	1	US-08-391-339-4
7	1160.8	89.6	1293	2	US-08-484-274A-4
8	1160.8	89.6	1689	1	US-08-391-339-3
9	1011.2	78.0	1296	1	US-08-391-339-8
10	1011.2	78.0	1296	2	US-08-484-274A-8
11	1006.4	77.7	1296	1	US-08-391-339-17
12	1006.4	77.7	1296	2	US-08-484-274A-17
13	69	5.3	69	1	US-08-391-339-30
14	69	5.3	69	1	US-08-391-339-33
15	69	5.3	69	2	US-08-484-274A-30
16	69	5.3	69	2	US-08-484-274A-33
17	68	5.2	68	1	US-08-391-339-32
18	68	5.2	68	2	US-08-484-274A-32
19	63.4	4.9	65	1	US-08-391-339-28
20	63.4	4.9	65	2	US-08-484-274A-28
21	62	4.8	62	1	US-08-391-339-27
22	62	4.8	62	2	US-08-484-274A-27
23	61	4.7	61	1	US-08-391-339-31
24	61	4.7	61	2	US-08-484-274A-31
25	41	3.2	41	1	US-08-391-339-29
26	41	3.2	41	2	US-08-484-274A-29

C 27	37.4	2.9	3292	1	US-07-814-964-12	Sequence 12, Appl
C 28	37.4	2.9	3292	1	US-08-238-442-12	Sequence 12, Appl
C 29	37.4	2.9	3292	2	US-08-328-809-7	Sequence 7, Appl
C 30	37.4	2.9	3292	6	PCT-US92-11107-12	Sequence 12, Appl
C 31	36.4	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C 32	34.4	2.7	3489	4	US-08-728-323A-1	Sequence 1, Appl
C 33	34.4	2.7	32207	3	US-08-770-379-20	Sequence 20, Appl
C 34	33.2	2.6	1694	2	US-08-698-551-9	Sequence 9, Appl
C 35	33.2	2.6	1694	3	US-08-602-228-9	Sequence 9, Appl
C 36	33.2	2.6	1694	3	US-08-494-440B-9	Sequence 9, Appl
C 37	33.2	2.6	1694	3	US-08-533-901B-9	Sequence 9, Appl
C 38	33.2	2.6	1694	3	US-08-839-032A-9	Sequence 9, Appl
C 39	33.2	2.6	1694	4	US-08-839-031A-9	Sequence 9, Appl
C 40	33.2	2.6	1694	6	PCT-US93-12724-9	Sequence 9, Appl
C 41	33	2.5	423	1	US-08-470-179-144	Sequence 144, App
C 42	33	2.5	2800	3	US-08-874-138-1	Sequence 1, Appl
C 43	33	2.5	2800	3	US-08-874-138-5	Sequence 5, Appl
C 44	32.8	2.5	543	7	5273901-6	Patent No. 5273901
C 45	32.6	2.5	3181	2	US-08-655-086-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-391-339-7
; Sequence 7, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F,
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-391-339-7

Query Match 100.0%; Score 1296; DB 1; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGGAATCGTTGGTGATATGCAC	60
Qy	61	GCTTTGATGCTTCAACGTCGTGGATTTCAAGATCACTTGATTTGACCGCAACCCCTCTGGC	120
Db	61	GCTTTGATGCTTCAACGTCGTGGATTTCAAGATCACTTGATTTGACCGCAACCCCTCTGGC	120
Qy	121	GAAGGTGCATCGTTTGGGAATGCCGATGCTTTCAACGGCTCATCGCTGCTCCCTATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATGCCGATGCTTTCAACGGCTCATCGCTGCTCCCTATGTCC	180
Qy	181	ATGCCGGGAACCTTGACGAGCTGCCGAAGTGGCTCTTGTACCCGATGGGGCCGTTGTCA	240
Db	181	ATGCCGGGAACCTTGACGAGCTGCCGAAGTGGCTCTTGTACCCGATGGGGCCGTTGTCA	240
Qy	241	ATCCGGTTCAAGCTATTTTTCAACCATCATCGCCCTGGTTGATTTCCGCTTTCTGTTAGCCCGA	300
Db	241	ATCCGGTTCAAGCTATTTTCCNACCATCATGCCCTGGTTGATTTCCGCTTTCTGTTAGCCCGA	300
Qy	301	AGACCAAAAGGTGAAGGACAGGCGGAAGACATCCCGCAATCTCATCAAGTCCACGGTG	360
Db	301	AGACCAAAAGGTGAAGGACAGGCGGAAGACATCCCGCAATCTCATCAAGTCCACGGTG	360
Qy	361	CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGGGAGGCATCTGATCGGCATCAAGGT	420
Db	361	CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGGGAGGCATCTGATCGGCATCAAGGT	420
Qy	421	CATCTGACCCTATATCGTGGAGAACGACACTTCGCCAAGGACCGGAGGTTGGSACTG	480
Db	421	CATCTGACCCTATATCGTGGAGAACGACACTTCGCCAAGGACCGGAGGTTGGSACTG	480
Qy	481	CGGGCTCTCAACGGTGTTCCGACGCAGATCCCTCTCTGCTGATGCTTTGCGTGATTTCCAT	540
Db	481	CGGGCTCTCAACGGTGTTCCGACGCAGATCCCTCTCTGCTGATGCTTTGCGTGATTTCCAT	540
Qy	541	CCTAACTTGTGCGATCGTTTACCNAAGGCACTTCTATAGAAGAGAAGCGGCACACGATT	600
Db	541	CCTAACTTGTGCGANTCGTTTACCNAAGGCACTTCTATAGAAGAGAAGCGGCACACGATT	600
Qy	601	AATCCGAAGGGCTGTGACCCCTCTTGTTCGGCGTTTATATCCCAACGGTGGCGAATTT	660
Db	601	AATCCGAAGGGCTGTGACCCCTCTTGTTCGGCGTTTATATCCGAACGGTGGCGAATTT	660
Qy	661	GTATCTCGCGCTGCATCGGTTTGGAGACTGAAGTTCGTCTCNAAGGCAATTACAACC	720
Db	661	GTATCTCGCGCTGCATCGGTTTGGAGACTGAAGTTCGTCTCNAAGGCAATTACAACC	720
Qy	721	ACTAACGGTGTTCGGCTGTGTAGCAGCTGTTGTTCGAGCTGGTGACACTCTAAATCA	780
Db	721	ACTAACGGTGTTCGGCTGTGTAGCAGCTGTTGTTCGAGCTGGTGACACTCTAAATCA	780
Qy	781	CTTGCTAAATTGCGTAGCGCATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840
Db	781	CTTGCTAAATTGCGTAGCGCATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840
Qy	841	ATCCGGAATCCGGAAGCCGCTCCACGCATTCGAGGACCGCATGCGTCAAGAAAAATTCATC	900
Db	841	ATCCGGAATCCGGAAGCCGCTCCACGCATTCGAGGACCGCATGCGTCAAGAAAAATTCATC	900
Qy	901	GCACACCTATGGAATGGGTCTTCGTGTTCGTGCTACTGTTGAGTTTGTCTGGTCTCACA	960
Db	901	GCACACCTATGGAATGGGTCTTCGTGTTCGTGCTACTGTTGAGTTTGTCTGGTCTCACA	960
Qy	961	GCTGCTCCTAACTGGAACGTCGGATGTGCTCTATACGCACGCTCGAAAACTCTTCCCA	1020
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Qy	1021	GCCCTCGCGCTCGGAGTTCTGAAGAACGATATCCAAATGGATGGGTTTTCGTCCTAGC	1080
Db	1021	GCCCTCGCGCTCGGAGTTCTGAAGAACGATATCCAAATGGATGGGTTTTCGTCCTAGC	1080

Qy	1081	ATTGCTGATTCTCTTCACGATGATTGGTCGTGGAACCTCGGTACACCGCAGGTAACTATGCT	1140
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Qy	1141	TTTGGTTCACGGTCATCTCGGTATGACAGGTGCTTCCAATGACITGCAACTCTCGTCTCAGAG	1200
Db	1141	TTTGGTTCACGGTCATCTCGGTATGACAGGTGCTTCCAATGACITGCAACTCTCGTCTCAGAG	1200
Qy	1201	CTCCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTTCGCAACCAACCGCTTTTGGT	1260
Db	1201	CTCCTCGCAGCGCAAAAGACCTCAATCGACATTTTCGCCCTTTCGCAACCAACCGCTTTTGGT	1260
Qy	1261	ATTGGCAAAATCCCAAGCAAAACGGGTCGGCAAGTTAA	1296
Db	1261	ATTGGCAAAATCCCAAGCAAAACGGGTCGGCAAGTTAA	1296

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RESULT      2
US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glycosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2879
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-7

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	Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches	0;	Gaps
	Matches 1296;	Conservative	0;	Indels	0;	Gaps
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Dd	1	ATGCGTGAGAACACAAAAAGTAGGCATCGCTGGAGCTGGAAATCGTTGGTGTATGCAC	60			
Qy	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACCTTGAATGACCCGAACCCCTCCTGGC	120			
Dd	61	GCTTTGATGCTTCAACGTCGTGGATTCAAAGTCACCTTGAATGACCCGAACCCCTCCTGGC	120			
Qy	121	GAAGGTGCATGCTTTGGGAATGCCGGAATGCTTCAACGGCGTCATCCGTCGTCCTCATGTCC	180			

Db 121 GAAGGTGCATCGTTGGGAATCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
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Qy 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
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Qy 361 CCTCTGATCAAGTATTTGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
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Qy 421 CATCTGACCGTATATCGTGAGAGAGCAGACTTCCGCAAGGACCGCGGAGGTTGGGAAGT 480
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Qy 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTTCGACGCGAGATCCTCTCTGCTGATGCTTTCGCTGATTTTCGAT 540
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Qy 601 AATCCGCAAGGGTCTGACGCTTCTTCTTTCGCGGTTTATCCGGAACGGTGGCGAATTT 660
Db 601 AATCCGCAAGGGTCTGACGCTTCTTCTTTCGCGGTTTATCCGGAACGGTGGCGAATTT 660
Qy 661 GTATCTGCGGCTGATCGGCTTTGAGACTGAAGGTGCTGCTCTCAAGGCAATTTACAACT 720
Db 661 GTATCTGCGGCTGATCGGCTTTGAGACTGAAGGTGCTGCTCTCAAGGCAATTTACAACT 720
Qy 721 ACTAACGGTCTTCTGCGTGTGATGACGCTGTTGTTGACAGCTGGTGCACACTCTAAATCA 780
Db 721 ACTAACGGTCTTCTGCGTGTGATGACGCTGTTGTTGACAGCTGGTGCACACTCTAAATCA 780
Qy 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Db 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Qy 841 ATCCGGAATCCGGAAGCGCTCCACGCAATTCGAGACCGATGCTCAGGAAATTCATC 900
Db 841 ATCCGGAATCCGGAAGCGCTCCACGCAATTCGAGACCGATGCTCAGGAAATTCATC 900
Qy 901 GCGACACCTATGGAATGGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 961 GCTGCTCCTAATCGGAACGTCGCGATGCTCTATACGACGCTCGAAGAACTTCTTCCA 1020
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Db 1021 GCCTCTGCGGCTCGGAGTCTGGAAGACGATATTCCAAATGGATGGGTTTTCGTCCTAGC 1080
Qy 1081 ATTCTGATTCCTCTTCCAGTATTTGGTGGTGAACCTGCTACACCCGACGTAATCTATGCT 1140
Db 1081 ATTCTGATTCCTCTTCCAGTATTTGGTGGTGAACCTGCTACACCCGACGTAATCTATGCT 1140
Qy 1141 TTTTGTACCGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCTCTCAGAG 1200
Db 1141 TTTTGTACCGGTCATCTCGGTATGACAGGTGCTCCAAATGACTGCAACTCTCTCTCAGAG 1200
Qy 1201 CTCTCTGCGAGGCGAAAGACCTCAATCGACATTTTCGCGCTTTCGACCAACCGCTTTGGT 1260
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Qy 1261 ATTGGCAAAATCCAAAGCAACGGGTCCGGCAAGTTAA 1296
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US-08-391-339-6
; Sequence 6, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/717,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-391-339-6

Query Match 92.7%; Score 1201.6; DB 1; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Db 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGCTATGCAC 60
Qy 61 GCTTTGATGCTTCAACGTCGCTGGATTCAAAAGTCACCTTGATTGACCCGAAACCTCCTGGC 120
Db 61 GCGCTGATGCTTCAAGCGCGCGGATTCAAAGTCACCTTGATTGACCCGAAACCTCCTGGC 120
Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGAATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCCGGAATGCTTCAACGGCTCATCCGTCGTCCTATGTC 180
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QY 241 ATCCGGTTTCAGCTATTTTCCAAACCATCATGCTCGCTTGTGATTCGCTTTCTGTAGCCGGA 300
Db 241 ATCCGGTTTCAGCTATTTTCCAAACCATCATGCTCGCTTGTGATTCGCTTTCTGTAGCCGGA 300
QY 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATCGAGGCATCTGATCGCCCATGAAGT 420
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Db 421 CATCTGACCGTATATCGTGGAGAGCAGACTTCGCCAAGACCGCGGAGGTTGGGAACGT 480
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QY 541 CCTAACTTCTGCATGCTTTTACCAAGGCACTTTATAGAAGAGAACGGTCCACAGATT 600
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QY 601 AATCCGAAGGCTCGTGACCTCTTTTTCGCGCTTTTATCCGCAACCGTGGCGAATTT 660
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QY 661 GTATCTGCGCGTCTATCGGTTTGGAGACTGAAGTCTGCTCTCAAGGCATTACAACC 720
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Db 721 ACGAAGCGGCTTTCGCGCTGATGAGCTGTTGTGACAGTGGTGCACACTCTAAATCA 780
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Db 781 CTTGCTAATTCCTAGGCGATGACATCCCGCTCGATACCGAAGCGTGATCATATCGTC 840
QY 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGACGACCGGATGCGTCAGAAATTCATC 900
Db 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGACGACCGGATGCGTCAGAAATTCATC 900
QY 901 GCGACACCTATGGAATGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 GCGACACCTATGGAATGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GCTGCTCTAATCGGAAAGCGTCCGATGCTGCTATACGCGCGCTCGAAGAACTTCTTCCA 1020
Db 961 GCGGCTCTAATCGGAAAGCGTCCGATGCTGCTATACGCGCGCTCGAAGAACTTCTTCCA 1020
QY 1021 GCGCTCGGCGCTCGAGTTCGAAGAAGCATATTCCAATGGATGGTTCGCTCTCTAGC 1080
Db 1021 GCGCTCGGCGCTCGAGTTCGAAGAAGCATATTCCAATGGATGGTTCGCTCTCTAGC 1080
QY 1081 ATTCTGATTCCTTCCAGTGAATGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 ATCCCGGATTCGCTCCCGTGTATGGCGGGCAACCCGCGACACCCGACGTAATCTATGCT 1140
QY 1141 TTTTGGTCACGGTCACTTCGGTATGACAGGTGCTCCAAATGACGTGCAACTCTGCTCTCAGAG 1200
Db 1141 TTCGCGCCACGGTCACTTCGGGATGACAGGGGCGCGGATGACCGCAACGCTCTCTCAGAG 1200
QY 1201 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCCCTTCGCCCAACCGCTTTGGT 1260
Db 1201 CTCCTCGCAGGCGAAAGACCTCAATCGACATTTTCGCCCTTCGCCCAACCGCTTTGGT 1260
QY 1261 ATTGGCAATCAAGCAACAGGGTCCGGCAAGTTAA 1296
Db 1261 ATTGGCAATCAAGCAACAGGGTCCGGCAAGTTAA 1296
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RESULT 4
US-08-484-274A-6
; Sequence 6, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6
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Query Match 92.7%; Score 1201.6; DB 2; Length 1296;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1237; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
Db 1 ATGGCTGAGAACCAACAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGCGGTATGCAAG 60
QY 61 GCTTTGATGCTTCAACGCTGCTGATTCAAAGTCAACCTTGAATGACCCGAACCCCTCTGCG 120
Db 61 GCGCTGATGCTTCAACGCTGCTGATTCAAAGTCAACCTTGAATGACCCGAACCCCTCTGCG 120
QY 121 GAAGTGGCATCGTTGGGAATGCCGATGCTTCAAGTCAACCTTGAATGACCCGAACCCCTCTG 180
Db 121 GAAGTGGCATCGTTGGGAATGCCGATGCTTCAAGTCAACCTTGAATGACCCGAACCCCTCTG 180
QY 181 ATGCCGGGAAACTTACGAGCGTGGCGAAGTGGCTCTTGAACCCGATGGGCGGTTGTCA 240
Db 181 ATGCCGGGAAACTTACGAGCGTGGCGAAGTGGCTCTTGAACCCGATGGGCGGTTGTCA 240
QY 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCTCGCTTGTGATTCGCTTTCTGTAGCCGGA 300
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCTCGCTTGTGATTCGCTTTCTGTAGCCGGA 300
QY 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
Db 301 AGACCAAAACAGGTGAAGGAGCAGGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG 360
QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATCGAGGCATCTGATCGCCCATGAAGT 420
Db 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATCGAGGCATCTGATCGCCCATGAAGT 420
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Qy 421 CATCTGACCGTATATCTGTTGAGAGACAGACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480
Db 421 CATCTGACCGTATATCTGTTGAGAGACAGACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480
Qy 481 CGGGCTCTCAACGGTGTTCGACGCGAGATCTCTCTCTGATGCTTTTCGCTGATTTCCGAT 540
Db 481 CGGGCTCTCAACGGTGTTCGACGCGAGATCTCTCTCTGATGCTTTTCGCTGATTTCCGAT 540
Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTATAGAGAGACGGTTCACACGATT 600
Db 541 CCGAACTTGTGCGATGCTTTTACCAAGGGCATTTCTATAGAGAGACGGTTCACACGATT 600
Qy 601 AATCCGAAGGGCTCGTACACCTCTTTCTTCGCGGTTTTATCGCGAAGCGTGGCGAATTT 660
Db 601 AATCCGAAGGGCTCGTACACCTCTTTCTTCGCGGTTTTATCGCGAAGCGTGGCGAATTT 660
Qy 661 GTATCTGCGCGTGTATCGGTTTGTAGACTGAAGTCTGCTCTCAAGGCATTACAACC 720
Db 661 GTATCTGCGCGTGTATCGGTTTGTAGACTGAAGTCTGCTCTCAAGGCATTACAACC 720
Qy 721 ACTAACGGTGTTCGGCTGTTGATGACAGCTGTTGTTGACGCTGTTGCTGCTTTCGCTCACA 780
Db 721 ACTAACGGTGTTCGGCTGTTGATGACAGCTGTTGTTGACGCTGTTGCTGCTTTCGCTCACA 780
Qy 781 CTTCGTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCCTC 840
Db 781 CTTCGTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCCTC 840
Qy 841 ATCGGGAATTCGGAGCGGCTCCAGCATTCGAGACCGATGCTCAGGAAAATTCATC 900
Db 841 ATCGGGAATTCGGAGCGGCTCCAGCATTCGAGACCGATGCTCAGGAAAATTCATC 900
Qy 901 GCGACACCTATGGAATGGGCTTCGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 960
Db 901 GCGACACCTATGGAATGGGCTTCGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 960
Qy 961 GCTGCTCTACTGGAACGTCGGATGCTCTATACGACAGCTCGGAAACTTCTTCCA 1020
Db 961 GCGGCTCTACTGGAACGTCGGATGCTCTATACGACAGCTCGGAAACTTCTTCCA 1020
Qy 1021 GCCCTCGCGCTGGAGTTCCTGAAGAACGATATCCAAATGATGGGTTTCGCTCTAGC 1080
Db 1021 GCCCTCGCGCTGGAGTTCCTGAAGAACGATATCCAAATGATGGGTTTCGCTCTAGC 1080
Qy 1081 ATTCTGATTTCTTCCAGTATGTTGCTGCTGCAACTCTGACACCGAGTAACTCTATGCT 1140
Db 1081 ATCCGGATTCGCTCCCGCTGATTGGCCGGCAACCCGACACCGAGCTAACTCTATGCT 1140
Qy 1141 TTTGGTCAAGGTCATCTCGGTATGACAGGTGCTTCCAATGACTGCAACTCTCTCTCAGAG 1200
Db 1141 TTTGGTCAAGGTCATCTCGGTATGACAGGTGCTTCCAATGACTGCAACTCTCTCTCAGAG 1200
Qy 1201 CTCCTCGGAGGGAAGACCTCAATCCACATTTTCGCCCTTCGCAACCAACCGCTTTGGT 1260
Db 1201 CTCCTCGGAGGGAAGACCTCAATCCACATTTTCGCCCTTCGCAACCAACCGCTTTGGT 1260
Qy 1261 ATTGGCAATCCAAGCAACGGTCCGGCAAGTTAA 1296
Db 1261 ATTGGCAATCCAAGCAACGGTCCGGCAAGTTAA 1296

RESULT 5

US-08-484-274A-3
: Sequence 3, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433

: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1692 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-484-274A-3

Query Match 92.3%; Score 1196.8; DB 2; Length 1692;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 1234; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 1 ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGAGCTGGAATCGTTGGTGTATGCACT 60
Db 120 ATGCTGAGAACCAAAAAAGTAGGCATCGCTGAGCGGGAATCGTCGGCGTATGCAGC 179
Qy 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAAGTCACTTTGATTGACCCGGAACCTCCTGCG 120
Db 180 GCGCTGATGCTTCAAGCGCGGATTTCAAGTCACTTTGATTGACCCGGAACCTCCTGCGC 239
Qy 121 GAAGTGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCTGCTATGTC 180
Db 240 GAAGTGTGATCGTTTGGGAATCCCGGATGCTTCAACGGCTCATCGTCTGCTATGTC 299
Qy 181 ATCCGGGAAACTTCACGAGCGTCCGGAAGTGGCTCTTACCCGATGGGCGCTTGTC 240
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Qy 241 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGA 300
Db 360 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGA 419
Qy 301 AGACAAACAGGTGAAGGAGGAGCGGAAGACACTTCGCAATCTCATCAAGTCCACGGTG 360
Db 420 AGACAAACAGGTGAAGGAGGAGCGGAAGACACTTCGCAATCTCATCAAGTCCACGGTG 479
Qy 361 CCTCTGATCAAGTCAATTCGCGGAGGAGGCTGATGCGAGCCATCTCATCGCCCATGAAGT 420
Db 480 CCTCTGATCAAGTCAATTCGCGGAGGAGGCTGATGCGAGCCATCTCATCGCCCATGAAGT 539
Qy 421 CATCTGACCGTATATCTGTTGAGAGACAGACTTCGCCAAGGACCGCGGAGGTTGGAACTG 480
Db 540 CATCTGACCGTATATCTGTTGAGAGACAGACTTCGCCAAGGACCGCGGAGGTTGGAACTG 599
Qy 481 CGCGCTCTCAACGGTGTTCGACGCGAGATCTCTCTCTGCTGATGCTTTGCGTCAATTCGAT 540
Db 600 CGCGCTCTCAACGGTGTTCGACGCGAGATCTCTCTCTGCTGATGCTTTGCGGATTTCCGAT 659
Qy 541 CCTAACTTGTGCGATGCTTTTACCAAGGGCATTTCTATAGAGAGAACGGTTCACACGATT 600
Db 560 CCGAACTTGTGCGATGCTTTTACCAAGGGCATTTCTATAGAGAGAACGGTTCACACGATT 719

Oy 661 GTATCTGCGCGTGTCTATCGGTTTTCAGACTGAAGTCTGTCTCTCAAGGCAATTAACAAC 720
Db 658 GTATCTGCGCGTGTCTATCGGTTTTCAGACTGAAGTCTGTCTCTCAAGGCAATTAACAAC 717
Oy 721 ACTAAGCGTGTCTGCGTGTTCATCCAGCTGTGTTGTCAGCTGGTGGCACACTCTAAATCA 780
Db 718 ACGAACGCGTGTCTGCGGCTTGTATGACGCGTGTGTCGAGCGCGGCACACTCGAAATCA 777
Oy 781 CTTCGTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCGTC 840
Db 778 CTTCGTAATTCGCTAGGCGATGACATCCGCTCGATACCGAAGTGGATATCATATCGTC 837
Oy 841 ATCGGGAATTCGGAAGCGCTCCAGCAATTCGACGACCGATGCGTCAGGAAATTCATC 900
Db 838 ATCGGGAATTCGGAAGCGCTCCAGCAATTCGACGACCGATGCGTCAGGAAATTCATC 897
Oy 901 CGGACACCTATGGAATGGGTCTTCGTCTGTCTGCTACTGTTCAGTTTTCGTCTCACA 960
Db 898 CGGACACCTATGGAATGGGTCTTCGCTGGCGGTACGGTTGAGTTTCGTCTGCGGTCTACA 957
Oy 961 GGTGCTCTTAATTCGGAAGCGTGGCATGTGCTCTATAGCACGCTCGGAAACTTCTTCCA 1020
Db 958 GCGCTCTTAATTCGGAAGCGTGGCATGTGCTCTATAGCACGCTCGGAAACTTCTTCCA 1017
Oy 1021 GCGTCTGCGGCTCGGAGTCTTGGAAGACGATATTCGAAATGGATGGGTTCGTCCTAGC 1080
Db 1018 GCGCTCGGCGCTCGGAGTCTTGGAAGACGATATTCGAAATGGATGGGTTCGTCCTAGC 1077
Oy 1081 ATTCCTGATCTCTTTCACAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1140
Db 1078 ATTCGCGATTCGCTCCCGCTGATTCGCGCGGCAACCGGACACCGAGTATCTATGCT 1137
Oy 1141 TTGTGTCAGGCTCATCTCGGTATGACAGTGTCTCAATGACTGCAACTCTCTGTCCTCAG 1200
Db 1138 TTGCGCATGTCATCTCGGCATGACAGGCGCGCATGACCGCAACCGTCTGTCCTCAG 1197
Oy 1201 CTCCTCGGAGGGAAGACCTCAATGACATTTTCGCGCTTCGCGCACCAACCGCTTTGGT 1260
Db 1198 CTCCTCGGAGGGAAGACCTCAATGACATTTTCGCGCTTCGCGCACCAACCGCTTTGGT 1257
Oy 1261 ATTCGCAATTCGCAACGCGTCCGCAAGTTAA 1296
Db 1258 ATTCGCAATTCGCAACGCGTCCGCAAGTTAA 1293

RESULT 7
US-08-484-274A-4
; Sequence 4, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.

; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1293
US-08-484-274A-4

Query Match 89.6%; Score 1160.8; DB 2; Length 1293;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;

Oy 1 ATGGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
Db 1 ATGCTGAGAACCAACAAAAAGTAGGCATCGCTGGAGCGGGAATCGTCGGCGTATGCACG 60
Oy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAAGTACCTTTGATTGACCCGGAACCCCTCCTGCG 120
Db 61 GCGCTGATGCTTCAGCGCGCGGATTCAAAGTACCTTTGATTGACCCGGAACCCCTCCTGCG 120
Oy 121 GAAGTGTGATCGTTTGGGAATCCCGGATTCACAGGCTCATCGTGTGCTATGTC 180
Db 121 GAAGTGTGATCGTTTGGGAATCCCGGATTCACAGGCTCATCGTGTGCTATGTC 180
Oy 181 ATGCGGGAACCTTCACGAGGTGCGGAAGTGGCTCTTGACCCGATGGGCGGTGTCA 240
Db 181 ATGCGGGAACCTTCACGAGGTGCGGAAGTGGCTCTTGACCCGATGGGCGGTGTCA 239
Oy 241 ATCCGGTTTCAAGTATTTTCCAAACCATCATGCTGCTGTTGATTGCTGTTTCTGTTAGCCGA 300
Db 240 ATCCGGTTTCAAGTATTTTCCAAACCATCATGCTGCTGTTGATTGCTGTTTCTGTTAGCCGA 297
Oy 301 AGACCAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 298 AGACCAACAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Oy 361 CCTCTGATCAAGTCAATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 358 CCTCTGATCAAGTCAATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
Oy 421 CATCTGACCGTATATCTGTTGAGAACGACACTTCGCCAAGGAGCGCGGAGGTTTGGGAAC 480
Db 418 CATCTGACCGTATATCTGTTGAGAACGACACTTCGCCAAGGAGCGCGGAGGTTTGGGAAC 477
Oy 481 CGGCGTCTCAACGCGTTCGACGAGATCCTCTCTGCTGATGCTTTCGGTGATTTCCAT 540
Db 478 CGGCGTCTCAACGCGTTCGACGAGATCCTCTCTGCTGATGCTTTCGGTGATTTCCAT 537
Oy 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATTCCTTATAGAAGACGAGGAGGAGGAGGAG 600
Db 538 CGGAACCTTGTGCGATGCTTTTACCAAGGCGATTCCTTATAGAAGACGAGGAGGAGGAGGAG 597
Oy 601 AATCGCAAGGCGCTCGTGACCTCTTTTTCGGCGTTCCTTATCGCGAAGCGGTCGCGAATTT 660
Db 598 AATCGCAAGGCGCTCGTGACCTCTTTTTCGGCGTTCCTTATCGCGAAGCGGTCGCGAATTT 657
Oy 661 GTATCTGCGCGTGTCTCGGTTTTCAGACTGAAGTCTGTCTCTCAAGGCAATTAACAAC 720
Db 658 GTATCTGCGCGTGTCTCGGTTTTCAGACTGAAGTCTGTCTCTCAAGGCAATTAACAAC 717
Oy 721 ACTAAGCGTGTCTGCGTGTTCATGACGCTGTTGTTGACGCTGGTTCACACTCTAAATCA 780
Db 718 ACGAACGCGTGTCTGCGCGTTCATGACGCGGTTGTCGACGCGGTCGCGAAGTCA 777

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QY 781 CTTGCTAATTGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 840
Db 778 CTTGCTAATTGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 837
QY 841 ATCGCGAATCCGAAGCGCTCCACGCAATCCGACGACCGATGCTCAGGAAAATTCATC 900
Db 838 ATCGCGAATCCGAAGCGCTCCACGCAATCCGACGACCGATGCTCAGGAAAATTCATC 897
QY 901 GCGACACCTATGGAATGGGTCTCGTGTTGCTGCTACTGTTGAGTTTGTGCTCTCACA 960
Db 898 GCGACACCTATGGAATGGGTCTCGTGTTGCTGCTACTGTTGAGTTTGTGCTCTCACA 957
QY 961 GCTGCTCTAATCGGAACGTCGCGATGCTCTATACGACGCTCGAATCTCTTCCA 1020
Db 958 GCGCTCTAATCGGAACGTCGCGATGCTCTATACGACGCTCGAATCTCTTCCA 1017
QY 1021 GCGCTCGCGCTCGGAGTCTGGAAGACGATATTCAAAATGGATGGTTCGTCCTAGC 1080
Db 1018 GCGCTCGCGCTCGGAGTCTGGAAGACGATATTCAAAATGGATGGTTCGCGCGAGC 1077
QY 1081 ATTCCTGATTTCTCTTCAGTGATTGGTCTGTCGCAACTCGTACACCCGACGTAATCTATGCT 1140
Db 1078 ATCCCGGATTCGCTCCCGGATTGGCGGGCAACCCGACACCCGACGTAATCTATGCT 1137
QY 1141 TTTGGTCACGGTANTCGGTATGACAGTGTCTCAATGACTGCAACTCTGCTCTCAGAG 1200
Db 1138 TTTGGGCAATGCTCTCTCGGCATGACAGGGGCGCGATGACCCGACGCTCGTCTCAGAG 1197
QY 1201 CTCTCGCAGCGAAGACCTCAATGACATTTTCGCCCTTCGCACCAACCGCTTTGGT 1260
Db 1198 CTCTCGCAGCGAAGACCTCAATGACATTTTCGCCCTTCGCACCAACCGCTTTGGT 1257
QY 1261 ATTGGCAATCCAAAGCAACGGGTTCGGCAAGTTAA 1296
Db 1258 ATTGGCAATCCAAAGCAACGGGTTCGGCAAGTTAA 1293

RESULT 8
US-08-391-339-3
: Sequence 3, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. BB4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
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: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1689 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-391-339-3

Query Match      89.6%; Score 1160.8; DB 1; Length 1689;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches 62; Indels 3; Gaps 3;

QY 1 ATGCTCGAGAACACAAAAAGTAGGCATCGCTGAGCTTGAATCGTTGGTGTATGACAT 60
Db 120 ATGCTCGAGAACACAAAAAGTAGGCATCGCTGAGCCGGAATCGTCGGCGTATGACAG 179
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAAAGTCACCTTTGATTGACCCGAAACCCCTCTCC 120
Db 180 GCCTGATGCTTCAGCGCCGCGGATTCAAAAGTCACCTTTGATTGACCCGAAACCCCTCTCC 239
QY 121 GAAGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATATGCC 180
Db 240 GAAGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATATGCC 299
QY 181 ATCCCGGAAACTTGACGAGCGTCCGCAAGTGGCTTCCTTACCCGATGGGCGCTTGTCA 240
Db 300 ATCCCGGAAACTTGACGAGCGTCCGCAAGTGGCTTCCTTACCCGATGGGCGCTTGTCA 358
QY 241 ATCCGGTTTACGCTATTTTCCAAACCATCATGCCCTGGTTGATTGCTTTCTTGTAGCCGGA 300
Db 359 ATCCGGTTTACGCTA-TTTTCCAAACCATCATG-CCTGGTTGATTGCTTTCTTGTAGCCGGA 416
QY 301 AGACCAAAACAAAGTGAAGGAGCAGGCGAAAGACACTCCGCAATCTCATCAAGTCACCGGTG 360
Db 417 AGACCAAAACAAAGTGAAGGAGCAGGCGAAAGACACTCCGCAATCTCATCAAGTCACCGGTG 476
QY 361 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT 420
Db 477 CCTCTGATCAAGTCATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT 536
QY 421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAAGT 480
Db 537 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAAGT 596
QY 481 CGCGCTCTCAACGGTGTTCGCACGACAGATCCTCTCTGCTGATGCTTTGCGTGTATTCGAT 540
Db 597 CGCGCTCTCAACGGTGTTCGCACGACAGATCCTCTGAGCTGAGGTCGCTCTCAAGGCAATTCAC 656
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATTTCTTATAGAAGAACGCTCACACGATT 600
Db 657 CCGAATTTGCGATGCGTTTACCAAGGCGATTTCTTATAGAAGAACGCTCACACGATT 716
QY 601 AATCCGCAAGGCTCGTGACCCCTCTTGTTCGGCGTTTATCGCGAACGCTGGCGAATTT 660
Db 717 AATCCGCAAGGCTCGTGACCCCTCTTGTTCGGCGTTTATCGCGAACGCTGGCGAATTT 776
QY 661 GTATCTCGCGGCTGTCATCGGTTTGGAGACTGAGGTCGCTCTCAAGGCAATTCACAC 720
Db 777 GTATCTCGCGGCTGTCATCGGTTTGGAGACTGAGGTCGCTTAAAGGCAATTCACAC 836
QY 721 ACTAAGCGCTTCTGCGTGTGATGAGCTGTTGTTGACGCTGCTGACACTCTAAATCA 780
Db 837 ACGAACGGCGTCTTGGCGGTTGATGACGCGGTTGTCGACGCCGCGCACAATCA 896
QY 781 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 840
Db 897 CTTGCTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGTGGATATCATATCGTC 956
QY 841 ATCGCGAATCCGAAGCGCTCCACGCAATCCGACGACCGATGCTCAGGAAAATTCATC 900
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Qy	961	GCTGCTCCTTAACTGGAAACGCTGGGATGTGCTCTATACGCACGCTCGAAACATTCCTTTCCA	1020
Db	961	GCTGCTCCTTAACTGGAAAGCGTCTACGTTCTCTACACTACGCTCGTAACTGCTTCTTCCA	1020
Qy	1021	GCCTCGCGCCTCGGAGTTCTGAAGACAGATATTCCTCAATGGATGGGTTTTCGTCCTTAGC	1080
Db	1021	GCTCTCGCTCCTCCCAAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCTCAAGC	1080
Qy	1081	ATTCTCTGATTCTCTCCACGTGATTTGGTCGTGCAACTCGTACACCCGACGTAATCTATGCT	1140
Db	1081	ATCCAGATTTCCCTTCCAGTGATTTGGTCGTGCTACCCGTACTCCAGACGTTATCTACGCT	1140
Qy	1141	TTTGGTCACGGTTCATCTCGGTATGACAGTGCTGCTCAATGACTGCAACTCTCGTCTCAGAG	1200
Db	1141	TTCGGTACGGTTCACCTCGGTATGACTGGTGCTCAATGACCGCAACCTCGTTTCTGAG	1200
Qy	1201	CTCCTCGCAGCGGAAAGACCTCAATCGACATTTTCGGCCTTTTCGCACCAACCCGTTTGGT	1260
Db	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTTTCGCACCAACCCGTTTCGGT	1260
Qy	1261	ATTGGCANAATCCAAAGCAACGGGTCCGGCAAGTTAA	1296
Db	1261	ATTGGTAAGTCTCAAGCAAACTGCTCGTCACTCTAA	1296

RESULT 10
US-08-484-274A-8
; Sequence 8, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glycosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:

Query Match	78.0%	Score 1011.2	DB 2	Length 1296
Best Local Similarity	86.3%	Pred. NO. 0		
Matches 1118	Conservative	0	Mismatches 178	Indels 0
				Gaps 0

Qy	1 ATGGCTGAGAACCAACAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCCACT 60
Db	1 ATGGCTGAGAACCAACAAAGGTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCCACT 60

Qy	61	GCTTGTGATGCTTCAACGTCGTGGGATTCAAAGTCACCTTGAATTGACCCGAACCCCTCTCC	TGGC	120
Db	61	GCTTGTGATGCTTCAACGTCGTGGGATTCAAAGTCACCTTGAATTGACCCGAACCCAGGT	120	
Qy	121	GAAGGTGCATCGTTTGGSAATGCGGATGCTTCAACGGCTCAATCCGTGCTGTCCTTATGTC	180	
Db	121	GAAGGTGCTTCTTTCGGTAGCGTGGTTCATCAACGGTTCCTCCGTTGTTTCCAATGTC	180	
Qy	181	ATGCGGGAAACTTGGAGAGCGTCCGAAGTGGCTCTTGACCCGATGGGCGGTGTGCA	240	
Db	181	ATGCGCAGAAACTTGAATAGCTAGCGTTCCAAGTGGCTTTCGACCAATGGTCCATTGTC	240	
Qy	241	ATCCGGTTCACCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGTTCTTGTCTGCTGA	300	
Db	241	ATCCGGTTCACCTACTTTCCAAACCATCATGCCCTGGTGTGATTCGTTCTTGTCTGCTGA	300	
Qy	301	AGACAAACAAAGGTGAAGGAGCAGCGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG	360	
Db	301	AGACAAACAAAGGTGAAGGAGCAAGCTTAGGCACTCCGTAACTCATCAAGTCCACTGTG	360	
Qy	361	CCTCTGATCAAGTCATTTGGCGGAGGAGCTGATGCGAGCCATCTGATCCGCCATGAAGT	420	
Db	361	CCTTGTGATCAAGTCTTTGGGCTAGGAGGCTGATGCTAGGCACCTTATCCGTCAACAGT	420	
Qy	421	CATCTGACCGTATATCTGTGGAGAGCAGACTCCGCCAAGGACCGGAGGTTCGGAACGTG	480	
Db	421	CACCTTACCGTGTACCTGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCGGAACTT	480	
Qy	481	CGGCGTCTCAACGGTGTTCGCAACGAGATCCTCTGCTGATGCTTTGGGTGATTTTCGAT	540	
Db	481	GCTGCTCTCAACGGTGTTCGTTACTCAAATCCTCAGGCTCATGCAATGGCTGATTTTCGAT	540	
Qy	541	CCTAACTTGTGCGATGCTTTTACCAAGGGCATCTTTATAGAAGAGACGGTCCACAGATT	600	
Db	541	CCTAACTTGTCTACGGCTTTTACCAAGGGAATCCTTTATCGAAGAGAACGGTCCACACATC	600	
Qy	601	AATCCGAAGGGCTCGTGACCCCTCTCTTTTCGGCGTTTATCCGAACCGGTGGCGAAATT	660	
Db	601	AACCCACAAGTCTCGTGACTCTCTGTTTCGTGCTTTCATCGCTAACGGTGGAGTTC	660	
Qy	661	GTATCTGGCGGTGATCATCGGTTTTGAGACTGAAGTGTGCTCTCAAGGCAATTTACAAC	720	
Db	661	GTGTCGTGCTGTATATTCGGAATTCGAGACTGAAGTGTGCTCTCAAGGATATCACACAC	720	
Qy	721	ACTAACGGTGTCTGCGCTGTGATGCAGCTGTGTTGTGACGTGGTGTGCACACTCTAAATCA	780	
Db	721	ACCAACGGTGTCTTCTGTTGTGATGCAGCTGTGTTGTGCAGCTGGTGTGCACACTCCAAAGTCT	780	
Qy	781	CTTGCTTAATTTGGCTPAGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATGCTC	840	
Db	781	CTTGCTAACTCCCTTGGTGTGATGATCCCATTTGGATACCGAACGTGGATACCATATCGTG	840	
Qy	841	ATCCGGAATCCGAAGCGCTCCACCATTTCCGACACACCGATCCGTTCAGGAAATTCATC	900	
Db	841	ATCCGAACCCCAAGCTGCTCCACGTATTTCCAACCTACCGATGCTTCTGGAAGTTCATC	900	
Qy	901	CGGACACTATGGAATAGGCTCTTCGTTGTGCTGGTACTGTTGAGTGTTCGTGGTCTCACA	960	
Db	901	GCTACTCTATGGAGATGGCTCTTCGTTGTGCTGGAAACCGTTTGAATTCGCTGCTCACT	960	
Qy	961	GCTGCTCTTAATCTGGAACGTGGCGATGTGCTCTATACCGACGCTTCGAAACTTCTCCCA	1020	
Db	961	GCTGCTCTTAATCTGGAAGCGTGTCACTCTCTATACACTCACGCTCGTAAGTGTGCTTCCA	1020	
Qy	1021	GCCCTCGCGCTCGGAGTCTCTGAAGAACGATATTCCAATGATGGTTCCTGCTCTAGC	1080	
Db	1021	GCTCTCGCTCTCGCCAGTCTCTGAAGAACGTTACTCCAAGTGGATGGTTCCTGCTCCAAGC	1080	
Qy	1081	ATTCCTGATCTCTTCCAGTGTATGCTGTGCAACTCTGTACACCGACGTAATCTATGCT	1140	
Db	1081	ATCCGAGATTCCTTCCAGTGTATGCTGTGCTGTACCGTACCTCCAGAGGTTATCTACGCT	1140	

Qy	1141	TTTGGTCACGGTCAATCTCGGTATGACAGGTGCTCAATGACTGCNACTCTCGTCTCAGAG	1200
Db	1141	TTTGGTCACGGTCACCTCGGTATGACTGCTGCTCAATGACCGAACCTCTGTTCTTGAG	1200
Qy	1201	CTCCTCGCAGGGGAAAGACCTCAATCGACATTTTCGCCCTTTGCGACCAAAACCGCTTTTGGT	1260
Db	1201	CTCCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGTTTCGGT	1260
Qy	1261	ATTGGCAAAATCCAAGCAAAACGGGTCTCGGCAAGTTAA	1296
Db	1261	ATTGGTAAAGTCCAAGCAAACTGGTCTCGCATCCTAA	1296

RESULT 11

```

US-08-391-339-17
: Sequence 17, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. BB4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1296 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (recombinant)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1296
US-08-391-339-17

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Query Match 77.7%; Score 1006.4; DB 1; Length 1296;
Best Local Similarity 86.0%; Pred. No. 4.8e-300;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

Qy	1	ATGCTGAGAACCAACAAAAAGTAGGATCGCTGGAGCTGGAATCGTTGGTGTATGCAC	60
	1		
	1	ATGGCTCAGAACCAACAAGAGTTGGTATCGCTCGAGCTGGAATCGTTGCTTTGCAC <td>60</td>	60
	1		
Qy	61	GCTTTGATGCTTCACGCTCGTGGATTCAAAGTCAACCTTGATGACCCGAACCCCTCTGGC	120

Db	61	GC	TTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGTGATGCCAAACCCACCAAGT	120
Qy	121	GA	AGGTGCATCGTTTGGGAATCCGGGATGCTTTCAACGGCTCATCCGTCGTCCCTATGTGCC	180
Db	121	GA	AGGTGCCCTTTTTCGGTAAAGGCTGGTTTTCGTTTCAACGGTTCCTCGTTTGCCTCAATGTCC	180
Qy	181	AT	GCCGGGAAACTTACGAGGCTGCCGAAGTGGCTTCTTGACCCGATGGGCGCGTTGTCA	240
Db	181	AT	GCCAGGAAACTTGACTAGCGTTTCCAAAGTGGCTTCTTTGACCCAAATGGGTCCAATTGTGCC	240
Qy	241	AT	CCGGTTACAGCTATTTCACCAACATCATGCCCTGGTTGCAATTCGCTGCTTCTGTTCGCCGGA	300
Db	241	AT	CCGTTTCGGCTACTTTCCAAACATCATGGCTTGGTTGATTTCTTCTGCTTGCCTGGA	300
Qy	301	AG	CAAAACAAAGTGAAGGAGCAGGCGAAAGACATCCGCAATCTCATCAAGTCCACCGGTG	360
Db	301	AG	CAAAACAAAGTGAAGGAGCAAGCTAAGGCATCCGTAACCTCATCAAGTCCACCTGTG	360
Qy	361	CCT	GTATCAAGTTCATTTGGGGAGGAGGCTGATTTGGAGGCATCTGATCCGCGCATGAAGGT	420
Db	361	CCT	TTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGCAAGGT	420
Qy	421	CAT	CTGACCGGTATATCGTGCAGAAAGCAGACTTCGGCAAGGACCGCGGAGGTTTGGGAATG	480
Db	421	CAC	CTTACCCTGTACCGTGAGGAGCAGACTTCGGCAGGGACCGTGGAGGTTTGGGAACCT	480
Qy	481	CG	CGCTTCAACCGTCTTCGACCGCAGATCTCTCTGCTGATGCTTTCGCTGATTTTCGAT	540
Db	481	CG	TCTCTCAACCGTGTTCGTACTCAATTCCTCAGCGCTGATGCAATTCGGTGATTTTCGAT	540
Qy	541	CCT	TAATTTGTCGATGCTTTTACCAAGGCACTTCTTAGAAGAGAACGGTCACACGATT	600
Db	541	CCT	TAATTTGCTCAGCGCTTTTACCAAGGCAATCCTTATGCAAGAGAACGGTCACACCATC	600
Qy	601	AAT	CCGCAAGGGCTCGTGACCCCTCTTTTTCGGCGTTTATGCGCAACGGTGGCGAATTT	660
Db	601	AAC	CCACAGGTCGTGTACTCTTTTTCGCTGCTTATCGCTTACCGGTCGGAGGTTTC	660
Qy	661	GT	ATCTCCGGCTGTCACTCGGTTTTTGTAGACTGAAGTTCGTGCTCTCAAAAGCAATTACAACC	720
Db	661	GT	GTCTCTCTCGTGTATTCCGATTCGAGACTGAAGTTCGTGCTCTCAAGGGTATACCAACC	720
Qy	721	ACT	AACGGTGTCTGCGCTGTGTATGCAGCTGTGTGTGCAGCTGGTGCACTCTAATATCA	780
Db	721	ACCA	AACGGTGTCTTGTGTTGTATGCAGCTGTGTGTGCAGCTGGTGCACTCTCAAGTCT	780
Qy	781	CT	TGCTAATTTTCGTAGCGGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC	840
Db	781	CT	TGCTAATCTCCCTTGGTGATGACATCCCAATTCGGATACCGAACGTGGATACCATCGTG	840
Qy	841	AT	CCGAAATCCGAAGCGCTCCACGCAATTCGACGACCGGATGCGCTCAGGAAATTCATC	900
Db	841	AT	CCCAACCCCAAGCTGCTCCACGTAATTCCACTACCGATGCTTCTTGGAAAGTTTCATC	900
Qy	901	GC	GACACTATGGAATGGGCTTCTCGTTGTGTGTTACTTGTGAGTTTTCGGTGGCTCACA	960
Db	901	GCT	ACTCTTATGAGATGGGCTTCTCGTTTGTGTGGAACCGTTGAGTTTCGCTGGCTCACT	960
Qy	961	GCT	GCTCCTTAACCTGGAACCGTGGCGATGTGCTCTATACGACGCTCGAAAATTCCTTCCA	1020
Db	961	GCT	GCTCCTTAACCTGGAAGCGTGTCTACGTTCTCTACACTCGCGCTCGTAAGTTGCTTCCA	1020
Qy	1021	GCC	TCCGCTCGGCTCGGATCTGAAGAACGATATTTCCAAATGGATGGGTTTTCGTCCTTACG	1080
Db	1021	GCT	CTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCTCAAGC	1080
Qy	1081	ATT	CCTGATTTCTTCCAGTGATTGTGCTGTGCAACTTCGTFACACCCGACGTAATCTATGCT	1140
Db	1081	AT	CCCGGATTTCCAGTGATTGTGCTGTGCTACCCGTACTTCCAGAGCTTATCTACGCT	1140
Qy	1141	TT	TGGTCACGGTTCATCTCGGTATGACAGGTGTCTCCAAATGACTTGCACACTCTCGCTCAAG	1200
Db	1141	TT	CGGTCACGGTCACCTCGGTATGACTGTGTGCTGTGCTCAATGACCGCAACCTCGTCTCTGAG	1200

QY 1201 CTCTCCGAGCGGAAAGACCTCAATCGACATTCGCCCTTCGACCAAAACCGTTTGGT 1260
Db 1201 CTCTCCGAGGTGAGAGACCTCTATCGACATCTCTCAATTCGACCAAAACCGTTTGGT 1260
QY 1261 ATTGGCAAAATCCAAAGCAAAACGGGTCCGGCAAGTTAA 1296
Db 1261 ATTGGTAAGTCCAAGCAAAACGGTCCCTGCATCCTAA 1296

RESULT 12

US-08-484-274A-17
; Sequence 17, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1296
US-08-484-274A-17

Query Match 77.7%; Score 1006.4; DB 2; Length 1296;
Best Local Similarity 86.0%; Pred. No. 4.8e-300;
Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
QY 1 ATGGCTGAGAACCAACAAAGTAGGCTCGCTGGAGCTGGAATCGTTGGTGATGCAC 60
Db 1 ATGGCTGAGAACCAACAAAGTAGGCTCGCTGGAGCTGGAATCGTTGGTGATGCAC 60
QY 61 GCTTTGATGCTTCAACGTCGTGGATTCAAAAGTCACCTTGATTGACCCGAAACCCCTCTGGC 120
Db 61 GCTTTGATGCTTCAACGTCGTGGATTCAAAAGTCACCTTGATTGATCCAAACCCACCCAGGT 120
QY 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
Db 121 GAAGGTGCCTCTTTCGGTAACCGTGGTGTCTTCAACGGTTCCTCTCGTTTCAATGTCC 180
QY 181 ATCCCGGGAAACCTTGACGAGCTGCGGAAGTGGCTCCTTGACCCGATGGGCGGTGTGTC 240
Db 181 ATCCCGGGAAACCTTGACGAGCTGCGGAAGTGGCTCCTTGACCCGATGGGTCGATGTCC 240

QY 241 ATCCGGTTTCAGCTATTTCACCAACCATCATGCCCTGGTGTGATTCGCTTTCTGTTAGCCGA 300
Db 241 ATCCGGTTTCAGCTATTTCACCAACCATCATGCCCTGGTGTGATTCGCTTTCTGTTAGCCGA 300
QY 301 AGACCAAAACAAAGGTGAAGAGCAGCGGAAAGCACTCCGCAATCTCATCAAGTCCACCTGTG 360
Db 301 AGACCAAAACAAAGGTGAAGAGCAGCGTAAAGCACTCCGTAACCTTCAATCAAGTCCACCTGTG 360
QY 361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
QY 421 CATCTGACCGTATATCGTGAGAGCAGACTTCGCCAAGGACCGCGGAGGTGGGAACTG 480
Db 421 CACCTTACCGTGTACCGTGAGAGCAGACTTCGCCAAGGACCGCTGGAGGTGGGAACTT 480
QY 481 CGCGGCTCAACGGTGTTCGACGCGAGATCCTCTCTCTGATGCTTTGCGTGTGATTTGCGAT 540
Db 481 CGTCTGCTCAACGGTGTTCGTAACCTCTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTCCGAT 540
QY 541 CCTAACTTGTGCGATGCTTTTACCAAGGCGATCTTTATAGAAGAGACGCTCACACGATT 600
Db 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTTATCAAGAGAACGCTCACACCATC 600
QY 601 AATCCGCAAGGCTCGTGACCCCTCTTTTTCGGCGTTCCTTATCGCGAACGCTGGCGAAATTT 660
Db 601 AATCCGCAAGGCTCGTGACCTCTCTTTGTTTCGCTGCTTTCATCGCTACGCTGGAGAGTTC 660
QY 661 GTATCTGCGCGTGTATCGTGGTTCGAGACTGGAAGTGGTCTCTCAAGGCAATTCACAC 720
Db 661 GTCTCTGCTGCTGTATTCGGATTCGAGACTGGAAGTGGTCTCTCAAGGCTATCACAC 720
QY 721 ACTAAGCGTGTCTGCTGTTGATGAGCTGTTGTCAGCTGTCACACTCTCAATCA 780
Db 721 ACCAAGCGTGTCTGCTGTTGATGAGCTGTTGTCAGCTGTCACACTCTCAAGTCT 780
QY 781 CTTCGTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Db 781 CTTCGTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
QY 841 ATCGCGAATTCGGAAGCGCTCCACGCAATTCGACGACCGATGCGTCAAGGCAATTCATC 900
Db 841 ATCGCGAATTCGGAAGCGCTCCACGCAATTCGACGACCGATGCGTCAAGGCAATTCATC 900
QY 901 GCGACACCTATGGAATTCGGTCTTCGTTGCTGGTACTGTTGAGTTTGTGCTCTCAC 960
Db 901 GCTACTCTATGAGATGGTCTTCGTTGCTGGAAACCGTTGAGTTCGCTGGTCTCTCACT 960
QY 961 GCTGCTCCTAACTTGGAAACCGTGGCGATGCTCTATACCGACCGCTCGAAACCTTCTTCCA 1020
Db 961 GCTGCTCCTAACTTGGAAACCGTGGCGATGCTCTCTACACTCGCGCTCGTAAGTTGCTTCCA 1020
QY 1021 GCCTCGCGCTCGGAGTTCGTAAGAACGATATTCGAAATGGATGGGTTTCGCTCTCTAGC 1080
Db 1021 GCTCTCGCTCTCGCCAGTTCTCGAAGAACGTTACTTCCAAAGTGGGTTTCGCTCTCAAGC 1080
QY 1081 ATTCCTGATTCTCTCCAGTGATTGGTGGCAACTCGTACACCCGACGTAATCTATGCT 1140
Db 1081 ATCCCGGATTCCTCTCCAGTGATTGGTGGCTGCTACCGCTACTCCAGACGTTATCTAGCT 1140
QY 1141 TTTGGTTCAGGTCATCTCGGTATGACAGTGTCCAAATGACTGCAACTCTCTGCTCAGAG 1200
Db 1141 TTTGGTTCAGGTCATCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTCTGAG 1200
QY 1201 CTCTCGCAGGCAAAAGACCTCAATCGACATTTTCGCCCTTCGACCAAAACCGCTTTGGT 1260
Db 1201 CTCTCGCAGGTCAGAGACCTCTATCGACATCTCTCAATTCGACCAAAACCGCTTTGGT 1260
QY 1261 ATTGGCAAAATCCAAAGCAAAACGGGTCCGGCAAGTTAA 1296
Db 1261 ATTGGTAAGTCCAAGCAAAACGGTCCCTGCATCCTAA 1296

RESULT 13
US-08-391-339-30
; Sequence 30, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-30

Query Match 5.3%; Score 69; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 714 TACACCACTAACGGTGTCTGGCTGTGATGCAGCTGTGTGCGACTGTGTGCGACTC 773
|||||
Db 1 TACACCACTAACGGTGTCTGGCTGTGATGCAGCTGTGTGCGACTGTGTGCGACTC 60
Oy 774 TAAATCACT 782
|||||
Db 61 TAAATCACT 69

RESULT 14
US-08-391-339-33
; Sequence 33, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F

; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-33

Query Match 5.3%; Score 69; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1128 CGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGACAGTGTCTCCAATGACTGCAAC 1187
|||||
Db 1 CGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGACAGTGTCTCCAATGACTGCAAC 60
Oy 1188 TCTCGTCTC 1196
|||||
Db 61 TCTCGTCTC 69

RESULT 15
US-08-484-274A-30
; Sequence 30, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-30

Query Match 5.3%; Score 69; DB 2; Length 69;
Best Local Similarity 100.0%; Pred.No. 2.5e-12;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 714 TACAACCACTAAGCGTGTCTGATGCGAGCTGTTGTCAGCTGGTGCACACTC 773
|||||
Db 1 TACAACCACTAAGCGTGTCTGATGCGAGCTGTTGTCAGCTGGTGCACACTC 60
QY 774 TAAATCACT 782
|||||
Db 61 TAAATCACT 69

Search completed: January 1, 2001, 03:18:19
Job time: 29323 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:46 ; Search time 3327.86 Seconds
(without alignments)
2407.829 Million cell updates/sec

Title: US-08-484-274-7
Perfect score: 1296
Sequence: 1 ATGGCTGAGAACCAAAAA.....AAACGGTCCGCAAGTTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_est3.*
4:	gb_est4.*
5:	gb_est5.*
6:	gb_est6.*
7:	gb_est7.*
8:	gb_est8.*
9:	gb_est9.*
10:	gb_est10.*
11:	gb_est11.*
12:	gb_est12.*
13:	gb_est13.*
14:	gb_est14.*
15:	gb_est15.*
16:	gb_est16.*
17:	gb_est17.*
18:	gb_est18.*
19:	gb_est19.*
20:	gb_est20.*
21:	gb_est21.*
22:	gb_est22.*
23:	gb_est23.*
24:	gb_est24.*
25:	gb_est25.*
26:	gb_est26.*
27:	gb_est27.*
28:	gb_est28.*
29:	gb_est29.*
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31:	gb_est31.*
32:	gb_est32.*
33:	gb_est33.*
34:	gb_est34.*
35:	gb_est35.*
36:	gb_est36.*
37:	gb_est37.*
38:	gb_est38.*
39:	gb_est39.*
40:	gb_est40.*
41:	em_estba.*
42:	em_estfun.*
43:	em_esthum1.*
44:	em_esthum2.*
45:	em_esthum3.*
46:	em_esthum4.*
47:	em_esthum5.*
48:	em_esthum6.*
49:	em_esthum7.*
50:	em_esthum8.*
51:	em_esthum9.*
52:	em_esthum10.*
53:	em_esthum11.*
54:	em_esthum12.*
55:	em_esthum13.*
56:	em_esthum14.*
57:	em_esthum15.*
58:	em_esthum16.*
59:	em_esthum17.*
60:	em_esthum18.*
61:	em_esthum19.*
62:	em_esthum20.*
63:	em_estin1.*
64:	em_estin2.*
65:	em_estin3.*
66:	em_estin4.*
67:	em_estom.*
68:	em_estov1.*
69:	em_estov2.*
70:	em_estpl1.*
71:	em_estpl2.*
72:	em_estpl3.*
73:	em_estpl4.*
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75:	em_estrol.*
76:	em_estro2.*
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79:	em_estro5.*
80:	em_estro6.*
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83:	em_estro9.*
84:	em_estro10.*
85:	em_estro11.*
86:	em_estro12.*
87:	em_estro13.*
88:	gb_gss1.*
89:	gb_gss2.*
90:	gb_gss3.*
91:	gb_gss4.*
92:	em_gsa1.*
93:	em_gsa2.*
94:	em_gss3.*
95:	em_gss4.*
96:	gb_gss5.*
97:	gb_gss6.*
98:	gb_gss7.*
99:	gb_gss8.*
100:	gb_gss9.*
101:	em_gss5.*
102:	em_gss6.*
103:	em_gss7.*
104:	em_gss8.*
105:	em_gss9.*
106:	em_gss10.*
107:	em_gss11.*
108:	gb_gss10.*
109:	gb_gss11.*
110:	em_gss12.*
111:	gb_gss12.*
112:	gb_gss13.*
113:	gb_gss14.*
114:	gb_gss15.*
115:	gb_gss16.*
116:	gb_gss17.*

Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

REFERENCE
JOURNAL
AUTHORS

2 (bases 1 to 805)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

TITLE
JOURNAL
REFERENCE
AUTHORS

3 (bases 1 to 805)
Unpublished
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1. .805
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="005C20"
/clone_lib="H"
/note="Genoscope sequence ID : C0H005BB10XE1-end : PUC-ori"

BASE COUNT 87 a 194 c 293 g 226 t 5 others

ORIGIN

Query Match 3.1%; Score 40.4; DB 123; Length 805;
Best Local Similarity 44.8%; Pred. NO. 0.28;
Matches 155; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 643 GCGNACGGTGGCAATTTGTATCTCGCGGTGCATCGGTTTGGACACTGAAGTGGTGGT 702
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 399 GCTACTGGTGGCAGTGGCTGCTACTGCTGTGCTGGTGGTGGTGGTGGTGGTGGT 458
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 703 CTCGAAGGCATTACAAACCACTAACCGCTGTTGCGCTGTTGATGCAGCTGTTTGCAGCT 762
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 459 GCAGCTGGTGGTACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 518
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 763 GGTGCACACTTAAATCACTTGTCAATTCGGTAGCGGATGACATCCCGCTCGATACCGAA 822
|||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 519 GGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 578
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 823 GTGGATATCATATGTCATCGGAATCCGNAAGCCGCTCCACGCAATCCGACGACCGAT 882
|||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 579 GGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 638
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 883 CGCTCAGGAAATTCATCCGACACTATGGAATGGGTCTTCGTGTTGCTGGTACTGTT 942
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 639 GGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 698
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 943 GAGTTTGGTGGTCTCACAGCTGCTCCTCACTGAGGAAACGTCGCCATG 988
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 699 GCTGCTGCTACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 744
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||

RESULT 3
CNS03H6V/c 970 bp DNA 17-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 026011 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL243904
VERSION AL243904.1 GI:7964916
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

1 (bases 1 to 970)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 970)
Unpublished
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1. .970
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="026011"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG026AH06LP1-end : T7"

BASE COUNT 311 a 298 c 194 g 152 t 15 others

ORIGIN

Query Match 3.1%; Score 40; DB 123; Length 970;
Best Local Similarity 45.0%; Pred. NO. 0.4;
Matches 145; Conservative 1; Mismatches 176; Indels 0; Gaps 0;

QY 648 CGGTGGCGAATTTGTATCTCGCGGTGCATCGGTTTGGAGACTGAAGTGGTGGTGGT 707
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 712 MGCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 708 AGGCATTACAACCACTAACCGGTGTTGCTGCTGTTGATGCAGCTGTTGTCAGCTGGTGC 767
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 652 TGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 593
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 768 ACACCTCTAAATCACTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGTGG 827
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 592 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 828 ATATCATATGCTCATCGGAATCCGGAAGCCGCTCCAGCATTCGACGACGACGATCGGTC 887
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 532 TGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 473
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 888 AGGAAATTCATCGCGACACCTATGGAATGGGTCTTCTGCTGTTGCTGCTGCTGCTGCT 947
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 472 TGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
|| | |||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
QY 948 TGCTGGTCTCACAGTGGTCTCT 969
|||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||
Db 412 TGCTGCTGCTGCTGCTGCTGCTGCT 391
|||| | || |||| | || |||| | || |||| | || |||| | || |||| | || ||||

RESULT 4
CNS0001K 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR01D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL050434

```
VERSION AL050434.1 GI:4930346
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
          Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
          - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pletier de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

FEATURES             Location/Qualifiers
     source           1..1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR01D09"
                     /note="end : TET3"

BASE COUNT  280 a  225 c  248 g  310 t  38 others
ORIGIN

Query Match      3.0%; Score 39.2; DB 121; Length 1101;
Best Local Similarity 55.0%; Pred. No. 0.73;
Matches 77; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY  631 CGCGGTTTATCGGACGGTGGCAATTGTATCTGCGGTGTATCTCGGTTTGTAGACT 690
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  493 CGGATTAGAAAGTGGAAAGACGCCATTTTCGGTTTGAAGCCGACGTCGCCATTTGCGGT 552
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  691 GAAGTGGTGTCTCTCAAGGCATTACACCACTAACGGTCTTCTGGCTGTGATGCCAGCT 750
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  553 GAGCTGCCATGCCATGCGCATTTGCGGTACTACCAATGCTGCTGTGTGCTGTGCT 612
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  751 GTTGTTCAGCTGGTGACA 770
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  613 GCTGCTGATGTGTGCANA 632

RESULT  5
FR0006944
LOCUS      F.rubripes GSS sequence, clone 133B16AC7, genomic survey sequence.
DEFINITION 290754
ACCESSION 290754
VERSION   290754.1 GI:1867968
KEYWORDS  GSS; genome survey sequence.
SOURCE    Fugu rubripes
           Fugu rubripes
           Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
           Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
           Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
REFERENCE 1 (bases 1 to 619)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
          Williams,G. and Brenner,S.
TITLE    Direct Submission
JOURNAL  Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource

Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V.type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES             Location/Qualifiers
     source           1..619
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 133B16"
                     /clone="133B16AC7"

BASE COUNT  75 a  150 c  116 g  175 t  103 others
ORIGIN

Query Match      2.9%; Score 38.2; DB 124; Length 619;
Best Local Similarity 45.3%; Pred. No. 1.2;
Matches 130; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY  684 TGAGACTGAAGTGGTCTCTCAAAGGCATTACAAACCACTAACGGTGTCTGGCTGTGA 743
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  68  TGTACTGCNACTACTGCTACTGCTGCTGCTACTGCTACTGCTACTGCTACTACTACTAC 127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  744 TGCAGCTGTTGTTGCAGCTGGTGCACACTCTTAATCTACTTGTCTAATTCGCTAGCGCATGA 803
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  128 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  804 CATCCCGCTCGATACCGAACGTGGATATCATATCGTATCGCGAATCCGGAAGCGCTCC 863
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  188 TACTGCTACTACTACTGCTGCTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  864 ACGATTCCGACGACCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  248 TACTACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 307
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  924 TCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  308 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT  6
AI689448/c
LOCUS      tx94b11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:227213 3',
DEFINITION mRNA sequence.
ACCESSION AI689448
VERSION   AI689448.1 GI:4900742
KEYWORDS  EST.
SOURCE    human.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
           Unpublished (1997)
JOURNAL  Contact: Robert Strausberg, Ph.D.
COMMENT  Tel: (301) 496-1550
           Email: Robert_Strausberg@nih.gov
           Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
           Emmert-Buck, M.D., Ph.D.
           CDNA Library Preparation: Life Technologies, Inc.
           CDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution Information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio.llnl.gov/bbrp/image/image.html
           Insert length: 2161 Std Error: 0.00
           Seq primer: -400P from Glbco
           High quality sequence position: 407.
```


Db 232 TGTCGGGCTGTGTGATGCTGCTGCTGCTGCTGCTGCCACCA 186

RESULT 11
BE253678/c

LOCUS
DEFINITION BE253678 816 bp mRNA EST 13-JUL-2000
601110742f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351490 5',
mRNA sequence.
ACCESSION BE253678
VERSION
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 816)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: LLCM149 row: c column: 11
High quality sequence stop: 719.

FEATURES
source Location/Qualifiers
1..816
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3351490"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(C). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 214 a 203 c 206 g 193 t
ORIGIN

Query Match 2.8%; Score 36.8; DB 34; Length 816;
Best Local Similarity 54.4%; Pred. No. 3.6;
Matches 74; Conservative 0; Mismatches 62; Indels 0; Gaps

Qy 640 ATCCGCAACGGTGGCGAATTGTATCTCGCGGTCTATCGGTCTTTCGACACTGAAGGTCTG 699
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 AGCGCGGACTGCGTCGGCGACGGGCTGAGCGGTGTTAGGCGTGGATCCGCGCATGCTGTG 227
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 700 GCTCTCAAGGCATTACAAACCACTAACCGGTGTTCTGGCTGTTGATCGACGCTGTTGTGCA 759
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 GCTCAAGCTGCCGTCGGCGCGGCTGGCCCTGTCGGGCTGTTGATGCTGCTGCTGCTGCT 167
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 760 GCTGGTGCACACTCTA 775
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 GCTGCTGCTCCACCA 151
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
CNS015Y8/c

LOCUS
DEFINITION CNS015Y8 922 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15P08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

```

ACCESSION      ALI06058
VERSION        ALI06058.1   GI:5619823
KEYWORDS       GSS.
SOURCE         Drosophila melanogaster fruit fly.
ORGANISM       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrdoidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 922)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT        - web : www.genoscope.cns.fr
                Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES             Location/Qualifiers
     source           1..922
                     /organism="Drosophila melanogaster"
                     /plasmid="pBelOBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="proSBAC"
                     /clone="BACN15P08"
                     /note="end : SP6"
BASE COUNT        359 a    147 c    154 g    24 t    238 others
ORIGIN

Query Match      2.8%; Score 36.8; DB 121; Length 922;
Best Local Similarity 32.2%; Pred. No. 3.7;
Matches 59; Conservative 45; Mismatches 79; Indels 0; Caps 0;

QY 113 CTCCTGCGGAAGGTGCATCGTTTCGGAAATGCCGATGCTTCAACGGCTCATCCGCGTC 172
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 727 YTTTTTGTCGGTGCATTYYYGGKSCCYCTVTTCGCCCYSCCSCCCCCCCC 668

QY 173 CTATGTCATCCCGGGAACATTGACGCGCTGCCGAAGTGGCTCTCTTGACC CGATGGGCG 232
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DB 667 CTYTGWMNTGMCMGMMMTHTMGHGACBTGMGHGIMGMTGWMTMGMGMGCGGG 608

QY 233 CGTTGTCANTCCGGTTTCAGCTATTTTCCAACCATCATGCCCTGGTGTATTCGCTTTCTGT 292
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 607 MGNTGGSGSMGGGGHHMMGMMMCMWMTTMWTMTTKCTTTTCTGTTTTT 548

QY 293 TAG 295
      |||
DB 547 TTG 545


RESULT 13
ALI350691/c
LOCUS            ALI350691              377 bp      mRNA                  EST               13-FEB-1999
DEFINITION      qq04a08.x1 Soares_Nhhmpu_S1 Homo sapiens cDNA clone IMAGE:1931510 similar to contains element MER22 repetitive element ;, mrna sequence.
ACCESSION       ALI350691
VERSION         ALI350691.1
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 377)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL

```

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 860 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 326.

FEATURES
source

1..377
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1931510"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"

/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not i;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NHMPu, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 91 a 128 c 105 g 53 t
ORIGIN

Query Match 2.8%; Score 36.6; DB 10; Length 377;

Best Local Similarity 58.9%; Pred. No. 3.2;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 669 GCGTGCATCGTTTGAGACTGAAGTCGTCTCTCAAAAGGCATTACAAACCCTAAACGG 728

Db 306 GCGTGTAGGCTGGATCCGGCCATGGTCGTGGCTCAAACTGCCTCGGCCGCGTGCC 247

QY 729 TGTCTCGCTGTGATGCACCTGTTGTCGACGCTGGTGCACACTCTA 775

Db 246 TGTCCGGCGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCCACCA 200

RESULT 14

BE210590 521 bp mRNA EST 29-JUN-2000
LOCUS so50401.y1 Gm-cl039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl039-1370 5' similar to TR:064760 O64760 PUTATIVE TRANSLATION
INITIATION FACTOR EIF-2B-EPSILON SUBUNIT. ;, mRNA sequence.

ACCESSION BE210590
VERSION BE210590.1 GI:8826860
KEYWORDS EST.

SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Glycine.

REFERENCE 1 (bases 1 to 521)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
A., Bolla, B., Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Rutter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE Public Soybean EST Project
JOURNAL Contact: Shoemaker R/Public Soybean EST Project
COMMENT Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 411.

FEATURES
source

1..521
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-1370"
/clone_lib="Gm-cl039"
/tissue_type="whole seedling without cotyledons"
/lab_host="DH10B"

/note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."
BASE COUNT 147 a 78 c 140 g 156 t
ORIGIN

Query Match 2.8%; Score 36.6; DB 34; Length 521;

Best Local Similarity 57.4%; Pred. No. 3.5;
Matches 66; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 689 CTGAAGTCGTCTCTCAAGGCATTACAAACCCTAAACGGCTGTCTCGCTGTTGATGCAG 748

Db 373 CTAAAGATAAAGTTATGGAGCAATTAAACTATGAAGATGATCTGGAGAAATGATGATA 432

QY 749 CTGTTGTTGACGCTGGGCGACACTCTAAATCACCTTGCCTAAATTCGCTAGGCGCATGA 803

Db 433 GTTTTCTCCAGCTCTCTGGAGAACTGAAACCTAAATTTCTAATTTATTCAGATGATGA 487

RESULT 15

CL13125 353 bp mRNA EST 28-DEC-1998
LOCUS CL13125 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
DEFINITION clone yk164d4 5', mRNA sequence.

ACCESSION CL13125
VERSION CL13125.1 GI:1560678
KEYWORDS EST.

SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 353)
AUTHORS Kohara, Y., Mochizuki, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano
M., Miyata, A. and Nishigaki, A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Gene Library Lab

National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..353
/organism="Caenorhabditis elegans"

FEATURES
source

/strain="CBI489 him-8(el489)"
/db_xref="taxon:6239"
/clone="yk164d4"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
115 a 76 c 78 g 76 t 8 others

BASE COUNT
ORIGIN

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Best Local Similarity		47.0%	Pred. No. 3.6;		
Matches 103;		Conservative 0;	Mismatches 116;	Indels 0;	Gaps 0;
Qy	385	GAGGCTGATCGAGCCATCTGATCCGCCATGAAGGTGATCTGACCGTATATCGTGGAGAA	444		
Db	236	GACGCTGCGAGCTCGTCTTGGGCTCCGGTGGTGATGAGGTGACCGAATNCCTTGTAGTC	177		
Qy	445	GCAGACTTCGCCAAGGACCGCGAGGTGGGAACTCGCGCGTCTCAACGGTGTTCGCACG	504		
Db	176	ANCTCTCTCTCCCTCGANTGGTGGCTTCCCTTTGACATAGCCCTTGACCTCATCCTCGTC	117		
Qy	505	CAGATCCTCTCTGCTGATGCTTTGCGTGATTTCGATCCTAACTTGTCCGATGCTTTTACC	564		
Db	116	TAATGGCTCTCCTCTCTTTTGAAGGATCTTGATAAGGTGCTCCTCTTGATCTTTCC	57		
Qy	565	ANGGGCATTTCTATAGAGAGACGGTCAACACGATTAAAT	603		
Db	56	GCAGTCCTCTTATCGAACATAGCAANAGCNCCACAAT	18		

Search completed: January 1, 2001, 01:12:53
Job time: 25792 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 03:15:47 ; Search time 7299.04 Seconds
(without alignments)
775.497 Million cell updates/sec

Title: US-08-484-274-8
Perfect score: 1296
Sequence: 1 ATGGCTGAGAACCAAGAA.....AAACTGGTCTCGATCCTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb_bal.*
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- 44: em_hum5.*
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- 82: gb_pr6.*
- 83: gb_pr7.*
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- 86: gb_htg22.*
- 87: gb_htg23.*
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- 90: gb_sts2.*
- 91: gb_sy.*
- 92: gb_un.*
- 93: gb_vil.*
- 94: gb_vil2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1296	100.0	1296	5	AR016595 Sequence
2	1296	100.0	1296	5	I15328 Sequence 8
3	1288	99.4	1296	5	AR016604 Sequence
4	1288	99.4	1296	5	I15337 Sequence 17
5	1205.2	93.0	1631	5	A59869 Sequence 1
6	1011.2	78.0	1296	5	AR016594 Sequence 7
7	1011.2	78.0	1296	5	I15327 Sequence 1
8	961.6	74.2	1296	5	AR016593 Sequence 6
9	961.6	74.2	1296	5	I15326 Sequence 6
10	960	74.1	1692	5	AR016591 Sequence
11	928.8	71.7	1293	5	AR016592 Sequence
12	928.8	71.7	1293	5	I15325 Sequence 4

13	928.8	71.7	1689	5	I15324	I15324 Sequence 3
14	66.2	5.1	3430	2	PSEAKSD	M69158 Pseudomonas
15	58.8	4.5	62	5	AR016613	AR016613 Sequence
16	58.4	4.5	62	5	I15346	I15346 Sequence 27
17	58.4	4.5	69	5	AR016616	AR016616 Sequence
18	58.4	4.5	69	5	I15349	I15349 Sequence 30
19	56.2	4.3	69	5	AR016619	AR016619 Sequence
20	56.2	4.3	69	5	I15352	I15352 Sequence 33
21	53.6	4.1	68	5	AR016618	AR016618 Sequence
22	53.6	4.1	68	5	I15351	I15351 Sequence 32
23	53	4.1	61	5	AR016617	AR016617 Sequence
24	53	4.1	61	5	I15350	I15350 Sequence 31
25	52.8	4.1	65	5	AR016614	AR016614 Sequence
26	52.8	4.1	65	5	I15347	I15347 Sequence 28
C 27	50.2	3.9	3334	11	AF036191	AF036191 Homo sapi
C 28	50	3.9	767	54	EIMAX	M30933 E.tenella a
C 29	50	3.9	2289	2	PSEKSDA	M69159 Pseudomonas
30	49.8	3.8	7218	5	I66494	I66494 Sequence 14
31	49.4	3.8	45438	39	AC017841	AC017841 Drosophil
C 32	49.4	3.8	23361	29	AE003724	AE003724 Drosophil
C 33	46.4	3.6	178553	47	AC024253	AC024253 Homo sapi
34	46.4	3.6	209973	57	AC037355	AC037355 Mus muscu
C 35	46	3.5	1586	88	MMU70653	U70653 Mus musculu
C 36	46	3.5	1598	88	MMU70653	U70654 Mus musculu
C 37	45.6	3.5	223469	56	AC069019	AC069019 Mus muscu
C 38	45.2	3.5	186935	48	AC022322	AC022322 Homo sapi
39	44.8	3.5	31202	37	AC013022	AC013022 Drosophil
C 40	44.8	3.5	302357	29	AE003443	AE003443 Drosophil
41	43.2	3.3	3540	2	EHU17017	U17017 Ectothiorho
42	43.2	3.3	186935	48	AC022322	AC022322 Homo sapi
C 43	42.8	3.3	3941	88	RNLAR2	X83546 R.norvegicu
C 44	42.6	3.3	4420	88	U67916	U67916 Mus musculu
C 45	42.6	3.3	5719	88	MWCATS1	AF051726 Mus muscu

ALIGNMENTS

RESULT	1
LOCUS	AR016595 1296 bp DNA PAT 05-DEC-1998
DEFINITION	Sequence 8 from patent US 5776760.
ACCESSION	AR016595
VERSION	AR016595.1 GI:3972872
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1296)
TITLE	Barry.G.Francis and Kishore,G.Murthy.
JOURNAL	Glyphosate tolerant plants
FEATURES	Patent: US 5776760-A 8 07-JUL-1998;
	Location/Qualifiers
source	1..1296
	/organism="unknown"
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ORIGIN	
Query Match	100.0%; Score 1296; DB 5; Length 1296;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1296:	Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 ATGCGTGAAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCACACT 60
Dd	1 ATGCGTGAAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCACACT 60
Qy	61 GCTTTGATGCTTCACGTCGGTGATTCAAGGTTACCTTGATTGATCCAAACCACCAAGGT 120
Dd	61 GCTTTGATGCTTCACGTCGGTGATTCAAGGTTACCTTGATTGATCCAAACCACCAAGGT 120
Qy	121 GAAGGTGCTTCTTTTCGGTAAGCGCTGGTTGCCTTCAACGGGTTCCCTCGGTGTGTTCCAATGTCC 180

Qy 1261 ATTGGTAAAGTCCAGCAAACTGGTCCGTCATCCCTAA 1296
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Db 1261 ATTGGTAAAGTCCAGCAAACTGGTCCGTCATCCCTAA 1296
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RESULT 2
I15328 I15328 1296 bp DNA PAT 02-APR-1996
LOCUS Sequence 8 from patent US 5463175.
ACCESSION I15328
VERSION I15328.1 GI:1250236
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 271 a 359 c 305 g 361 t
ORIGIN
Query Match 100.0%; Score 1296; DB 5; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGTGAAGACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGGCACT 60
Db 1 ATGCGTGAAGACCAAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGGCACT 60
Qy 61 GCTTTGATGCTTCAACGTCGCGGATTCAGGTTACCTGATTGATCCAAACCCACCAAGGT 120
Db 61 GCTTTGATGCTTCAACGTCGCGGATTCAGGTTACCTGATTGATCCAAACCCACCAAGGT 120
Qy 121 GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGCTTCCCTCGTTGTTCCAAATGCC 180
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Qy 181 ATGCCAGAACTTGACTAGAGGTTCCAAAGTGGCTTCTTGACCAAGAGGGTCCATGTGCC 240
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Qy 241 ATCCGTTTCAGCTACTTTCCAAACCATCATGCTTGGTTGATTGCTTCTTCTGCTGGA 300
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Qy 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360
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Qy 361 CCTTTGATCAAGTCCCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGAACTT 480
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGAACTT 480
Qy 481 CGTCTCTCAACGGTGTTCGTTACTCAAACTCCTCAGCGCTGATGATTCCGTTGATTCCAT 540
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Qy 541 CCTAACTTGTCTACGCGCTTTACCAAGGGAATCCTTATCGAAGAGACGGTCCACACCATC 600
Db 541 CCTAACTTGTCTACGCGCTTTACCAAGGGAATCCTTATCGAAGAGACGGTCCACACCATC 600
Qy 601 AACCACAAAGTCTCGTGACTCTCTTGTTCGTTCTGTTTCATCGCTTAACGGTGGAGAGTTC 660
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Db 601 AACCACAAAGTCTCGTGACTCTCTTGTTCGTTCTGTTTCATCGCTAAGGTTGGAGAGTTC 660
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Db 661 GTGTCTGCTCGTTATATCGGATTCGAGACTGAAGGTCGTCTCTCAAGGGTATCACCAACC 720
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Db 841 ATGCCCAACCCAGAGCTGCTCCACGATATCCAACTACCGATGCTTCTGGAAGTTTCATC 900
Qy 901 GCTACTCCTATGGAGATGGGTCCTTCTGCTGGAACCGTTGAGTTGCGTCTGCTCACT 960
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Qy 961 GCTGCTCTAACTGGAAGCGTGCACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020
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Qy 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAGCGTTACTCCAAAGTGGATGGGTTTCCGTCCTCAAGC 1080
Db 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAGCGTTACTCCAAAGTGGATGGGTTTCCGTCCTCAAGC 1080
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Db 1081 ATCCAGATTCCTTCCAGTGATTGGTGGTCTACCCGCTACTCCAGAGCTTATCTACGCT 1140
Qy 1141 TTCGCTCAGCGTCACTCGGTTGATGACTGGTCTCCAATGACCGCAACCTCGTTCTGAG 1200
Db 1141 TTCGCTCAGCGTCACTCGGTTGATGACTGGTCTCCAATGACCGCAACCTCGTTCTGAG 1200
Qy 1201 CTCTCCGAGTGAGAGACCTCTATCGACATCTCTCCATTCGACCAACCGTTTCGCT 1260
Db 1201 CTCTCCGAGTGAGAGACCTCTATCGACATCTCTCCATTCGACCAACCGTTTCGCT 1260
Qy 1261 ATTGGTAAAGTCCAGCAAACTGGTCCGTCATCCCTAA 1296
Db 1261 ATTGGTAAAGTCCAGCAAACTGGTCCGTCATCCCTAA 1296
RESULT 3
AR016604 AR016604 1296 bp DNA PAT 05-DEC-1998
LOCUS Sequence 17 from patent US 5776760.
DEFINITION AR016604
ACCESSION AR016604
VERSION AR016604.1 GI:3972881
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN
Query Match 99.4%; Score 1288; DB 5; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGGCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTGGCACT 60

|||||
Db 1 ATGGCTGAGAACACAGAAGGTTGGTATTCGCTGGAGCTGGAATCGTTGGTTGCACCT 60
QY 61 GCATTGATGCTTCACAGTCGTGATTCACAGGTTACCTTGGATTGATCCAAACCCACACAGGT 120
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QY 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAAGCGTTCCCTCCGTTGTTCCTCAATGTCC 180
Db 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAAGCGTTCCCTCCGTTGTTCCTCAATGTCC 180
QY 181 ATGCCAGGAACCTTGACTACCGTTTCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240
Db 181 ATGCCAGGAACCTTGACTACCGTTTCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240
QY 241 ATCCGTTTACAGTACTTTTCCAAACCATCATGCCTTGGTTGATTCTGTTCTTGGTTGCTTGGGA 300
Db 241 ATCCGTTTTCGGCTACTTTTCCAAACCATCATGCCTTGGTTGATTCTGTTCTTGGTTGCTTGGGA 300
QY 301 AGACCAAAACAGGTGAAGGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 360
Db 301 AGACCAAAACAGGTGAAGGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 360
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Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 480
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 480
QY 481 CGTCTGCTCAACCGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGTTGCTTTCGAT 540
Db 481 CGTCTGCTCAACCGTGTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGTTGCTTTCGAT 540
QY 541 CCTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACACATC 600
Db 541 CCTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACACATC 600
QY 601 AACCCACAAGGTCTCGTGACTCTCTTTTTCGTCGTTTATCGATCTTAACGGTGGAGAGTTC 660
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QY 661 GTGTCGTCTGCTGTTATTCGGATTTCGAGACTGAAGGTGCTGCTCAAGGGTATCACCAAC 720
Db 661 GTGTCGTCTGCTGTTATTCGGATTTCGAGACTGAAGGTGCTGCTCAAGGGTATCACCAAC 720
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QY 781 CTTGCTTAAGTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCGTGGATACCAATCGTG 840
Db 781 CTTGCTTAAGTCCCTTGGTGATGACATCCCATTTGGATACCGAAGCGTGGATACCAATCGTG 840
QY 841 ATGCCCAACCCAGAGCTGCTCCACGTATTCACACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATGCCCAACCCAGAGCTGCTCCACGTATTCACACTACCGATGCTTCTGGAAAGTTTCATC 900
QY 901 GCTACTCTTATGGAGATGGGTCTTCGCTGTTGCTGGAAACCGTTGAGTTCCGTTGCTTCACT 960
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QY 961 GGTGCTCTTAAGTGAAGGCTGCTACGTTCTCTACACTCACCTCGTAAAGTTCCTTCCA 1020
Db 961 GGTGCTCTTAAGTGAAGGCTGCTACGTTCTCTACACTCACCTCGTAAAGTTCCTTCCA 1020
QY 1021 GCTCTCGCTCTGCCAGTTCGTAAGAACGTTTACTCCAAAGTGGATGGGTTTCGCTCCAAAG 1080
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QY 1081 ATCCCCAGATTCCCTTCCAGTGATTGGTCTGCTTACCCGCTACTCCAGACGTTTATCTACGCT 1140
|||||

Db 1081 ATCCCGGATTCCCTTCAGCTGATTGGTGTGCTACCCGTTACTCCAGACGTTATCTACGCT 1140
QY 1141 TTCCGGTCACAGTCACCTCGCTATGACTGTGCTCCCAATGACCGCAACCCCTCTTCTGAG 1200
Db 1141 TTCCGGTCACAGTCACCTCGCTATGACTGTGCTCCCAATGACCGCAACCCCTCTTCTGAG 1200
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Db 1201 CTCTCCGAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGTTTCGGT 1260
QY 1261 ATTGGTAAAGTCCAAAGAACTGGTCTCGATCTCTAA 1296
Db 1261 ATTGGTAAAGTCCAAAGAACTGGTCTCGATCTCTAA 1296
RESULT 4
LOCUS I15337 115337 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 17 from patent US 5463175.
ACCESSION I15337
VERSION I15337.1 GI:1250245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 17 31-OCT-1995;
FEATURES Location/Qualifiers
source
1..1296
/organism="unknown"
BASE COUNT 267 a 360 c 309 g 360 t
ORIGIN
Query Match 99.4%; Score 1288; DB 5; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATCGCTGAGAACACAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCTTGCACCT 60
Db 1 ATCGCTGAGAACACAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCTTGCACCT 60
QY 61 GCATTGATGCTTCACAGTCGTGATTCACAGGTTACCTTGGATTGATCCAAACCCACACAGGT 120
Db 61 GCATTGATGCTTCACAGTCGTGATTCACAGGTTACCTTGGATTGATCCAAACCCACACAGGT 120
QY 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAAGCGTTCCCTCCGTTGTTCCTCAATGTCC 180
Db 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTCGTTCAAGCGTTCCCTCCGTTGTTCCTCAATGTCC 180
QY 181 ATGCCAGGAACCTTGACTACCGTTTCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240
Db 181 ATGCCAGGAACCTTGACTACCGTTTCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTGTCC 240
QY 241 ATCCGTTTACAGTACTTTTCCAAACCATCATGCCTTGGTTGATTCTGTTCTTGGTTGCTTGGGA 300
Db 241 ATCCGTTTTCGGCTACTTTTCCAAACCATCATGCCTTGGTTGATTCTGTTCTTGGTTGCTTGGGA 300
QY 301 AGACCAAAACAGGTGAAGGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 360
Db 301 AGACCAAAACAGGTGAAGGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 360
QY 361 CTTTTCATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 361 CTTTTCATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 480
Db 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCCCTGCTTGGTTGCTTGGGA 480
QY 481 CGTCTGCTCAACCGGTTTCGTACTCAAACTCCTCAGCGCTGATGCAATTCGTTGCTTTCGAT 540

Db	481	CGTGCTCAACGGTGTTCGTAACAAATCTCAGCGTGTGATGCGTGGATTTCGAT	540
Qy	541	CCTAACTTGTCTCAGCGCTTTACCAAGGCAATCTTATCGAAGAGAACGGTTCACACCAATC	600
Db	541	CCTAACTTGTCTCAGCGCTTTACCAAGGCAATCTTATCGAAGAGAACGGTTCACACCAATC	600
Qy	601	ANCCACAAAGTCTCGTGACTCTCTTGTTCGTGCTTTCATCGCTAACGGTGGAGAGTTC	660
Db	601	AACCCACAAGTCTCGTGACTCTCTTGTTCGTGCTTTCATCGCTAACGGTGGAGAGTTC	660
Qy	661	GTGTCTGCTGCTTATCGGATTCGAGACTCAAGSTCGTCTCAAGGGTATCACCAACC	720
Db	661	GTGTCTGCTGCTTATCGGATTCGAGACTCAAGSTCGTCTCAAGGGTATCACCAACC	720
Qy	721	ACCAACGGTGTTCGTGCTGCTGAGCTTGTTCAGCTGGTGCACACTCCAAAGTCT	780
Db	721	ACCAACGGTGTTCGTGCTGCTGAGCTTGTTCAGCTGGTGCACACTCCAAAGTCT	780
Qy	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCGTG	840
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAAGTGGATACCATCGTG	840
Qy	841	ATCGCCAAACCAGAGTGTCTCCAGTATTCCTCAACTACCGATGCTTCTGGAAAGTTCATC	900
Db	841	ATCGCCAAACCAGAGTGTCTCCAGTATTCCTCAACTACCGATGCTTCTGGAAAGTTCATC	900
Qy	901	GCTACTCTCATGGAGATGGTCTTCGTGCTTGTGGAACCGTGTGAGTTCGGTCTCACT	960
Db	901	GCTACTCTCATGGAGATGGTCTTCGTGCTTGTGGAACCGTGTGAGTTCGGTCTCACT	960
Qy	961	GCTGCTCCTAACTGGAAGCGTCTCAGCTTCTCTACACTCAGCTCGCTTAAGTTCCTTCCA	1020
Db	961	GCTGCTCCTAACTGGAAGCGTCTCAGCTTCTCTACACTCAGCTCGCTTAAGTTCCTTCCA	1020
Qy	1021	GCTCTCGTCTCTGCCAGTCTTGAAGAAGTTCCTCCAAAGTGGATGGTTCCTGCTCCAAAGC	1080
Db	1021	GCTCTCGTCTCTGCCAGTCTTGAAGAAGTTCCTCCAAAGTGGATGGTTCCTGCTCCAAAGC	1080
Qy	1081	ATCCGAGATTCCTTCCAGTGTATGGTGTCTACCCCTACTCCAGAGCTTATCTACGCT	1140
Db	1081	ATCCGAGATTCCTTCCAGTGTATGGTGTCTACCCCTACTCCAGAGCTTATCTACGCT	1140
Qy	1141	TTCCGGTACAGGTACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTCTGAG	1200
Db	1141	TTCCGGTACAGGTACCTCGGTATGACTGGTGTCTCAATGACCGCAACCCCTCGTTCTGAG	1200
Qy	1201	CTCCTCGAGGTGAGAAGACCTCTATCCACATCTCTCCATTCGCACCAACCCGTTTCGGT	1260
Db	1201	CTCCTCGAGGTGAGAAGACCTCTATCCACATCTCTCCATTCGCACCAACCCGTTTCGGT	1260
Qy	1261	ATTGTTAAGTCCAAAGCAACTGGTCTGCATCCTTAA	1296
Db	1261	ATTGTTAAGTCCAAAGCAACTGGTCTGCATCCTTAA	1296
RESULT	5		
LOCUS	A59869	1631 bp	DNA
DEFINITION	Sequence 1 from Patent WO9706269.	PAT	06-MAR-1998
ACCESSION	A59869		
VERSION	A59869.1	GI:3715060	
KEYWORDS	Arabidopsis sp.		
SOURCE	Arabidopsis sp.		
ORGANISM	Eukaryota; Virdiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Caprales; Brassicaceae; Arabidopsis.		
REFERENCE	Jepson, I.		
AUTHORS	INDUCIBLE HERBICIDE RESISTANCE		
TITLE	Patent: WO 9706269-A 1 20-FEB-1997;		
JOURNAL	ZENECA LTD (GB)		

FEATURES	source	Location/Qualifiers
BASE COUNT	342 a	454 c
ORIGIN	454 t	
Query Match	93.0%;	Score 1205.2; DB 5; Length 1631;
Best Local Similarity	95.3%;	Pred. No. 0;
Matches 1283;	Conservative 0;	Mismatches 13; Indels 50; Gaps 2;
Qy	1	ATGGCTGAGAACCAAGAGTGGTATCGCTGGAGCTGGAATCGTTGGTGGTACT 60
Db	274	ATGGCTGAGAACCAAGAGTGGTATCGCTGGAGCTGGAATCGTTGGTGGTACT 333
Qy	61	GCTTTGATGCTTCAACGCTCGTGAATTCAGGTTACCTTTGATTGATCCAAACCCACCAAGT 120
Db	334	GCTTTGATGCTTCAACGCTCGTGAATTCAGGTTACCTTTGATTGATCCAAACCCACCAAGT 393
Qy	121	CAAGTGTCTTCTTCGGTAAACGCTGGTTGCTTCAACGCTTCTCTCGTTGTTTCCAAATGTCC 180
Db	394	CAAGTGTCTTCTTCGGTAAACGCTGGTTGCTTCAACGCTTCTCTCGTTGTTTCCAAATGTCC 453
Qy	181	ATGCCAGAAACTTGTACTAGCGTTCCAAAAGTGGCTTCTTTGACC----- 223
Db	454	ATGCCAGAAACTTGTACTAGCGTTCCAAAAGTGGCTTCTTTGGATCCTGTTCGAATTCAAAGC 513
Qy	224	-----CAATGGGTCATTTGTCATCCGTTTTCAGCTACTTTTCCAAACATCATGCCCTTG 275
Db	514	TTACGGATCCAATGGGTCCTCATCCGTTTTCAGCTACTTTTCCAAACATCATGCCCTTG 573
Qy	276	GTTGATTCCTTTTCTTGTCTTGAAGACCAACAAAGTGAAGGAGCAAGCTTAAGGCACT 335
Db	574	GTTGATTCCTTTTCTTGTCTTGAAGACCAACAAAGTGAAGGAGCAAGCTTAAGGCACT 633
Qy	336	CCGTAACCTCATCAAGTCCACTGTGCCCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGC 395
Db	634	CCGTAACCTCATCAAGTCCACTGTGCCCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGC 693
Qy	396	TAGCACCTTATCCGTCACGAAGTTCACCTTACCGTCTACCGTGGAGAGAGAGCTTCGC 455
Db	694	TAGCACCTTATCCGTCACGAAGTTCACCTTACCGTGGAGAGAGAGAGCTTCGC 753
Qy	456	CAAGACCGTGGAGTGGGAACCTCGTCTCTCAACGGTGTTCGTAACCTCCTCAG 515
Db	754	CAAGACCGTGGAGTGGGAACCTCGTCTCTCAACGGTGTTCGTAACCTCCTCAG 813
Qy	516	CGTGTGATGCTTGGTGTGATTTGATGCTTAACTGTCTCACGCTTTTACCAAGGAATCCT 575
Db	814	CGTGTGATGCTTGGTGTGATTTGATGCTTAACTGTCTCACGCTTTTACCAAGGAATCCT 873
Qy	576	TATCGAAGAGAACGTCACACCATCAACCCACAGGTCCTCGTGACTCTCTCTTTCGTCG 635
Db	874	TATCGAAGAGAACGTCACACCATCAACCCACAGGTCCTCGTGACTCTCTCTTTCGTCG 933
Qy	636	TTTCATCGCTAACCGTGGAGAGTTCGTCCTCTCTTATTCGGATTCGAGACTGAAGG 695
Db	934	TTTCATCGCTAACCGTGGAGAGTTCGTCCTCTCTTATTCGGATTCGAGACTGAAGG 993
Qy	696	TCGTGCTCTCAAGGGTATCACCAACCAAGGTTTCTTCTGCTGTGATG----- 745
Db	994	TCGTGCTCTCAAGGGTATCACCAACCAAGGTTTCTTCTGCTGTGATGCTGCTGCTGCT 1053
Qy	746	-----CAGCTGTTGTCAGCTGGTGGACACTTCCAAAGTTCATCGCTACTCCTA 790
Db	1054	GTGAATTCAGGCTTACTCGAGTGTGTCAGCTGGTGGACACTTCCAAAGTCTCTTGTCTA 1113
Qy	791	CCCTTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACACATCTGCTGATCGCAACC 850
Db	1114	CCCTTGGTGTGATGACATCCCATTTGGATACCGAAGTGGATACACATCTGCTGATCGCAACC 1173
Qy	851	CAGAAGCTGCTCCACGTAATCCAACTACCGATGCTTCTTGAAAGTTCATCGCTACTCCTA 910

Db	1174		CAGAAGTGTCTCCACGATATTTCCAACTACCGATGCTTCTGGAAAGTTTCATCGCTACTCCTA	1233				
Qy	911		TGAGATGGGTCTTGGTGGTGGAAACCGTTGAGTTCGGCTGGTCTCACTGCTGCTCCTA	970				
Db	1234		TGAGATGGGTCTTGGTGGTGGAAACCGTTGAGTTCGGCTGGTCTCACTGCTGCTCCTA	1293				
Qy	971		ACTGGAAGCGTGTCTACAGTCTCTACACTCACGCTCGTAAGTTGCTTCCAGCTCTCGCTC	1030				
Db	1294		ACTGGAAGCGTGTCTACAGTCTCTACACTCGTCTCGTAAGTTGCTTCCAGCTCTCGCTC	1353				
Qy	1031		CTGCCAGTTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCCGTCCAAGCATCCAGATT	1090				
Db	1354		CTGCCAGTTCTGAAGAAGCTTACTCCAAGTGGATGGGTTTCCGTCCAAGCATCCAGATT	1413				
Qy	1091		CCCTTCCAGTGATTGGTGGTGGTACCGGTACTCCAGACGTTATCTACGCTTTCGGTCACG	1150				
Db	1414		CCCTTCCAGTGATTGGTGGTGGTACCGGTACTCCAGACGTTATCTACGCTTTCGGTCACG	1473				
Qy	1151		GTCACTCGGTATGACTGGTGGTCCCAATGACCGCAACCCCTCGTTCTGAGCTCCTCGCAG	1210				
Db	1474		GTCACTCGGTATGACTGGTGGTCCCAATGACCGCAACCCCTCGTTCTGAGCTCCTCGCAG	1533				
Qy	1211		GTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAAAACCGTTTCGGTATTGGTAAGT	1270				
Db	1534		GTGAGAAGACCTCTATCGACATCTCTCCATTTCGCACCAAAACCGTTTCGGTATTGGTAAGT	1593				
Qy	1271		CCAAGCAAACTGGTCTGTCATCTAA 1296					
Db	1594		CCAAGCAAACTGGTCTGTCATCTAA 1619					
RESULT 6								
AR016594								
LOCUS	AR016594	1296 bp	DNA	PAT 05-DEC-1998				
DEFINITION	Sequence 7 from patent US 5776760.							
ACCESSION	AR016594							
VERSION	AR016594.1 GI:3972871							
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 1296)							
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.							
TITLE	Glyphosate tolerant plants							
JOURNAL	Patent: US 5776760-A 7 07-JUL-1998;							
FEATURES	Location/Qualifiers							
Source	1..1296							
BASE COUNT	287 a	344 c	332 g	333 t				
ORIGIN	/organism="unknown"							
Query Match 78.0%; Score 1011.2; DB 5; Length 1296;								
Best Local Similarity 86.3%; Pred. No. 1.5e-274;								
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;								
Qy	1	ATGGCTGAGAACCAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGGTTTGCAC	60					
Db	1	ATGGCTGAGAACCAAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT	60					
Qy	61	GCCTTTCATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGG	120					
Db	61	GCCTTTCATGCTTCAACGTCGTGGATTCAAAAGTCACCTTGATTGACCCGAACCCCTCG	120					
Qy	121	GAAGTGGCTTCTTCCGTTAACCGTGGTTCCTTCAACGGTTCCTCCGTTGTTCCAATGTCC	180					
Db	121	GAAGTGGCATCGTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGCTCCCTATGTCC	180					
Qy	181	ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAAAATGGGTCCATTGTCC	240					
Db	181	ATGCCGGGAACCTTGACGAGCGTGCCGAGTGGCTCTCTTACCCGATGGGGCGCTTGTCA	240					

QY	241	ATCCGTTTACGCTACTCTTCCAAACCATCATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGG	300
Db	241	ATCCGTTTACGCTACTCTTCCAAACCATCATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGG	300
QY	301	AGACCAACCAAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACCTCATCAAGTCCACTGTG	360
Db	301	AGACCAACCAAGGTGAAGGAGCAAGCTAAGGCACCTCGTAACCTCATCAAGTCCACTGTG	360
QY	361	CCCTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
Db	361	CCCTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
QY	421	CACCTTACCGTGTACCGTGGAGAGCAAGCTTCCGCCAAGGACCGTGGAGGTTGGGAAC	480
Db	421	CATCTGACCGTATATCGTGGAGAGCAAGCTTCCGCCAAGGACCGGAGGTTGGGAAC	480
QY	481	CGTGGCTTCAACGCTGCTTCTACTCAATCCTCAGCGCTGATGCATGCTGCTGCTGCTG	540
Db	481	CGCGCTCTCAACGCTGCTTCCGACGCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTG	540
QY	541	CCTAACCTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGACGCTCACACCATC	600
Db	541	CCTAACCTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGACGCTCACACCAT	600
QY	601	AACCCACAAGGTCTCGTGGTCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	660
Db	601	AATCCGCAAGGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	660
QY	661	GTCTGCTGCTGCTTATCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCA	720
Db	661	GTATCTCGCGCTGCTATCGGTTTGGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCA	720
QY	721	ACCAAGGCTGCTTCTGCTGTTGATGCAAGCTGTTGTTGCAGCTGGTGCACACTCTCA	780
Db	721	ACTAACGCTGCTTCTGCTGTTGATGCAAGCTGTTGTTGCAGCTGGTGCACACTCTCA	780
QY	781	CTTGTCAACTCCCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	840
Db	781	CTTGTCAATTCGCTAGCGGATGACATCCCGCTCGATACCGCAAGCTGGATATCAT	840
QY	841	ATCCGCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAGGTTCA	900
Db	841	ATCCGCAATCCGGAAGCGCTCCAGCAATTCGCAAGCGGATGCGTCAGGAAAATTCAT	900
QY	901	GCTACTCTTATGAGATGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	960
Db	901	GCAGACCTATGGAATGGGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	960
QY	961	GCTGCTCCTAACTGGAGCGTGTCTACAGTTCCTTACACTCACGCTCGTAAGTTCCTCA	1020
Db	961	GCTGCTCCTAACTGGAAACGTCGTCATATACGCAAGCTGCTCTTCTGCAAACTCTT	1020
QY	1021	GCTCTCGCTCCTGCCAGTCTGAAGAACGTTACTCCAAAGTGGATGGGTTCCGTC	1080
Db	1021	GCCCTCGCGCTCGGAGTCTGAAGAACGATATTCGCAAAATGGATGGGTTTCGTC	1080
QY	1081	ATCCAGATTCCTTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1140
Db	1081	ATTCTCTGATCTCTTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1140
QY	1141	TTCGGTCAAGGTCACCTCGGTATGACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1200
Db	1141	TTTGGTCACGGTCATCTCGGTATGACAGGTCCTCAATGCTGCAACTCTCGTCTCAG	1200
QY	1201	CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCG	1260
Db	1201	CTCCTCGCAGGGAAGAACCTCAATCGACATTTTCGCGCTTCGCAACCAACCGTTTCG	1260
QY	1261	ATTGGTAAGTCCAAAGCAACTGGTCTGCTGATCTCTAA 1296	
Db	1261	ATTGGCAAAATCCAAAGCAAGCGGTCCGGCAAGTTAA 1296	

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RESULT 7
LOCUS I15327 115327 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 7 from patent US 54631175.
ACCESSION I15327
VERSION I15327.1 GI:1250235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.F. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 54631175-A 7 31-OCT-1995;
FEATURES Location/Qualifiers
source 1.1296
BASE COUNT 287 a 344 c 332 g 333 t
ORIGIN

Query Match 78.0%; Score 1011.2; DB 5; Length 1296;
Best Local Similarity 86.3%; Pred. No. 1.5e-274;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACACAGAAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
Db 1 ATGGCTGAGAACACAAAAGTAGGCAATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60

Qy 61 GCTTTGATGCTTCAACGTCGTTGATTCAGGTTACCTTGATGATCCAAACCCACCAAGT 120
Db 61 GCTTTGATGCTTCAACGTCGTTGATTCAGGTTACCTTGATGATCCAAACCCACCTCTCGG 120

Qy 121 GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTTCCTCGTTGTTCCAAATGCC 180
Db 121 GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTTCCTCGTTGTTCCAAATGCC 180

Qy 181 ATGCCAGAAATGACTAGGCTTCCAAAGTGGCTTCTTTGACCCNATGGGTCCATTTGCC 240
Db 181 ATGCCGGGAAATTTGACGAGGGTGCCGAAGTGGCTTCTTGACCCGATGGGCGCGTTGTCA 240

Qy 241 ATCCGTTACGCTACTTTCCAAACCATCATGCTTGGTTGATTCGTTCTTCTGCTCGGA 300
Db 241 ATCCGTTACGCTATTTTCCAAACCATCATGCTTGGTTGATTCGTTCTTCTGTTAGCCGA 300

Qy 301 AGACAAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
Db 301 AGACAAACAAGGTGAAGGAGCAGGCAAGCACTCCCGCAATCTCATCAAGTCCACGGTG 360

Qy 361 CCTTTGATCAAGTCTCTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTACCAAGGT 420
Db 361 CCTCTGATCAAGTCTATTTGGCGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGT 420

Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGCTTCCGCAAGGACCGTGGAGGTGGCAACTT 480
Db 421 CATCTGACCGTATATCTGTGGAGAGCAGCTTCCGCAAGGACCGCGGAGGTGGGAATG 480

Qy 481 COTGCTCTCAACGGTGTTCGTACTCAAACTCCTACGCGCTGATGCAATTCGCTGATTCGAT 540
Db 481 CGGGCTCTCAACGGTGTTCGCGACGAGATCTCTCTGCTGATGCTTTTCGCTGATTCGAT 540

Qy 541 CTTAACTTGTCTACGCCCTTTTACCNAGGGAATCTTATTCGAAGAGAACGGTCAACACATC 600
Db 541 CTTAACTTGTCTGCGATGCTTTTACCAGGGCATTTCTTATAGAAGAGAACGGTCAACAGAT 600

Qy 601 AACCCACAAGGTCTGCTGACCTCTCTGTTGTTTCGTTTCATCGCTTAACGGTGGAGAGTTC 660
Db 601 ATCCGAAAGGGCTGCTGACCCCTCTGTTTCGCGGTTTTATCGCGAAGCGGTGGCGAATTT 660

Qy 661 GTGCTGCTGCTGATATCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGGTATCAACACC 720
Db 661 GTATCTGGCGCTGATCATCGGTTTGTAGACTGAAGGTCTGCTCTCAAGGGCATTAACACC 720
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Qy 721 ACCAACGGTGTCTTCTGCTGTTGATGCGAGCTGTTGTTGCGAGCTGGTGGACACTTCCAAGTCT 780
Db 721 ACTAACGGTGTCTTCTGCTGTTGATGCGAGCTGTTGTTGCGAGCTGGTGGACACTTCTAAATCA 780

Qy 781 CTTGCTAACTCCCTTTGGTGATGACATCCCAATTGGATACCGAAGCTGGATACCAATCCGTG 840
Db 781 CTTGCTAAATTCGCTAGGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840

Qy 841 ATGCCCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATCGCGAATCCGAAGCGCTCCAGCATTCGAGCAGCCGATGCGTCAAGAAAATTCATC 900

Qy 901 GCTACTCTATGGAGATGGGTCTTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 901 CGCACCTATGGAATGGGTCTTTCGTTGCTGCTACTGTTGAGTTCGCTGGTCTCACA 960

Qy 961 GCTGCTCCTAACTGAAGCGTGCACGTTCTCTACACTCACGCTCGCTAAGTTCGTTCTCCA 1020
Db 961 GCTGCTCCTAACTGGAACGTCGCGATGTCTATAGCACGCTCGAANAACCTCTTCTCCA 1020

Qy 1021 GCTCTCGCTCCGTCAGTCTCTGAAGAACGTTTACTCCAAAGTGGATGGTTCGCTCCAAGC 1080
Db 1021 GCCCTCGCGCTCGAGTTCTGAAGAACGATATTCCAAATGGATGGTTCGTCCTAGC 1080

Qy 1081 ATCCAGATATCCCTTCCAGTATTTGGTCTGCTACCCGCTACTCCAGAGCTTATCTACGCT 1140
Db 1081 ATTCTGATTTCTTCTCCAGTGAATTTGGTCTGCAACTCTGTACACCGAGCTAATCTATGCT 1140

Qy 1141 TTCCGTCACGCTACCTCGGTATGACTGCTGCTCCAATGACGCAACCTCGTTTCTGAG 1200
Db 1141 TTTGGTCACGCTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG 1200

Qy 1201 CTCCTCGCAGGTGAGAACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTTCGCT 1260
Db 1201 CTCCTCGCAGCGAAAAGACCTCAATCGACATTTGCGCCTTCGCAACCAACCGCTTGGT 1260

Qy 1261 ATTGGTAGTCCAGCAAACTGGTCTCGATCCCTAA 1296
Db 1261 ATTGGCAATCCAAAGAACGGGTCCGGCAAGTTAA 1296

RESULT 8
LOCUS AR016593 1296 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5776760.
ACCESSION AR016593
VERSION AR016593.1 GI:3972870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 6 07-JUL-1998;
FEATURES Location/Qualifiers
source 1.1296
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN

Query Match 74.2%; Score 961.6; DB 5; Length 1296;
Best Local Similarity 83.9%; Pred. No. 1.5e-260;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGTTGGTATCGCTGGAGCTGGAAATCGTTGGTGGTGGTGGTGGTGGT 60
Db 1 ATGGCTGAGAACCAAAAAAGTAGGATCGCTGGAGCGGAATCGTGGCGGTATGTCACG 60

Qy 61 GCTTTGATGCTTCAACGCTGCTGGATTCAGGTTACCTTGATGATCCAAACCCACCAAGT 120
Db 61 GCGCTGATGCTTACGCGCGGCGGATTCAGGTTACCTTGATGATCCAAACCCCTCTCGC 120
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Qy 121 GAAGGTGCTTCTTCGGTAACGGTGTGTGCTTCAACGGTTCCTCCGTTGTGTTCGAATGTCC 180
Db 121 GAAGGTGCATCCTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
Qy 181 ATGCCAGGAACCTTGACTAGCGTTCGAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240
Db 181 ATGCCAGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA 240
Qy 241 ATCCGTTTACGTACTTTCACCAACCATCATGCCCTGGTGTGATTCGTTTCTGCTTGTCTGGA 300
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTCTGTAGCCGGA 300
Qy 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACCTGTG 360
Db 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCACTCCGCAATCTCATCAAGTCCACCTGTG 360
Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTATCCGTCAGGAGGT 420
Db 361 CCTCTGATCAAGTCTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAAGCTTCCCAAGACCGTGGAGGTGGGAATTT 480
Db 421 CATCTGACCGTATATCTGTGAGAGAGCACTTCCCAAGACCGCGGAGGTGGGAATTT 480
Qy 481 CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCATTCGCTGATTTCCGAT 540
Db 481 CGCGCTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCGATGCTTTCGCGGATTTCCGAT 540
Qy 541 CCTAACTTGTCTACGCGCTTTACCAAGGGAATCCTTATCGAAGAGACGGTCACACATC 600
Db 541 CCGAAGTGTGCGATGCTTTTACCAAGGGAATCCTTATAGAAGAGACGGTCACACATTT 600
Qy 601 AACCCACAAGTCTCGTACTCTCTCTTCTGCTGCTTTCATCGCTAACGGTGGAGAGTTC 660
Db 601 AATCCGAAGGGTCTGTGACCCCTTCTTTCGGGGTTTTATCCGGAACGGTGGCGAATTT 660
Qy 661 GTGTCTCTCTGTGTATTCGGAATTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACACCC 720
Db 661 GTATCTCGCGTGTATCTCGGCTTTGACACTGAAGGTAGGCGCTTAAAGGCATTTACAACC 720
Qy 721 ACCAAGCGTGTCTGTCTGTGATGAGCTGTGTTGTCAGCTGGTGCACACTCCAAGTCT 780
Db 721 ACGAAGCGTGTCTGCGCGTGTGATGAGCGGTGTGTCAGCGCGGCGCACACTCGAATCA 780
Qy 781 CTGTCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCATCGTG 840
Db 781 CTGTCTAACTCTAGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Qy 841 ATGCCCAACCCAGAGTGTCTCACGATTTTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Db 841 ATCCGGAATCCGGAAGCGCTCCACGCAATTTCCGACGACCGATGCTCAGGAAATTCATC 900
Qy 901 GCTACTCTATGAGATGGGTCTCGGTGTGCTGGAACCGTGTGATTCGCTGGTCTCACT 960
Db 901 GCGACACTATGAAATGGGGTCTCGGTGGGGGTACGGTGTGATTCGCTGGGCTCACA 960
Qy 961 GCTGCTCTAACTCGAAGCGTGTCTACGTTCTCTACACTCACGCTCGTAAGTTCCTTCCA 1020
Db 961 GCGGCTCTAACTCGGAACGTCGSCATGTCTATACGACGCTCGAANAATCTTCCA 1020
Qy 1021 GCTCTCGCTCCGAGTTCTGAAGAACGTTACTTCCAAAGTGGATGGTTCCTGTCGAAGC 1080
Db 1021 GCGCTCGCGCTCGAGTTCTGAAGAACGATATTTCCAAATGGATGGGGTTCGCGCCGAGC 1080
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Qy 1141 TTCGGTCAACGGTCAACCTCGGTATGACTGTGTGCTCAATGACCGCAACCCGCTTCTGAG 1200
Db 1141 TTCGGCACGCTCATCTCGCATGACAGGGGCGCGGATGACCGAAGCGTCTGTCAGAG 1200

Qy 1201 CTCCTCGAGGTGAGAAGACCTCTATCGACATCTCTCAATTCGACCAAAACCGTTTCGGT 1260
Db 1201 CTCCTCGAGGTGAGAAGACCTCAATCGACATCTCGCCCTTCGCAACAAACCGCTTTGGT 1260
Qy 1261 ATTGGTAAAGTCCCAAGCAAACTGGTCCCTGCATCTCTAA 1296
Db 1261 ATTGGCAATTCCAAGCAAAACGGGTCCGCAAGTTAA 1296
RESULT 9
LOCUS I15326 1296 bp DNA PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5463175.
ACCESSION I15326
VERSION I15326.1 GI:1250234
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1296)
AUTHORS Barry,G.P. and Kishore,G.M.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5463175-A 6 31-OCT-1995;
FEATURES Location/Qualifiers
source I. 1296
BASE COUNT 286 a 368 c 361 g 281 t
ORIGIN
Query Match 74.2%; Score 961.6; DB 5; Length 1296;
Best Local Similarity 83.9%; Pred. No. 1.5e-260;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
Qy 1 ATGGCTCAGAACCAACAGAGGTGGTATCGCTGCAGCTGGAATCGTTGGTGTGGACT 60
Db 1 ATGGCTCAGAACCAACAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAG 60
Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAAGT 120
Db 61 GCGCTGATGCTTACGCCCGCGGATTCAAAGTCACTTGATTGACCCGAACCCCTCCCTGGC 120
Qy 121 GAAGGTGCTTCTTCGGTAACGGTGTGTGCTTCAACGGTTCCTCCGTTGTGTTCGAATGCC 180
Db 121 GAAGGTGCATCGTTTGGGAATGCCGATGCTTCAACGGCTCATCCGTCGTCCTTATGTCC 180
Qy 181 ATGCCAGGAACCTTGACTAGCGTTCGAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240
Db 181 ATGCCAGGAACCTTGACGAGCGTCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA 240
Qy 241 ATCCGTTTACGTACTTTCACCAACCATCATGCCCTGGTGTGATTCGTTTCTGCTTGTCTGGA 300
Db 241 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTGTGATTCGCTTCTGTAGCCGGA 300
Qy 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCACTCCGTAACCTCATCAAGTCCACCTGTG 360
Db 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCACTCCGCAATCTCATCAAGTCCACCTGTG 360
Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCAGGAGGT 420
Db 361 CCTCTGATCAAGTCTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAAGCTTCCCAAGACCGCTGGAGGTGGGAATTT 480
Db 421 CATCTGACCGTATATCTGTGAGAGAGCACTTCCCAAGACCGCGGAGGTGGGAATTT 480
Qy 481 CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTGATGCATTCGCTGATTTCCGAT 540
Db 481 CGCGCTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCGATGCTTTCGCGGATTTCCGAT 540
Qy 541 CTTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGACGGTCAACACATC 600
Db 541 CCGAAGTGTCTCAGCGCTTTTACCAAGGGAATCCTTATAGAAGAGACGGTCAACACATTT 600

[illegible]

RESULT	10
AR016591	DNA
LOCUS	Sequence 3 from patent US 5776760.
DEFINITION	AR016591
ACCESSION	GI:3972868
VERSION	.
KEYWORDS	Unknown..
SOURCE	Unknown..
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1692)
AUTHORS	Barry,G.Francis and Kishore,G.Murthy.
TITLE	Glyphosate tolerant plants
JOURNAL	Patent: US 5776760-A 3 07-JUL-1998;
FEATURES	location/Qualifiers 1..1692 /organism= "unknown"
source	381 a 480 c 469 g 361 t
BASE COUNT	1 others
ORIGIN	

Query Match 74.1%; Score 960; DB 5; Length 1692;
Best Local Similarity 83.8%; Pred. No. 4.3e-260;

QY	1081	ATCCAGATTCCCTTCCAGTGATTGGTCTGCTACCGTACTCCAGACGTTATCTACGCT	1140
Db	1200	ATCCCGGATTTCGCTCCCGGATTGGCGGCAACCGGACACCGAGCTAATCTATGCT	1259
QY	1141	TTCCGGTCAAGGTACCTCGGTATGACTGGTCTCAATGACCGCAACCTCGTTCTGAG	1200
Db	1260	TTCCGGCATGGTCTATCTCGGCATGACAGGGGCGCGATGACCGCAACGCTCGTCTCAGAG	1319
QY	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCCGACCAACACCGTTTCGGT	1260
Db	1320	CTCCTCGCAGGCAAGACCTCAATCGACATTTCCGCTTCGCAACCAACCGCTTTGGT	1379
QY	1261	ATTGGTAAGTCCAAAGCAAACTGCTCTCGCATCTCTAA	1296
Db	1380	ATTGGCAAAATCCAAAGCAACGGGTCCGCAAGTTAA	1415
RESULT 11			
AR016592			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 1086; Conservative			
0; Mismatches 207; Indels 3; Gaps 3;			
QY	1	ATGGGTGAGAACACAAAGAGTGTGTATCGCTGGAGCTGGAATCGTTGGTGTTCACCT	60
Db	1	ATGCTCTGAGAACACCAAAAAAGTAGGCATCGCTGGAGCGGAATCTCGCGCGTATGCACG	60
QY	61	GCTTTGATGCTTCAAGCTCGTGATTCAGGTTACCTTTGATTGATCCAAACCCACCAAGGT	120
Db	61	GCCTGATGCTTCAGCGCGCGGATTCAAGTCAACCTTGATTGACCGCAACCCCTCTGGC	120
QY	121	GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTTCTCCGTTGTTCCAAATGTCC	180
Db	121	GAAGGTGCATCGTTTGGGAATCCGGATGCTTCAACGGCTATCCGCTCGCTATGTCC	180
QY	181	ATGCCAGAACTTGACTAGCGCTTCAAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC	240
Db	181	ATGCCGGGAACTTGACGAGCGTGCCGAAGTGGCTCTCTTGACCCGATGGG-CCGTTTGTC	239
QY	241	ATCCGTTTTCAGCTACTTTCACACCATCATCGCTTGGTTGATTCGTTTCTGCTGTGGA	300
Db	240	ATCCGTTTTCAGCTA-TTTCACCATCATGCTCC-TGGTTGATTGCTTCTGTTAGCCGA	297
QY	301	AGACCAAAAGGTGAAGGCAAGCTTAAGCACTCCGTAACCTCATCAAGTCCACTGTG	360
Db	298	AGACCAAAAGGTGAAGGCAAGCGCAAGCACTCCGCAATCTCAAGTCCACGGTG	357
QY	361	CTTTGATCAAGTCTTGGCTGAGGAGGTGATGTAGCCACCTTATCCGTTCACGAAGT	420
Db	358	CTCTCATCAAGTCATTGGCGGAGGAGGTGATGCGAGCCATCTGATCCGCCATGAAGT	417
QY	421	CACCTTACCGTGTACCGTGGAGNAGCAGACTTCGCCAAGCAGCGTGGAGACTT	480

Db	418	CATCTGACCCTATATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTGGGAAC	477
QY	481	CGTCGCTCAACGGTGTTCGTACTCAAACTCCTCAGCGCTCATGCATTCGCTGATTCGAT	540
Db	478	CGCGCTCAACGGTGTTCGACGCGAGATCCTCAGCGCCGATCGTTCGCGGATTCGAT	537
QY	541	CCTAACTGTCTCACGCCCTTTACCAAGGGAATCCTTTATCGAAGAGAACGGTTCACACCAT	600
Db	538	CCGAACCTTGTCGATCGCTTTACCAAGGCGATTCCTATACAGAGAAGCGTTCACAGATT	597
QY	601	AACCCACAAGGTCTCGTACTCTCTTGTTCGTCGTTTCATTCGCTAACGGTGGAGAGTTC	660
Db	598	AATCCCAAGGGTCTGTGACCTCTTTGTTTCGCGCTTTTATCGCAACGGTGGCGAATTC	657
QY	661	GTCTCTGCTGCTGTATTCGGATTTCGAGACTGAAGGTGCTGCTCTCAAGGGGTATCACCA	720
Db	658	GTATCTGCCGCTGCTATCGGCTTTGAGACHGAAGGTAGGGCGCTTAAAGGCATTTACAA	717
QY	721	ACCAACGGTGTCTTCTGCTGTGATGACGCTGTTGTTGCAGCTGTGTGCACACTCCAAAGTCT	780
Db	718	ACGAACGGCGTTCGTGCGCTTGATGACGCGTTCGTCAGCGCGCACACTCGAAATCA	777
QY	781	CTTGTCTAACTCCCTTGGTGATGACATCCCAATTCGATACCGAACGTCGATACCACTCGT	840
Db	778	CTTGTCTAAATTCGTAGCGGATGACATCCCGCTCGATACCGAACGTCGATATCATATCGT	837
QY	841	ATGCCCAACCCAGAAGCTGCTCCACGTAATTCACAACTACCGATGCTTCTGGAAAAGTTCA	900
Db	838	ATCGCGAATCCGAAGCGCTCCACGCTTCGACGACCGATTCGCGACGCGTTCGATACCT	897
QY	901	GCTACTCTTATGAGATGGTCTTCTGCTGTTGCTGGAAACCGTTGAGTTCGCTGCTCTCAT	960
Db	898	GCACACCTTATGCAAAATGGGCTTCGCGTGGCGGTTACGTTTCAGTTTCGCTGGCTCACA	957
QY	961	GCTGCTCTTAACTTGAAGCGTGTCTCAGCTTCTACACTCACGCTCGTAAGTTCCTTCCA	1020
Db	958	GCCTCTCTTAACTTGAAGCGTGTCTCAGCTTCTACACTCACGCTCGTAAGTTCCTTCCA	1017
QY	1021	GCTCTCGCTCTGCCAGTTCTGAAGAACGTTTACTCCTCAAGTGGATGGTTTCCTGTCCTCA	1080
Db	1018	GCCTCTCGCGCTCGGAGTTCTGAAGAACGATATTCCTCAATGGATGGGTTCCGCGCGAGC	1077
QY	1081	ATCCAGATTCCCTTCCAGTGATTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140
Db	1078	ATCCCGGATTTCGCTCCCGTGATTGGCGGGCAACCGGACACCGGACGTAATCTATGCT	1137
QY	1141	TTCCGGTCAAGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
Db	1138	TTCCGGCATGGTCTATCTCGGCGATGACAGGGGCGCGGATGACCGCAACGCTGCTCAGAG	1197
QY	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAACACCGTTTCGCT	1260
Db	1198	CTCCTCGCAGGTGAGAAGACCTCTCAATCGACATTCGCGCTTCGCAACCAACCGCTTGGT	1257
QY	1261	ATTGGTAAGTCCAAAGCAAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1296
Db	1258	ATTGGCAAAATCCAAAGCAACCGTTCGCGCAAGTTAA	1293

RESULT 12			
LOCUS	I15325	Sequence 4 from patent US 5463175.	PAT 02-APR-1996
DEFINITION	I15325	Accession	
VERSION	I15325.1	GI:1250233	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1293)		
AUTHORS	Barry,G.F. and Kishore,G.M.		
TITLE	Glyphosate tolerant plants		
JOURNAL	Patent: US 5463175-A 4 31-OCT-1995;		

FEATURES		source		Location/Qualifiers	
		1. .1293			
BASE COUNT		286 a 367 c 359 g 281 t			
ORIGIN					
Query Match 71.7%; Score 928.8; DB 5; Length 1293;					
Best Local Similarity 83.8%; Pred. No. 2.8e-251;					
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps					
Qy	1	ATGCCTGAGAACCAACAGAGGTTGGTATCGCTGGAGCTGGGAATCGTTGGTGTTCGCACT	60		
Db	1	ATGTCTGAGAACCAACAAAAGTAGGCATCGCTGGAGCGCGGAATCGTCGGCGTATGTCAGG	60		
Qy	61	GCTTTGATGCTTCAACCTTCGTGGATTCAAGGTTCACGTTCACCTTGAATCATCCAAACCCACCAAGT	120		
Db	61	CGCTGATGCTTCAGCGCCGCGGATTCANAAGTCACCTTGATTGACCCGAACCTCTCTGGC	120		
Qy	121	GAAGGTGTTCTTTTCGTGAAGCTGTGTGTTCAACGGTTCCTCGTTGTCCAAATGTCC	180		
Db	121	CAAGCTGCATCGTTTGGGAATGCGGATGCTTCAAGGGCTCATCCGTCGTCCTATGTCC	180		
Qy	181	ATGCCAGGAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCATGGGTCCATTGTCC	240		
Db	181	ATGCCGGGAACTTTGACGAGCGTCCGAAGTGGCTCCTTGACCCGATGGG -CGGTTGTCA	239		
Qy	241	ATCGCTTTACGCTACTTTTCCAAACCATCATGCCCTTGGTTGATTTCGTTTCCTTGGTCTGCA	300		
Db	240	ATCGGGTTCAGTA -TTTCCAAACCATCATGCC -TGGTTGATTGCTTCTGTTAGCCGA	297		
Qy	301	AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAAACCTCATCAAGTCCACTGTG	360		
Db	298	AGACCAACAAAGGTGAAGGAGCAGCGCAAGACACTCCGCAATCTCATCAAGTCCACGGTG	357		
Qy	361	CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATTCGTCACGAAAGT	420		
Db	358	CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGGAGCCATCTGATCCGCCATGAAGT	417		
Qy	421	CACCTTACCCTGTACCCTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGGAACCT	480		
Db	418	CATCTGACCGTATATCTGGAGAAAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAAGT	477		
Qy	481	CGTCTCTCAACGGGTTCGTACTCAAACTCCTCAGCGCTGATGCATTCGCTGATTTTCGAT	540		
Db	478	CGGGCTCTCAACGGGTTCGACGCGCAGATCCTTCAGCGCCGATCGCTTCGGGATTTTCGAT	537		
Qy	541	CCTAACCTTGCTCAGCGCTTTACCAAGGGAACTCCTTATCGAAGAGAACGGTCACACCATC	600		
Db	538	CCGAACCTTGTGCGATGCGTTTACCAAGGGCAATCTTATAGAAGAGAACGGTCACACGATT	597		
Qy	601	AACCCACAAGCTTCGTGACTCTCTCTTTTCGTCTTTCATCTGCTAACGCTGGAGAGTTC	660		
Db	598	AATCCGCAAGGGCTCGTGACCCCTCTGTTTCGGCGGTTTTATCCGGAACGGTGGCGAATTC	657		
Qy	661	GTGTCTGCTGCTGTTATCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCACT	720		
Db	658	GTATCTGCGGTGTCATCGGCTTTGAGACTGAAGTAGGCGGCTTAAAGGCATTTACAACC	717		
Qy	721	ACCAACGGTGTCTTGCTGTTGATGCAAGCTTGTTTGTGCAAGTGGTCCACACTCCCAAGTCT	780		
Db	718	ACGAACGGCGTCTTGGCCGTTGATGACAGCGGTTGTGCGAGCGCGGCGCACACTCGAAATCA	777		
Qy	781	CTTTCCTTAACCTCCCTTGCTGATGACATCCCATTCGATACCGAAGCTGGATACCACTCGTG	840		
Db	778	CTTTCCTTAATTCGCTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATCATATCGTCT	837		
Qy	841	ATGCCCAACCCAGAACTGCTCCACGTAATTCCTCAACTACCGATGCTTCTCGGAAGTTTCATC	900		
Db	838	ATCCGGAATCCGGAAGCGGCTCCACGCAATTTCCGACGACCGATCGCTCAGGAAATTCATC	897		
Qy	901	GCCTACTCCTATGGAGATGGGTCTCTGTTGCTGGAAACCGTTGAGTTCGCTGCTCACT	960		

Db	417		AGACCAACAAAGTGAAGGACGAGCGAAGACACTCCGCAATCTCATCAAGTCCACGGTG	476
QY	361		CTTTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATCTAGCCACCTTATCCGCTCACGAAGGT	420
Db	477		CTCTGTATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT	536
QY	421		CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGACCGTGGAGGTGGGAACCTT	480
Db	537		CATCTGACCGCTATATCGTCGAGAAGCAGACTTCGCCAAGACCGCGAGGTTGGGAACGTG	596
QY	481		CGTCGCTCAACCGTGTCTGTACTCAATCCTCAGCGCTGATGCATTCGCTGATTTTCGAT	540
Db	597		CGCGCTCTCAACCGTGTCTGCACGCGAGATCCTCAGCGCGATCGTTCGCGGATTTTCGAT	656
QY	541		CTTAACCTTGTCTCACCGCTTTACCAAGGGAATCTTATCGAAGAGAACGCTCACACATC	600
Db	657		CGAATCTGTGCGTTCGCTTACCAAGGCAATCTTATAGAGAGAACGCTCACAGATT	716
QY	601		AACCCACAAAGGTCTCGTGACTCTCTTGTTCGTGCTTTCATCGCTAACGGTGGAGATTC	660
Db	717		AATCCGCAAGGGCTCGTGACCTCTCTTTCGGCGTTCATCGCAACGGTGGCGAATTC	776
QY	661		GTGCTGCTCGTGTATTCGGAATTCGGAAGTGAAGTGTGCTCTCAAGGGTATCACCAAC	720
Db	777		GTATCTGCGGCTGTATCGGCTTTGAGACTGAAGTGAAGGCTTAAAGCATTTACAAC	836
QY	721		ACCAACGGTGTCTGCTGTTGATGAGCTGTTGTTGTCAGCTGCTGCACACTCCAAGTCT	780
Db	837		ACGAAGCGGCTTGTGCGGTTGATGACGCGGTTGTGCGACGGCGGCACACTCGAATCA	896
QY	781		CTTGCTAACTCCCTTGGTGATGACATCCCATTTGATACCGAAGCTGGATACCACTCGTG	840
Db	897		CTTGTCTAACTTCGCTAGCGGATGATCCCGCTCGATACCGCAACGCTGGATCATATCGTC	956
QY	841		ATCGCCAAACCCAGAGTGTCTCACGATTAATTCGAATACCGATGCTCTGGAAGTTCATC	900
Db	957		ATCGCGAATCCGGAAGCGGCTCCACGATTTCCGACGACCGCATCGTCAGGAAATTCATC	1016
QY	901		GCTACTCTATGAGATGGGTCTCGTGTGCTGGAACCGTTGAGTTCGGTGGTCTCACT	960
Db	1017		GCACACCTATGGAATGGGCTTCGCTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA	1076
QY	961		GCTGCTCCTAACTTGAAGCGTGTACGTTCTCTACACTCACGCTCGTAAGTTCCTTCCA	1020
Db	1077		GCGGCTCCTAACTTGAAGCGTGTGCGCATGTCTATACGACGCTCGAAAACTTCTCCA	1136
QY	1021		GCCTCGCTCTCCAGTCTCTGAAGACGTTACTCCAAGTGGATGGTTTCGCTCCAAGC	1080
Db	1137		GCCCTCGGCTCGGAGTCTGAAGAACGATATTCCAAAATGGATGGGTTTCGCGCGAGC	1196
QY	1081		ATCCAGATTCCTTCCAGTGAATGGTTCGTGCTACCGGTACTCCAGACGTTATCTACGCT	1140
Db	1197		ATCCCGGATTCGCTCCCGTGATGGCGGGCAACCCGGACCCGACGTAATCTATGCT	1256
QY	1141		TTCCGGTACAGGTCACCTCGGTATGACTGGTGTCCCAATACCGCAACCCCTGTTCTGAG	1200
Db	1257		TTCCGGCATGGTCTATCGGCATGACAGGGCGCGCATGATACCGCAACGCTCGTCTCAG	1316
QY	1201		CTCCTCGCAGGTGAGAGACCTCTATGACATCTCTCCATTCGCAACCAACCGTTTCGGT	1260
Db	1317		CTCCTCGCAGGCAAGAACCTCAATCGACATTTTCGCGCTTCGCAACCAACCGCTTGGT	1376
QY	1261		ATTGGTAAGTCCAAAGAACTGCTCTCATCTCTAA	1296
Db	1377		ATTGGCAATCCAAAGCAAGGGTCCGCGCAAGTTAA	1412

RESULT 14
PSEAKSD
LOCUS
DEFINITION

PSEAKSD 3430 bp DNA BCT 26-APR-1993
Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.

ACCESSION	M69158
VERSION	M69158.1
KEYWORDS	GI:150981
SOURCE	ketoglutarate semialdehyde dehydrogenase.
ORGANISM	Pseudomonas putida
REFERENCE	Bacteria: Proteobacteria; gamma subdvlslon; Pseudomonas group; Pseudomonas.
AUTHORS	1 (bases 1 to 3430)
TITLE	Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
JOURNAL	Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas
FEATURES	Unpublished (1991)
source	Location/Qualifiers
gene	1..3430
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	/codon_start=1
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	RRTCTQLRTFARVVRAGWLDVRYDNAQPERQLPRADLRQVAGLGPVAVPGSNF
	PLAFSVAGDTSALAAQGVVYKAHSHPQSELVQVAQVAKLGGPAGVFSLLY
	GGREVGIALVSDPRIKAVFTGSSRGALCOATQARPEPIFYAEMSEINPVFLFE
	AALQARAEALAQFVASLTQGGAGFCTNPGLVIAQGPALQREIPYDAEMSEIVRAAQT
	MUTPGFSAYQAGVGGLAGNANAAGSAGQGNQCOALPVTQOAEFLADPALQA
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BASE COUNT	562 a 1140 c 1157 g 571 t
ORIGIN	

Query Match	5.1%;	Score 66.2;	DB 2;	Length 3430;
Best Local Similarity	47.7%;	Pred. No. 1.2e-07;		
Matches 194;	Conservative 0;	Mismatches 213;	Indels 0;	Gaps 0;
QY	29	TCGCTGGAGCTGGAATCGTTGGTGTGTTTGCACCTGCTTTGATGCTTCAACGCTCGTGGATTCA	88	
Db	2214	TGGTGGCGCGGGATTGTGCGGCTTCCCTGTCGCTTCAACCTGGCCCGCAGGCGCTCC	2273	
QY	89	AGGTTACCTTGTATGTATCCAAACCCACAGGTGAAGTGTCTTTCGGTAACGCTGGTT	148	
Db	2274	GGGTGCTTATTTGGTCGACCGCAGCACCGCCCATGCGGGGTCTCTATGGAACCGCGGC	2333	
QY	149	GCCTCAACGGTCTCTCGTGTGTTCCAAATGTCCATGCCAGGAACTTCACTAGCCTTCCAA	208	
Db	2334	ACCTGGCCACGAGCAGGTGTTCGGATTCGCGACCTGTCGATCCTCAAGCGCTTGC	2393	
QY	209	AGTGGCTTCTTGACCCCAATGGGTCCATTTGTCCTTTCAGTACTTTCCAACCATCA	268	
Db	2394	GCATGCTGCTGGACCGCATGGCCCACTGCGCCTGGACTGGAAGTACTCTGCCACGCGCA	2453	
QY	269	TGCGTTGGTTGATTCGTTTCTTGTCTGGAAGACCAACAAAGGTGAAGAGCAAGCTA	328	
Db	2454	TGCGCTGGTTTACCGCGCTGCTGCTCAACCTTGC	2513	
QY	329	AGGACATCCCGTAACCTCATCAAGTCCACTGTGCTTTGATCAAGTCTTTCGCTGAGGAGG	388	
Db	2514	CCGGCATCCCGACGCTGAACGAAGGACGCTGGGTGATGGCAGCGCTGCTGGGCTCGA	2573	
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RESULT 15
AR016613 AR016613 62 bp DNA PAT 05-DEC-1998
LOCUS Sequence 27 from patent US 5776760.
DEFINITION AR016613
ACCESSION AR016613
VERSION AR016613.1 GI:3972890
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 62)
AUTHORS Barry.G.Francis and Kishore,G.Murthy.
TITLE Glyphosate tolerant plants
JOURNAL Patent: US 5776760-A 27 07-JUL-1998;
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BASE COUNT 12 a 12 c 19 g 19 t
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Query Match 4.5% Score 58.8; DB 5; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.4e-05;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 CCCTGGAGCTGGAATCGTTGCTGATGACAC7GCTTTGATGCTTCAACGCTCGTGGATTCAA 60
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Qy 90 GG 91
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Db 61 AG 62
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: January 1, 2001, 03:43:13 ; Search time 263.11 Seconds
(without alignments)
1850.400 Million cell updates/sec
Title: US-08-484-274-8
Perfect score: 1296
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 480022 seqs, 187831343 residues
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1296	100.0 1296 13	Q20835 Synthetic glyphosa
2	1296	100.0 8418 20	X57309 Sugar beet T-DNA c
3	1205.2	93.0 1631 18	T85664 CPT1-GOX gene fusi
4	1009.6	77.9 1321 13	Q20834 Modified glyphosat
5	960	74.1 1321 13	Q20833 Manipulated glypho
6	956.8	73.8 1692 13	Q22705 Glyphosate oxidore
7	925.6	71.4 1689 13	Q20832 Glyphosate oxidore
8	897	69.2 8012 20	X57305 Sugar beet T-DNA c
9	897	69.2 8798 20	X57308 Sugar beet T-DNA c
10	39.8	3.1 32207 20	V73805 KSHV LTR DNA (nucl
11	39.8	3.1 137507 19	V19941 KSHV long unique c
12	37.4	2.9 397 20	X89891 Spinocerebellar at

c 13	35.6	2.7	6558	21	Z45602
c 14	35.2	2.7	6794	21	Z45597
c 15	35	2.7	2004	17	T13952
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c 18	35	2.7	2010	15	Q74683
c 19	35	2.7	2576	17	T13945
c 20	35	2.7	2576	18	T74006
c 21	35	2.7	2576	19	V16181
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c 23	35	2.7	2655	17	T13951
c 24	35	2.7	2655	17	T13954
c 25	35	2.7	2655	18	T73996
c 26	35	2.7	2655	18	T74001
c 27	35	2.7	2655	19	V16169
c 28	35	2.7	2655	19	V16174
c 29	35	2.7	4031	17	T13947
c 30	35	2.7	4031	18	T74010
c 31	35	2.7	4031	19	V16189
c 32	35	2.7	10266	17	T33007
c 33	34.6	2.7	543	13	Q23092
c 34	34.4	2.7	1291	20	X87940
c 35	34.4	2.7	2852	19	V64558
c 36	34.4	2.7	2852	19	V44449
c 37	34.4	2.7	2852	20	Z19359
c 38	34.4	2.7	2852	20	Z19147
c 39	34.4	2.7	4888	20	X13244
c 40	34.2	2.6	9551	20	Z22301
c 41	34.2	2.6	54548	21	Z45596
c 42	34.2	2.6	138169	21	A34791
c 43	34.2	2.6	141589	21	A35005
c 44	34.2	2.6	141589	21	A35030
c 45	34	2.6	1001	16	Q80734

ALIGNMENTS

RESULT 1	
Q20835	
ID Q20835 standard; DNA; 1296 BP.	
XX Q20835;	
XX 01-MAY-1992 (first entry)	
XX Synthetic glyphosate oxidoreductase gene.	
XX Recombinant; GOR; resistance; ss.	
XX Synthetic.	
XX Key Location/Qualifiers	
FT CDS 1..1296	
FT /*tag= a	
XX WO9200377-A.	
XX 09-JAN-1992.	
XX 24-JUN-1991; 91WO-US04514.	
XX 24-JUN-1991; 91US-0717370.	
XX 25-JUN-1990; 90US-054236.	
XX (MONS) MONSANTO CO.	
XX Kishore GM, Barry GF;	
XX WPI; 1992-041559/05.	
XX P-PSDB; R20642.	
XX Gene encoding glyphosate oxido-reductase enzyme - used to	

PT transform plants to produce plants tolerant to glyphosate
XX herbicide

Claim 1: Page 1032; 142pp; English.

The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtained so that weeds can be selectively controlled in fields containing crops.

See also Q20832-Q20841 and Q22705.

XX Sequence 1296 BP: 271 A; 359 C; 305 G; 361 T; 0 other;

Query Match 100.0%; Score 1296; DB 13; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGAGAACACAGANGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60
DB 1 atggctgagaaacacagaagggttggtatcgctggagctggaatcggttggttgcact 60

QY 61 GCTTTGATGCTTCAACGTCCTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGGT 120
DB 61 gctttgatgcttcaacgctggtatgattcaagggttaaccttgattgatccaaacccaccaggt 120

QY 121 GAAGTGTCTTTTCGGTAACGCTGGTGTGCTTCAACGGTTCCTCCGTTGTTTCCAAATGTCC 180
DB 121 gaagtgtctcttcggtaacgctggttgcttcaacgggttcctccggttggttccaaatgtcc 180

QY 181 ATGCCAGGAACCTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240
DB 181 atgccaggaaaccttgactagcgttccaaagtggcttcttgacccaatgggttccattgtcc 240

QY 241 ATCCGTTTCAAGTACTTCCAAACCATCATGCTTGGTTGATTGCTTCTTGGTTGTGGA 300
DB 241 atccgtttcaagtacttccaaacctcatgcttggattgattgcttcttggttgtgga 300

QY 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACTGTG 360
DB 301 agaccaaaacagggtgaaggagcagactaaggcactccgtaacctcatcaagtccactgtg 360

QY 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAGGT 420
DB 361 cctttgatcaagcccttggctgaggagctgatagctagccaccttattccgttcacgaagt 420

QY 421 CACCTTACCGTGTACCGTGGAGAGGAGACTTCCGCCAAGGACCGTGGAGGTTGGGAACCTT 480
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QY 721 ACCAACGGTGTCTTGTGCTGTTGATGACAGCTGTTGTTGTCAGCTGGTGACACTCCNAAGTCT 780

DB 721 accaaagggtgtcttctgctgttgatgcaagctgttgttgcagctggtgcacactccaaagtct 780

QY 781 CTTCGCTAACTCCCTTGGTGTGATGACATCCCATTTGCGATACCGAAGCTGGATACCCATCGTG 840

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DB 901 gctactctctatggagatgggtctctcggttgcgtggaacggttgagttcgctggtctcact 960

QY 961 GCTGCTCTTAACCTGGAAGCGTGTCTACGTTTCTTACACTCACGCTCGTAAAGTTGCTTTCCA 1020

DB 961 gctgctcttaactggaaagcgtgtcctacgttctctacactcaacgctgtaagttgcttcca 1020

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DB 1021 gctctgctctctgccagttctgaagaacgttactccaaagtggatgggtttccgtccaaagc 1080

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DB 1141 ttgggtcaacgctcacctccggtatgactggtgctccaaatgacccgaacccctcgttctcga 1200

QY 1201 CTCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAAAACCGTTTCGGT 1260

DB 1201 ctctcgcaggtgagaagacctctatcgacatctctctccttcgacccaacccgtttcgggt 1260

QY 1261 ATTGGTAAAGTCCAAAGCAAACTGGTCCCTGCATCCCTAA 1296

DB 1261 attggtaaagtccaaagcaaaactggctcgatccctaa 1296

RESULT 2

XX X57309

ID X57309 standard; DNA; 8418 BP.

XX X57309;

XX X57309;

DT 26-JUL-1999 (first entry)

XX Sugar beet T-DNA containing cp4/epsps #2.

DE Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;

XX 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX Beta vulgaris.

XX W0923232-A1.

PN X57309

XX 14-MAY-1999.

XX 29-OCT-1998; 98WO-EP06859.

XX 31-OCT-1997; 97US-0112003.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Mannerloef M, Steen P, Tenning PP;

XX

PT glyphosate, avoids constitutive expression and minimises development
XX of herbicide tolerant weeds
PS
XX
XX Example 3; Fig 7; 59pp; English.
CC A chemically inducible plant gene expression cassette which comprises an
CC inducible promoter linked to a gene (I) that confers resistance to a
CC herbicide, is claimed. (I) imparts resistance to N-phosphonomethyl-
CC glycine (glyphosate) or its salts, but may also be a gene for resistance
CC to, e.g. chloracetanilides, glufosinate, sulphonyl ureas, imidazoles,
CC etc. The inducible promoter (e.g. alca, alcr, alda or other alcr-induced
CC gene promoter) is operatively linked to an alcr regulator sequence.
CC Induced expression of (I) avoids the risk that constitutive expression
CC may interfere with plant development; allows volunteer plants to be
CC controlled by herbicide applied without inducer and minimises the chance
CC that herbicide-resistant strains of weeds will arise. The expression
CC cassette is strictly controlled and suitable for general use in plants
CC (both mono- and dicotyledons). The alca/alcr gene switch was exemplified
CC with genes conferring resistance to glyphosate. The switch was used to
CC drive inducible expression of glyphosate oxidase (GOX) in plants.
CC Switchable GOX was expressed alone or in conjunction with constitutive
CC expression of 5-enol-pyruvylshikimate 3-phosphate (EPSPS) CP4. Constructs
CC were optimised for expression in mono- and dicotyledonous crop species.
CC The present sequence comprises a fusion of the GOX gene fused to the
CC chloroplast transit sequence 1 from Arabidopsis RUBISCO (CPT1). This
CC sequence was ligated into pMJB1 (see T85666) and used in construction of
CC dicot vectors.
XX
SQ Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

Query Match 93.0%; Score 1205.2; DB 18; Length 1631;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1283; Conservative 0; Mismatches 13; Indels 50; Gaps 2;
QY 1 ATGGCTGAGAACACACAGAGGTGGTATCGCTGGAGCTGGATCGTTGGTTCGACT 60
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DB 334 gctttgatgcttcaacgctcggtgatcaaggttaccttggatgatccaaacccacacaggt 393
QY 121 GAGGTGCTTCTTTTCGGTAACGCTGGTGTGCTTCAACGGTTCTCCGTTGTTCACATGTCC 180
DB 394 gaaggtgcttcttcgttaacgctggttgcctcaacggttcctccgttgttccaatgtcc 453
QY 181 ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGGCTTCTTGACC----- 223
DB 454 atgccaggaacacttgactagcgttccaaagtggcttcttgatcctctgttgatccaagc 513
QY 224 -----CAATGGGTCATTTGTCATTCCTGCTTTCAGTACTTTCACACCATCATGCTTG 275
DB 514 ttacggatccaatgggttccatgtccatccgttttcagctacttccaaacacatgctcttg 573
QY 276 GTTGATTCGTTTCTGCTTGTCTGGAGACCAACAAAGGTGAAGGAGCAAGCTAAGGCAC 335
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XX
AC Q20834;
XX
DT 01-MAY-1992 (first entry)
XX
DE Modified glyphosate oxidoreductase gene.
XX
KW Recombinant; GOR; resistance; ss.
XX
OS Bacterial isolate LBAA.
XX
FH Key Location/Qualifiers
FT 9..1304
FT CDS /tag= a
FT /notes 'encodes wlld type glyphosate oxidoreductase'

```
XX PN W09200377-A.
XX PD 09-JAN-1992.
XX PP 24-JUN-1991; 91WO-US04514.
XX PP 24-JUN-1991; 91US-0717370.
XX PR 23-JUN-1990; 90US-0343236.
XX PS (MONS ) MONSANTO CO.
XX PI Kishore GM, Barry GF;
XX PR WPI; 1992-041559/05.
XX DR P-PSDB; R20642.
XX PT Gene encoding glyphosate oxido-reductase enzyme - used to
XX PT transform plants to produce plants tolerant to glyphosate
XX PT herbicide
XX PS Claim 1; Page 102; 142pp; English.
XX CC The sequence is that of the gene encoding a glyphosate oxidoreductase
XX CC (GOR) enzyme which has been modified using mutagenic primers. The
XX CC gene sequence was redesigned to eliminate as much as possible the
XX CC following sequences or sequence features (while avoiding the
XX CC introduction of unnecessary restriction sites), stretches of G's
XX CC and C's of 5 or more; A + T rich regions (predominantly) that could
XX CC function as polyadenylation sites or potential RNA destabilisation
XX CC regions, and codons not frequently found in plant genes. The G + C%
XX CC of the GOR gene was reduced from 56% in the manipulated version
XX CC (Q20833) to 52% in the modified version. However it still encodes
XX CC the wild type GOR enzyme. It was obt'd. from bacterial isolate LBAA.
XX CC It is used to transform plants such that they express the enzyme
XX CC sufficiently to enhance the glyphosate tolerance of the plant.
XX CC Transformed plants resistant to glyphosate can be obt'd. so that
XX CC weeds can be selectively controlled in fields contg. crops.
XX CC See also Q20832-Q20841 and Q22705.
XX PS Sequence 1321 BP: 293 A; 349 C; 339 G; 340 T; 0 other;

Query Match 77.9%; Score 1009.6; DB 13; Length 1321;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1117; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAAGAGGTGGTATCGCTGGAGCTGGAATCGTTGGTGGTCACT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGTGATTCACCAACCCACCAAGGT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 69 gctttgatgttcaacgtcgtggattcaagtcacgttgattgaccggaacccctctcggc 128
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 GAAGGTGCTTCCTTTTCGGTACGCTGGTGGTTCAACGGTTCCTCGCTGGTTTCCAAATGTCC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 129 gaagtgcatcgtttgggaaatgcgcgatgtctcaacggctcactcgtcgtccctatgtcc 188
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 ATGCCAGCAACTTGACTACGCTTCCAAAGTGGCTTCTTTCACCCCAATCGGTCCATTGTCC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 189 atgcgggaaacttgacgagcgtgcgaagtgcgcctcttgaccgagtggggcccgttgca 248
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 ATCGGTTAGCTACTTTCACCAACCATCATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 249 atccggttcagctattttccaaaccatcatgcccctggttgattcgtcttctgttagccgga 308
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 AGACCAACCAAGGTGAAGGAGCAAGCTTAAGCCACTCCGTAACCTTCATCAATCCACATGTG 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 309 agacaaacaaggltgaagggagcaggcgaaagcactccgcgaatctcatcaagtccacggtg 368
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTTCACTAGCTAGCCACCTTATCCGTCACGAAGT 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 369 cctctgtcaagtcaatttgcggaggaggctgagtgcggccatctgtatccgccatgaaggt 428
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCCTGGAGGTGGGAACATT 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 catctgaccgtatatcgtggagaagcagacttcgccaagaccgcggaggttggaactg 488
Qy 481 CGTCGCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCCCTGATGCATTCGCTGATTTTCAT 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 489 cggcgtctcaacgggttcgcacgcagatcctctctctgctgcttgcgtgatttcgat 548
Qy 541 CCTAACTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGAACGGTGCACACCATC 600
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 549 cctaaactgtcgaatgcttttaccgaaggcattctctatagaagaagacggttcacacgatt 608
Qy 601 AACCCACAAGGTCTCGTGAATCTCTTCTTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 609 aatccgcaaggctcgtgaccctcttcttcggcgctttatcgcgaacggttgcggaattt 668
Qy 661 GTGTCTGCTCGTGTTCGGATTCGAGACTTCGAGAGTTCGCTCTCAAGGATGATCACCACC 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 669 gtaactgcgctgcatcgcggttttgagactgaaggctcgtctctcaaaaggcattacaacc 728
Qy 721 ACCAACGGTGTCTTGTGCTGTGATGCAGCTGTTTGTTCAGCTGGTGCACACTCCAAGTCT 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 729 actaacggttcttcgctgttgatgcagctgttcttcgagctggcgacactctcaatca 788
Qy 781 CTTGCTAACCTCCCTTGTGTGATGACATCCCATTTGGATACCGAACCTGGATACCATCGTG 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 789 ctgttaattcgcgtagcgcatgacatccgctcgatcaccgaacgtggtatcatatcgtc 848
Qy 841 ATGCCCAACCCAGCAAGCTGCTCCAGATTTTCCAACTACCGATGCTTCTGGAAATTTTCATC 900
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 849 atcgcgaatccggaagcgcctccacgcatctccgacgaccgcatgctcaggaaaaattc 908
Qy 901 GCTACTCCTTATGAGATGGGTCTTCGTGGTGTCTGCAACCGTTGAGTTTCGGTGGTCTCACT 960
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 909 gcgaacactatggaaatgggtcttcctcgttgcgtggttactgttcgagtttgcgtgg 968
Qy 961 GCTGCTCCTTAACGTGAAGCGTGTCTCAGCTTCTCTACACTCAGCGTCTGAAGTTGCTTCCA 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 969 gctgctcctaactggaaacgtgcgcattgctctatatacgcaacgctcgaaaactcttcca 1028
Qy 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTTACTTCCAAAGTGGATGGTTCCTGCTCCAGC 1080
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1029 gccctcgcctcgcagttcttgaagaacgatatctccaaatggatgggttttctcctcagc 1088
Qy 1081 ATCCACGATTCCTCCAGTGTGGTGGTCTACCGCTACTCCAGACGTTATCTACGCT 1140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1089 attcctgattctctctccagtgattgcgtgcgaactcgtacaccccgacgtaactatgct 1148
Qy 1141 TTCGGTCAACGCTCACCTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTGCTTCTGAG 1200
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1149 ttgtgtcacggtcatctcgttatgacaggtgctccaatgactgcaactctcgtctcag 1208
Qy 1201 CTCTCCAGGTGAGAGACCTCTATCGACATCTCTTTCATTCATTCGACCAACCGTTTCGGT 1260
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1209 ctctcgcaggcgaaaagacctcaatcgacatttgcctctgcacccaacacggttgggt 1268
Qy 1261 ATTGGTAAAGTCCAAAGCAACTGGTCTTCATCTCTAA 1296
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1269 attggcaaatccaaagcaaacgggtccgggcaagttaa 1304

RESULT 5
ID Q20833 standard; DNA; 1321 BP.
XX AC Q20833;
XX XX
DT 01-MAY-1992 (first entry)
XX DE Manipulated glyphosate oxidoreductase gene.
XX XX
```


Db 1197 atccccgattcgctccccgtgatggcgccggcaaccgcggacacccgcagctaatctatgct 1256

Qy 1141 TTCGGTCACGGTCACCTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTGTTTCTGAG 1200

Db 1257 ttccggccatggtcatctcggcatgacagggcgccgatgaccgcgaacgctcgtctcagag 1316

Qy 1201 CTCTCTCCGAGTGAGAACCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260

Db 1317 ctctctcagcgcaagaaacccaatcgacatttcgcccttcgcaccaaaaccgctttggt 1376

Qy 1261 ATTGGTAAGTCCAAAGCAAACTGGTCTCGCATCCTTAA 1296

Db 1377 attcgcaaatccaagcaaaacgggtcccgcaagtttaa 1412

RESULT 8

X57305

ID X57305 standard; DNA; 8012 BP.

XX

AC X57305;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps fragment.

XX

XX

KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX

PN WO9923232-A1.

XX

PD 14-MAY-1999.

XX

XX 29-OCT-1998; 98WO-EP06859.

XX

PR 31-OCT-1997; 97US-0112003.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX

PI Mannerloef M, Steen P, Tenning PP;

XX

DR WPI; 1998-313347/26.

XX

XX Glyphosate resistant transgenic sugar beet plants

XX

PS Claim 8; Page 24-29; 55pp; English.

XX

CC This invention describes a novel sugar beet plant, including its

CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase

CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium

CC mediated transformation with a gene allowing expression of cp4/epsps

CC in plants, where the plant lacks both right and left T-DNA border

CC sequences. The transgenic sugar beet plants of the invention are capable

CC of tolerating herbicide treatment with glyphosate (also known as

CC N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.

XX

SQ Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;

Qy 1 ATCGCTGAGACCAACAGAGGTTGGTATCGCTCGAGCTGGAATCGTTGCTTTGCACT 60

Db 7116 atgsgctgagaaccacaagaaggttggtatcgctgagctggaatcgttggtgttgcaact 7175

Qy 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACGAGT 120

Db 7176 gctttgatgcttcaacgctcgtggaattcaaggttaccttgattgatccaaacccaccaggt 7235

Qy 121 GAAGTGTCTTCTTTCGGTAAACGCTGGTTCCTTCAACGGTTCCTCGTTCCTTCCAAATGTC 180

Db 7236 gaagggtctcttcggtaacgctggttgcttcaacggttctctcgttgcttccaatgtcc 7295

Qy 181 ATGCCAGGAACACTTCAGCTAGGTTTCCAAAGTGGCTTCCTTGACCCCAATGGGTCCATTTGCC 240

Db 7296 atgcaggaacttgactagcgttccaaagtggctctcttgacccaatgggtccatgtgtcc 7355

Qy 241 ATCCGTTTCAGCTACTTTTCCAAACCATCATGCTTGGTTGATTTCGTTTCTTGGTCTGCTGA 300

Db 7356 atccggttcagctacttccaaacctaatgctctggttgattcgttcttctgcttgctgga 7415

Qy 301 AGACCAACAAGGTGAAGGAGCAAGCTTAAGGCATTCCTTAACCTCATCAAGTCCACTGTG 360

Db 7416 agaccaaacaagggtgaaggagcaagctaacctccgtaacctcatcaagctccactgtg 7475

Qy 361 CCTTTGATCAAGTTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTTATCCGTCACCAAGGT 420

Db 7476 cctttgatcaagtccttggtgagaggtgatgtagccaccttatccgtccacgaaggt 7535

Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTGGGAACCT 480

Db 7536 caccttaacctgtaccgttgagagaagcagacttcgccaaggacctggaaggttgggaactt 7595

Qy 481 CGTGTCTCAACGGTGTTCGTACTCAAAATCCCTACGCGTGTATGCAATTCGCTGATTTCCGAT 540

Db 7596 cgtcgtctcaacgggtgttctcgtaactcaaatcctcagcgtgtagcatlgcgtgatttctgat 7655

Qy 541 CCTAACTTGTCTCACGCCCTTTACCAAGGGAATCCTTATCGAAGAGAACGGTCACACCATC 600

Db 7656 cctaaacttgtctcagcctttaccaaagggaatcctta tcgaagagaacgggtccacccatc 7715

Qy 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTTCCTTTCATCGCTTAACGGTGGAGAGTTC 660

Db 7716 aaccacaaggctctgtaactctctgttctcgtctgttcaatcgctlaaagggttggagagttc 7775

Qy 661 GTGTCTGCTGTGTTATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATACACCACC 720

Db 7776 gtgtcgtcgtgttatctcggaattcgagactgaaggtcgtgctctcaagggtatccacc 7835

Qy 721 ACCAAGGTTCTTTCGCTGTTGATGCACGCTGTTGTTGAGCTGGTGCACACTCCAGTCT 780

Db 7836 accaaggttctctgtgtgtgatgagctgtgtgtcagctgtgtgtcagctgtgtgcacactccaagtct 7895

Qy 781 CTTCGTAACCTCCCTGGTGATGACATCCCATTCGATACCGAACGTCGATACCCATCGTG 840

Db 7896 ctgctaactccctggtgatgagatcccatggataccgaaacgttggataccacatcgtg 7955

Qy 841 ATCCGCCAACCCAGAGCTGCTCCACGTTATTCCAACTACCGATGCTTCCTGGAAAGTTC 897

Db 7956 atgcgaaccacagaagctgctccacgtatcccaactaccgatgctctcgtggaagtcc 8012

RESULT 9

X57308

ID X57308 standard; DNA; 8798 BP.

XX

AC X57308;

XX

DT 26-JUL-1999 (first entry)

XX

DE Sugar beet T-DNA containing cp4/epsps.

XX

KW Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;

KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;

KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.

XX

OS Beta vulgaris.

XX

PN WO9923232-A1.

XX

PD 14-MAY-1999.

XX 29-OCT-1998; 98WO-EP06859.
XX 31-OCT-1997; 97US-0112003.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Mannerloef M, Steen P, Tenning PP;
XX WPI; 1999-313347/26.
XX
XX Glyphosate resistant transgenic sugar beet plants
XX
XX Claim 11; Page 31-36; 55pp; English.
XX
XX This invention describes a novel sugar beet plant, including its
XX descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
XX (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
XX mediated transformation with a gene allowing expression of cp4/epsps
XX in plants, where the plant lacks both right and left T-DNA border
XX sequences. The transgenic sugar beet plants of the invention are capable
XX of tolerating herbicide treatment with glyphosate (also known as
XX N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
XX
XX Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;
SQ

Query Match 69.2%; Score 897; DB 20; Length 8798;
Best Local Similarity 100.0%; Pred. No. 8.1e-266;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAGAAGGTGGTATCGCTGGAGCTGGAATCGTTGGTTTGCACCT 60
|||||
Db 7205 atggctgagaaacacacagaaggttggtatcgctggagctggaatcgttggtttgcact 7264
|||||

QY 61 GCTTTGATGCTTCAACGTCGCTGGATTCAAGTTACCTTGATGATCCAAACCCACCAAGGT 120
|||||
Db 7265 gctttgatgcttcaacgctcggtgattcaaggtttaccttgattgatccaaacccaccaggt 7324
|||||

QY 121 GAAGGTGCTTCTTCGGTAACGCTGCTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180
|||||
Db 7325 gaaggcgctcttcctcggttaacgctggtgcttcaacggttcctcccgttgttccaaagctcc 7384
|||||

QY 181 ATGCCAGGAACTTGACTACGCTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCATTGTCC 240
|||||
Db 7385 atgccaggaacttgactagcttccaaagtggcttcttgacccaatgggtccatgtcc 7444
|||||

QY 241 ATCCGTTTCAGCTACCTTCCAAACCATCATGCTGCTGGTTGATTCGTTTCCTGTTGCTGGA 300
|||||
Db 7445 atccggttcagctactttccaaacatcatgcttggtgattgattcgttcttctgcttgctgga 7504
|||||

QY 301 AGACCAAAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360
|||||
Db 7505 agaccaaaacaaggtgaaggagcaagctaaaggcaactccgtaacctcatcaagtcactgtg 7564
|||||

QY 361 CTTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGGCACCTTATCCGTCCACGAAGGT 420
|||||
Db 7565 cetttgatcaagtcccttgctgaggaggtgatgctagccaacttatccgtcacgaaggt 7624
|||||

QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCCAAGACCGGTGGAGTGGGAACATT 480
|||||
Db 7625 caccctaccgtgtaccgtggagaagcagacttcgcaaggaacggtggaggttgggaactt 7684
|||||

QY 481 CGTCGCTCAACGGTGTTCGTACTCAATCCCTCAGGCGTGATGTCATTGCGTGTGATTCGAT 540
|||||
Db 7685 cgtcgtctcaacaggttgctcgtactcaaaacctcagcgcgtgagctgctgattccgat 7744
|||||

QY 541 CCTAACTTCTCAGCCCTTTACCAAGGAATCCTTTATCGAAGAGAACGGTTCACACCATC 600
|||||
Db 7745 cctaaactgtctcagccctttaccaagggaaatccttlatcgaagagacggttcacacalc 7804
|||||

QY 601 AACCCACAAGTCTCGTGACTCTCTTCTGCTGTTTCATCGCTAACCGTGGAGAGTTTC 660
|||||

Db 7805 aaccacaaggctcgtgactctctgttctcgtcgttctcgtcgttaacggtgagagttc 7864
|||||

QY 661 GTGCTGCTGCTGTTATCGGATTTCGAGACTGAAGGTGCTGCTCTCAAGGCTATCACCACC 720
|||||

Db 7865 gtgctcgtcgtcttctcgttcgagactcgagagctgagaggtcgtcgtctcgaaggtatcacacc 7924
|||||

QY 721 ACCAACGGTGTCTTCTGCTGTTGATGTCAGCTGTTGTTGTCAGCTGCTGCACACTCCAACTCT 780
|||||

Db 7925 accaagcgtgttctcgtctgattgatcagctgttgttgacgtggtgcacactccaaagtct 7984
|||||

QY 781 CTTCCTTAACCTCCCTTGGTGTGATGATACATCCCATTCGATACCCAACTCGATACCATCTGTG 840
|||||

Db 7985 cttgctaactcccttggtgatgacatcccatgtgataccgaagctggataccacatcgtg 8044
|||||

QY 841 ATCGCAACCCAGCAAGCTGCTGCACGCTATTTCCAACTACCGATGCTTCTGGAAGTTTC 897
|||||

Db 8045 atcgcaaacccagaagctgctcacgtattcccaactacacgactcgtcttcttggaagttc 8101
|||||

RESULT 10
V73805
ID V73805 standard; DNA; 32207 BP.
XX
AC V73805;
XX
DT 25-FEB-1999 (first entry)
XX
DE KSHV LUR DNA (nucleotides 105,301-137,507).
XX
KW Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
KW dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;
KW diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV;
KW glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2;
KW v-adi; G-protein coupled receptor; FGARAT; ds.
XX
OS Kaposi's sarcoma-associated herpesvirus.
XX
PN US5849564-A.
XX
PD 15-DEC-1998.
XX
PF 29-NOV-1996; 96US-0770379.
XX
PR 29-NOV-1996; 96US-0770379.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX WPI; 1999-069741/06.
XX
PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
PT dihydrofolate reductase and is useful for treatment, prophylaxis
PT or diagnosis of Kaposi's sarcoma
XX
PS Disclosure; Column 155-182; 109pp; English.
XX
XX This sequence is a fragment of the Kaposi's sarcoma-associated
CC herpesvirus (KSHV) LUR (long unique region). This fragment contains
CC coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67
CC which encodes tegument protein IV, ORF68 which encodes a glycoprotein,
CC ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D,
CC ORF73 which encodes immediate early protein (IEP), K14 which encodes
CC OX-2 (v-adi), ORF74 which encodes G-protein coupled receptor, ORF75
CC which encodes tegument protein/FGARAT, K15. KSHV is a new human
CC Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the
CC most common form of neoplasm occurring in persons with acquired immune
CC deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,
CC prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma
CC and for detecting expression of a DNA virus associated with Kaposi's
CC sarcoma in a cell.
XX

Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;

```
Query Match      3.1%; Score 39.8; DB 19; Length 137507;
Best Local Similarity 47.7%; Pred. No. 0.3;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 727 GGTGTTCTTGGTGTGATGAGCTGTTGTCAGCTGGTGCACACTCCAAAGTCCTTTGGCT 786
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125142 gctgctcatcctgctgctgctcatcctgctgctgctgctgctgctgctgctgct 125201

QY 787 AACTCCCTTGGTGTATGATCCCATTTGGATACCGAAGCTGGATACCAATCGTGATCGCC 846
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125202 catcctgctgctgctcatcctgctgctgctgctcatcctgctgctgctgctgctgct 125261

QY 847 AACCCAGAAAGCTGCTCCACAGTATTCCAACTACCGATGCTTCTTGAAAGTTTCATCGCTACT 906
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125322 catcctgctgctgctcatcctgctgctgctgctcatcctgctgctgctgctgctgct 125381

QY 907 CCTATGGAGATGGGTCCTGCTGTTGCTGGAAACCGTTGAGTTGCGTGGTCTCAGTGGCTGCT 966
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125322 catcctgctgctgctcatcctgctgctgctgctcatcctgctgctgctgctgctgct 125381

QY 967 CCT 969
  |||||
Db 125382 cat 125384

RESULT 12
X89891/c
ID X89891 standard; DNA; 397 BP.
XX AC X89891;
XX DT 05-NOV-1999 (first entry)
XX DE Spinocerebellar ataxia type III (SCAIII) gene fragment.
XX KW Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation;
KW PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
KW SCAIII syndrome; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT repeat_region 137..355
FT /*tag= a
FT repeat_unit 137..139
FT /*tag= b
FT /*note= "trinucleotide repeat"
XX PN WO9943852-A1.
XX PD 02-SEP-1999.
XX PF 18-FEB-1999; 99WO-KR00078.
XX PR 26-FEB-1998; 98KR-0006278.
XX (JIND/) JIN D K.
PA (SMSU ) SAMSUNG FINE CHEM CO LTD.
XX JIN DK;
XX WPI; 1999-527634/44.
XX DR Diagnosis of spinocerebellar ataxia type III (SCA III) syndrome
PT using techniques which ensure highly accurate diagnosis
XX Claim 1; Page 12-13; 28pp; English.
XX The invention relates to the diagnosis of spinocerebellar ataxia type
CC III (SCAIII) syndrome using reverse dot hybridisation or PCR-microplate
CC hybridisation (PCR-MPH). The method comprises attaching a portion of the
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CC SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit
CC (the present sequence) to a substrate, and hybridising with amplified
CC testee genomic DNA containing copies of the trinucleotide units. PCR
CC amplified with labeled primers (X89889-90). The new method is useful for
CC diagnosis of SCAIII syndrome, and for determining the severity of the
CC disease. The present sequence represents the SCAIII gene fragment
CC containing 73 trinucleotide (TNR) repeats.
XX SQ Sequence 397 BP; 124 A; 104 C; 104 G; 65 T; 0 other;

Query Match      2.9%; Score 37.4; DB 20; Length 397;
Best Local Similarity 47.0%; Pred. No. 0.084;
Matches 116; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 726 CGGTGTTCTTGTCTTATGATGACGCTGTTTGGACGCTGGTGCACACTCCAAAGTCTCTTGC 785
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298

QY 786 TAATCCCTTTGGTGTATGACATCCCATTTGGATACCGAAGCTGGATACCAATCGTGATCGC 845
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238

QY 846 CAACCCAGAAAGCTGCTCCACGATATTCCAACTACCGATGCTTCTTGAAAGTTTCATCGCTAC 905
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 178

QY 906 TCCTATGAGATGGTCTTCTGCTGTTGCTGGAAACGTTGAGTTGCTGCTCAGTGGCTGTC 965
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 118

QY 966 TCCTAAC 972
  |||||
Db 117 CTGAAC 111

RESULT 13
Z45602/c
ID Z45602 standard; cDNA; 6558 BP.
XX AC Z45602;
XX DT 06-APR-2000 (first entry)
XX DE cDNA sequence of a murine OPA gene.
XX KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
KW mental retardation; autism; depression; bipolar affective disorder;
KW hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
XX OS Mus sp.
XX PN WO9955915-A2.
XX PD 04-NOV-1999.
XX PF 29-APR-1999; 99WO-US09365.
XX PR 29-APR-1998; 98US-0083465.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (IOWA ) UNIV IOWA RES FOUND.
XX Philibert RA, Ginns EI;
XX WPI; 2000-126357/11.
XX DR Identification of polymorphisms in the PCTG4 region of xql3 for
PT diagnosing mental retardation or autism .
XX Example 7; Page 78-81; 100pp; English.
XX The present sequence represents the cDNA sequence of the murine OPA
```

PI	Philibert RA, Ginns EI;
XX	
DR	WPI; 2000-126357/11.
XX	
PT	Identification of polymorphisms in the PCTG4 region of Xql3 for
PT	diagnosing mental retardation or autism -
XX	
PS	Example 7; Page 68-71; 100pp; English.
XX	
CC	The present sequence represents the cDNA sequence of the human OPA
CC	gene, which is derived from the human PCTG4 region of chromosome Xql3.
CC	Polymorphisms in this region are associated with mental retardation,
CC	autism, depression, bipolar affective disorder or hypothyroidism.
CC	One 12 bp insertion polymorphism occurs within the coding region of
CC	the human OPA gene, and introduces a 4 amino acid insertion in a
CC	putative OPA domain. This domain has been shown to be involved in tissue
CC	specific expression. Another polymorphism consists of a pentanucleotide
CC	repeat approximately 7 kb upstream of the 12 bp polymorphism. Another
CC	polymorphisms consists of a dinucleotide repeat approximately 4.5 kb
CC	downstream of the 12 bp polymorphism. The specification describes a
CC	method for screening for polymorphisms in a PCTG4 nucleic acid sequence
CC	obtained from a subject. The PCTG4 related sequences within the q13
CC	region of the X chromosome have polymorphisms associated with
CC	neuropsychiatric disorders. The methods can be used to screen for the
CC	presence of a heritably linked form of mental retardation, autism,
CC	depression, bipolar affective disorder or hypothyroidism.
XX	
SQ	Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;
Query Match	2.7%; Score 35.2; DB 21; Length 6794;
Best Local Similarity	54.7%; Pred. No. 1.7;
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps	
QY	543 GCTAACGGTGCAGAGTCTGCTGCTGCTGTTATCGGATTCGAGACTGAAGTCTGCT 702
Db	6289 GCTGCTGCCCGAGGATCTGCTGCTGCTGCTGCTGCCGATGTGGTACTGCTGCTGCT 6230
QY	703 CTCGAAGGGTATCACCAACGCGTGTCTTGCTGTTGATGCAGCTGTTGTGCAGCT 762
Db	6229 GCTGCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6170
QY	763 GGTGCACA 770
Db	6169 GCTGCTCA 6162
RESULT/ 15	
TI13952/c	
ID	TI13952 standard; DNA; 2004 BP.
XX	
AC	TI13952;
XX	
DT	15-AUG-1996 (first entry)
XX	
DE	Maize-optimized VIPI1A(a) gene.
XX	
XX	
KW	Pesticide; insecticide; biological control agent; Lepidoptera;
KW	Coleoptera; transgenic plant; maize; Zea mays; Insect resistance;
KW	VIPI; Bacillus cereus; western corn rootworm;
KW	Diabrotica vergifera vergifera; ss.
XX	
OS	Synthetic.
XX	
PN	WO9610083-A1.
XX	
PD	04-APR-1996.
XX	
PF	27-SEP-1995; 95WO-EP03826.
XX	
PR	05-JUN-1995; 95US-0463483.
XX	
PR	28-SEP-1994; 94US-0314594.
XX	

```
PA (CIBA ) CIBA GEIGY AG.
XX
PI Carr B, Desai NM, Duck NB, Estruch JJ, Kostichka K;
PI Koziel MG, Mullinsma, Nye GJ, Warren GW;
XX
DR WPI; 1996-200921/20.
XX
XX Bacillus strain producing insecticidal protein during vegetative
PT growth - used in the control of Lepidoptera and Coleoptera pests
XX
PS Claim 48; Page 136-138; 242pp; English.
XX
CC A synthetic gene (Tl3952) comprises a version of the Bacillus
CC cereus strain AB78 80-kDa Vip1A(a) gene (see also Tl3941) with
CC codon usage optimised for expression in maize. The synthetic
CC gene encodes Vip1A(a) (R91240), an insect-specific protein
CC showing activity against western corn rootworm. Vip1A(a) can be
CC expressed in transgenic maize to protect the plant from insect
CC attack.
XX
SQ Sequence 2004 BP; 586 A; 659 C; 530 G; 229 T; 0 other;

Query Match 2.7%; Score 35; DB 17; Length 2004;
Best Local Similarity 44.8%; Pred. No. 1;
Matches 134; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 735 TCCTGTTGATGCAGCTGTTGTCAGCTGGTGACACTCCCAAGTCTCTTGTAACTCCCT 794
Db ||||| || | ||| ||| || | || | ||| ||| |||
QY 1546 TGCTGATGGGGTTGCTCTTGATGTTGGCGGATGATGCCAGCGGCTTGTTGTCCT 1487
Db || ||| || | ||| ||| || | || | ||| ||| |||
QY 795 TGGTGATGACATCCCATTTGGATACCGAACGTTGGATACCACTCGTGATCGCCCAACCCAGA 854
Db || ||| || | ||| ||| || | || | ||| ||| |||
QY 1486 TGTTCACGTTTCACGGTCTTGGTGGTGGTGGTATATCTCCCGTCGATGGTGATCGC 1427
QY 855 AGCTGCTCCACGATATCCCACTACCGATGCTTCTGGAAAGTTTCATCGCTACTCCTAACTG 914
Db || ||| || | ||| ||| || | || | ||| ||| |||
QY 1426 ACTGGGTGTTCTTCGCTCTTATGATACAGGCTGATGTAGTACGCGGTTCCTTGTCA 1367
QY 915 GATGGGTCTTTCGTGTTGCTGGAACCGTTGAGTTGCGTGGTCTCACTGCTGCTCTAACTG 974
Db || ||| || | ||| ||| || | || | ||| ||| |||
QY 1366 GCCTTCCTGGCGCTCGGTGTTTCAGGGTCAGTTGGCGTCGGGGTTGTTGCTGCTACT 1307
QY 975 GAAGCGTGCTCAGCTCTCTACACTCAGCTCGTAAGTTGCTTCCAGCTCTCGCTCCTG 1033
Db || ||| || | ||| ||| || | || | ||| ||| |||
QY 1306 GCTTCTTGGCGTTGTTGCCCGCTCAGCATGTTGGTGTGGTCCACTTCCCGATGCTG 1248
```

Search completed: January 1, 2001, 03:45:17
Job time: 20325 sec

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCTGAGAACACACAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACT	60
Db	1	ATGGCTGAGAACACACAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACT	60
QY	61	CTTTTGATGCTTCAACGTCGTGATTCAGAGTTACCTTGATTCATCCAAACCCACCAAGT	120
Db	61	CTTTTGATGCTTCAACGTCGTGATTCAGAGTTACCTTGATTCATCCAAACCCACCAAGT	120
QY	121	GAAGGTGCTTCTTTCGGTACGCTGGTTGCTTCAAGGGTTCCTCCGTTGTTCCTCAATGTC	180
Db	121	GAAGGTGCTTCTTTCGGTACGCTGGTTGCTTCAAGGGTTCCTCCGTTGTTCCTCAATGTC	180
QY	181	ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGGCTTCTTGACCAATGGGTTCCTATGTC	240
Db	181	ATGCCAGGAACCTTGACTAGCTGTTCCAAAGTGGCTTCTTGACCAATGGGTTCCTATGTC	240
QY	241	ATCCGTTTACGCTACCTTCCAAACATCATCCCTTGGTTGATTCCTTTCCTTGGTGGGA	300
Db	241	ATCCGTTTACGCTACCTTCCAAACATCATCCCTTGGTTGATTCCTTTCCTTGGTGGGA	300
QY	301	AGACCAACAAAGTGAAGGAGCAAGCTAAGSCACTCGTAAACCTCATCAAGTCCACTGTG	360
Db	301	AGACCAACAAAGTGAAGGAGCAAGCTAAGSCACTCGTAAACCTCATCAAGTCCACTGTG	360
QY	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
Db	361	CCTTTGATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT	420
QY	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCAAGAACCGTGGAGTTGGGAACCTT	480
Db	421	CACCTTACCGTGTACCGTGGAGAGCAGACTTCCGCAAGAACCGTGGAGTTGGGAACCTT	480
QY	481	CGTCGCTCAACGSGTTCCTACTCAATCCTCAGCGCTGATGCATTCGCTGATTCGAT	540
Db	481	CGTCGCTCAACGSGTTCCTACTCAATCCTCAGCGCTGATGCATTCGCTGATTCGAT	540
QY	541	CCTAACTGTCTCACGCCCTTTACCAAGGAATCCTTATCGAAGAACCGTTCACACATC	600
Db	541	CCTAACTGTCTCACGCCCTTTACCAAGGAATCCTTATCGAAGAACCGTTCACACATC	600
QY	601	AACCCACAAGGTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGCTGGAGAGTTC	660
Db	601	AACCCACAAGGTCGTGACTCTCTTGTTCGTCGTTTCATCGCTAACGCTGGAGAGTTC	660
QY	661	GTCTGCTGCTGTTATCGGATTCGAGACTGAAGTGCCTCTCAAGGCTATCACACC	720
Db	661	GTCTGCTGCTGTTATCGGATTCGAGACTGAAGTGCCTCTCAAGGCTATCACACC	720
QY	721	ACCAAGGTTCTTCTGCTGTTGATGAGCTGTTGCTTGCAGCTGGTGACACTCCAAGTCT	780
Db	721	ACCAAGGTTCTTCTGCTGTTGATGAGCTGTTGCTTGCAGCTGGTGACACTCCAAGTCT	780
QY	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAACTGGATACCAATCGTG	840
Db	781	CTTGCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAACTGGATACCAATCGTG	840
QY	841	ATCGCCAAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAGTTCATC	900
Db	841	ATCGCCAAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAGTTCATC	900
QY	901	GCTACTCCTATGAGATGGGTCTTCGTTGCTGGAACCGTTGAGTTCGCTGCTCACT	960
Db	901	GCTACTCCTATGAGATGGGTCTTCGTTGCTGGAACCGTTGAGTTCGCTGCTCACT	960
QY	961	GCTGCTCTTAACTTGAAGCGTGCTACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA	1020
Db	961	GCTGCTCTTAACTTGAAGCGTGCTACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA	1020
QY	1021	GCCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAAGTGGATGGTTTCCTCCAAAGC	1080
Db	1021	GCCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAAGTGGATGGTTTCCTCCAAAGC	1080

0;

60

60

120

120

180

180

240

240

300

300

360

360

420

420

480

480

540

540

600

600

660

660

720

720

780

780

840

840

900

900

960

960

1020

1020

1080

1080

RESULT 2

US-08-484-274A-8

; Sequence 8, Application us/08484274A

; Patent No. 5776760

; GENERAL INFORMATION:

; APPLICANT: Kishore, Ganesh M.

; TITLE OF INVENTION: Glyphosate Tolerant Plants

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,274A

; FILING DATE: 07 June 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Patterson, Melinda L.

; REGISTRATION NUMBER: 33,062

; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A

; TELEPHONE: (713)789-2679

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1296 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (synthetic)

US-08-484-274A-8

Query Match

Best Local Similarity 100.0%; Score 1296; DB 2; Length 1296;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCTGAGAACACACAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACT	60
Db	1	ATGGCTGAGAACACACAGAGTTGGTATCGCTGGAGCTGGAATCGTTGGTTGCACT	60
QY	61	GCTTTGATGCTTCAACGCTCGTGGATTCGAAGTTACCTTGATTCATCCAAACCCACCAAGT	120
Db	61	GCTTTGATGCTTCAACGCTCGTGGATTCGAAGTTACCTTGATTCATCCAAACCCACCAAGT	120
QY	121	GAAGGTGCTTCTTTCGGTACGCTGGTTGCTTCAAGGGTTCCTCCGTTGTTCCTCAATGTC	180

Db	121	GAAGGTGCTTCTTTTCGGTAACGCTGGCTTGCCTTCAACGGTTCCTCCGTTGTTTCCAATGTCC	180
Qy	181	ATGCCAGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCAATTGTCC	240
Db	181		
Db	181	ATGCCAGAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGGTCCAATTGTCC	240
Qy	241	ATCCGTTTCAGCTACTTTTCCAAACCATCATGCGCTCGTTGATTCGTTTCTTCTGTTTGGTGGGA	300
Db	241		
Db	241	ATCCGTTTCAGCTACTTTTCCAAACCATCATGCGCTCGTTGATTCGTTTCTTCTGTTTGGTGGGA	300
Qy	301	AGACCAACAAGGTGAAGCAGCAAGCTTAGGCACATCCGTAACCTCATCAAGTCCACATCTG	360
Db	301		
Db	301	AGACCAACAAGGTGAAGCAGCAAGCTTAGGCACATCCGTAACCTCATCAAGTCCACATCTG	360
Qy	361	CCTTTGTATCAAGTCCTTGGCTGAGGAGGTGATGTAGCCACCTTTATCCGTACAGAAAGTT	420
Db	361		
Db	361	CCTTTGTATCAAGTCCTTGGCTGAGGAGGTGATGTAGCCACCTTTATCCGTACAGAAAGTT	420
Qy	421	CACCTTTACCGTGTACCGTGGGAAGCAGACTTTCGCCAAGGACCGTGGAGGTTGGGAATTT	480
Db	421		
Db	421	CACCTTTACCGTGTACCGTGGGAAGCAGACTTTCGCCAAGGACCGTGGAGGTTGGGAATTT	480
Qy	481	CGTCGCTCAACGGTTCGTACTCAATCTCTACCGCTGATGCATTCGCTGATTTTCGAT	540
Db	481		
Db	481	CGTCGCTCAACGGTTCGTACTCAATCTCTACCGCTGATGCATTCGCTGATTTTCGAT	540
Qy	541	CCTAACTTTGTCTCACGCCTTTACCAAGGGAATCTTTATCGAAGAGAACGGTACACCATC	600
Db	541		
Db	541	CCTAACTTTGTCTCACGCCTTTACCAAGGGAATCTTTATCGAAGAGAACGGTACACCATC	600
Qy	601	AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTTCATCGCTAACGGTGGAGAGTTC	660
Db	601		
Db	601	AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTTCATCGCTAACGGTGGAGAGTTC	660
Qy	661	GTGTCTGCTCGTGTATTCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACCAACC	720
Db	661		
Db	661	GTGTCTGCTCGTGTATTCGGATTCGAGACTGAAGGTCTGCTCTCAAGGGTATCACCAACC	720
Qy	721	ACCAACGGTGTTCCTGCTGTGATGCAGCTGTGTTCAGCTGGTGTGCACACTCCAAGTCT	780
Db	721		
Db	721	ACCAACGGTGTTCCTGCTGTGATGCAGCTGTGTTCAGCTGGTGTGCACACTCCAAGTCT	780
Qy	781	CTTGCTAACTCCCTTGGTGATGACATTCGCATTTGGATACCGAACGTGGATACCAATCGTG	840
Db	781		
Db	781	CTTGCTAACTCCCTTGGTGATGACATTCGCATTTGGATACCGAACGTGGATACCAATCGTG	840
Qy	841	ATGCCCAACCCAGAACCTGCTCCAGTATTTCCAACCTACCGATGCTTCTTGGAAGATTCATC	900
Db	841		
Db	841	ATGCCCAACCCAGAACCTGCTCCAGTATTTCCAACCTACCGATGCTTCTTGGAAGATTCATC	900
Qy	901	GCTACTCCTATGGAGATGGGTCTTCGTGTGCTGCAACCGTTGAGTTCGGCTGGTCTCACT	960
Db	901		
Db	901	GCTACTCCTATGGAGATGGGTCTTCGTGTGCTGCAACCGTTGAGTTCGGCTGGTCTCACT	960
Qy	961	GCTGCTCCTAACTGGAAAGGTGCTCACGTTCTTACACTACGCTCGTAAAGTTCCTTCCA	1020
Db	961		
Db	961	GCTGCTCCTAACTGGAAAGGTGCTCACGTTCTTACACTACGCTCGTAAAGTTCCTTCCA	1020
Qy	1021	GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTCCTGTCGAAGC	1080
Db	1021		
Db	1021	GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTCCTGTCGAAGC	1080
Qy	1081	ATCCCAGATTTCCCTTCCAGTATGGTCTGTGCTACCCGTACTCCAGACGTTTATCTACGCT	1140
Db	1081		
Db	1081	ATCCCAGATTTCCCTTCCAGTATGGTCTGTGCTACCCGTACTCCAGACGTTTATCTACGCT	1140
Qy	1141	TTCCGTCACGGTCAACCTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTGTTCTGAG	1200
Db	1141		
Db	1141	TTCCGTCACGGTCAACCTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTGTTCTGAG	1200
Qy	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCTCCAATTCGCAACCAACCGTTTCGGT	1260
Db	1201		
Db	1201	CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCAATTCGCAACCAACCGTTTCGGT	1260

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Qy 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCTCAA 1296
      |||||||
Db 1261 ATTGGTAAGTCCAAGCAAACTGGTCTGCATCTCAA 1296

RESULT 3
US-08-391-339-17
: Sequence 17, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
:   APPLICANT: Kishore, Ganesh M.
:   APPLICANT: Barry, Gerard F.
:   TITLE OF INVENTION: Glyphosate Tolerant Plants
:   NUMBER OF SEQUENCES: 33
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Dennis R. Hoerner, Jr.,
:     ADDRESSEE: Monsanto Co. BB4F
:     STREET: 700 Chesterfield Village Parkway
:     CITY: St. Louis
:     STATE: Missouri
:     COUNTRY: USA
:     ZIP: 63198
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patent in Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/391,339
:     FILING DATE:
:     CLASSIFICATION: 800
:     PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US/08/156,968
:     FILING DATE:
:     APPLICATION NUMBER: US/07/717,370
:     FILING DATE:
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Hoerner, Dennis R., Jr.
:     REGISTRATION NUMBER: 30,914
:     REFERENCE/DOCKET NUMBER: 38-21(10533)
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (314)537-6099
:     INFORMATION FOR SEQ ID NO: 17:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 1296 base pairs
:         TYPE: nucleic acid
:         STRANDEDNESS: double
:         TOPOLOGY: linear
:       MOLECULE TYPE: DNA (recombinant)
:       FEATURE:
:         NAME/KEY: CDS
:         LOCATION: 1..1296
:   US-08-391-339-17

```

	Query Match	99.4%	Score 1288;	DB 1;	Length 1296;	
	Best Local Similarity	99.6%;	Pred. No. 0;	Mismatches	5; Indels	0; Gaps
	Matches 1291;	Conservative	0;			
Qy	1	ATGCGTAGAACCCACAGAAAGGTGGTATCCTCGAGCTGGAATCGTTGGTTTGCACT	60			
Dd	1	ATGCGTAGAACCCACAGAAAGGTGGTATCCTCGAGCTGGAATCGTTGGTTTGCACT	60			
Qy	61	GCTTTGATTGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCACCAAGGT	120			
Dd	61	GCTTTGATTGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCACCAAGGT	120			
Qy	121	GAAGGTGCTCTTTCCGGTTAAGCGTGGTTGCCTTCAACGGTTCCTCCGTTGTTCCAATGTCC	180			
Dd	121	GAAGGTGCTCTTTCCGGTTAAGCGTGGTTGCCTTCAACGGTTCCTCCGTTGTTCCAATGTCC	180			
Ov	181	ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTCTCTTGACCCAAATGGGTGCCATGTGCC	240			

Db 181 ATGCGAGAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC 240
QY 241 ATCGGTTTCAAGTACTTTCACCAACATCATGCTTGGTGTGATTCGTTTCTTGTCTGTGGA 300
Db 241 ATCGGTTTCCGGCTACTTTCACCAACATCATGCTTGGTGTGATTCGTTTCTTGTCTGTGGA 300
QY 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCATCGTAAACCTCATCAAGTCCACTGTG 360
Db 301 AGACCAACAAAGGTGAAGGAGCAAGCTTAAGGCATCGTAAACCTCATCAAGTCCACTGTG 360
QY 361 CTTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT 420
Db 361 CTTTGTATCAAGTCCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTACGAAGGT 420
QY 421 CACCTTACCCTGTACCGTGTGAGAGCACTTCGCCAAGGACCGTGGAGGTGGGAACCTT 480
Db 421 CACCTTACCCTGTACCGTGTGAGAGCACTTCGCCAAGGACCGTGGAGGTGGGAACCTT 480
QY 481 CGTGTCTCAACGGTCTTCTACTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540
Db 481 CGTGTCTCAACGGTCTTCTACTCAAACTCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540
QY 541 CTTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACCAATC 600
Db 541 CTTAACTTGTCTCAGCGCTTACCAAGGGAATCCTTATCGAAGAGAACGGTTCACCAATC 600
QY 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTATCGTACGCTAACGGTGGAGGTTT 660
Db 601 AACCCACAAGGTCTCGTGACTCTCTTGTTCGTCTGTTTATCGTACGCTAACGGTGGAGGTTT 660
QY 661 GTGTCTGCTCTGCTGTTATPCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCA 720
Db 661 GTGTCTGCTCTGCTGTTATPCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACCA 720
QY 721 ACCAAGGTTGTTCTGCTGTTGATGAGCTGTTGTTGCGAGCTGGTGCACACTCCAAGTCT 780
Db 721 ACCAAGGTTGTTCTGCTGTTGATGAGCTGTTGTTGCGAGCTGGTGCACACTCCAAGTCT 780
QY 781 CTTTGTCAACTCCCTTGGTGATGATGCCATTTGGATACCGAAGCTGGATACCAACATCGTG 840
Db 781 CTTTGTCAACTCCCTTGGTGATGATGCCATTTGGATACCGAAGCTGGATACCAACATCGTG 840
QY 841 ATCGCAACCCAGAAAGCTGCTCCACGTATTCACACTACCGATGCTTCTGGAAGTTTCATC 900
Db 841 ATCGCAACCCAGAAAGCTGCTCCACGTATTCACACTACCGATGCTTCTGGAAGTTTCATC 900
QY 901 GCTACTCCTATGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGCTCACT 960
Db 901 GCTACTCCTATGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGCTCACT 960
QY 961 GCTGCTCCTAACTGGAAGCTGCTCAGCTTCTTACACTCACGCTCGTAAGTTGCTTCCA 1020
Db 961 GCTGCTCCTAACTGGAAGCTGCTCAGCTTCTTACACTCGCGCTCGTAAGTTGCTTCCA 1020
QY 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCGTCCTCAAGC 1080
Db 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCGTCCTCAAGC 1080
QY 1081 ATCCAGATATCCCTTCCAGTGATTTGCTGCTGCTACCGGTACTCCAGACGTTATCTACGCT 1140
Db 1081 ATCCAGATATCCCTTCCAGTGATTTGCTGCTGCTACCGGTACTCCAGACGTTATCTACGCT 1140
QY 1141 TTCCGTCACGGTCACCTTCGGTATGACTTGGTGTCTCCAAATGACCAACCTCGTTTCTGAG 1200
Db 1141 TTCCGTCACGGTCACCTTCGGTATGACTTGGTGTCTCCAAATGACCAACCTCGTTTCTGAG 1200
QY 1201 CTCCTCGCAGGTGAGAAGACCTTATCGACATCTCTCCATTCGACACCAACCGTTTCGCT 1260
Db 1201 CTCCTCGCAGGTGAGAAGACCTTATCGACATCTCTCCATTCGACACCAACCGTTTCGCT 1260
QY 1261 ATTGGTTAAGTCCAAAGCAAACTGGTCTCTGCAATCCTAA 1296
|||||

Db 1261 ATTGGTTAAGTCCAAAGCAAACTGGTCTCTGCAATCCTAA 1296
RESULT 4
US-08-484-274A-17
; Sequence 17, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; NAME/KEY: CDS
; LOCATION: 1..1296
US-08-484-274A-17

Query Match 99.4%; Score 1288; DB 2; Length 1296;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGSAATCGTTGCTGTTGCACT 60
|||||
Db 1 ATGGCTGAGAACCAAGAGGTTGGTATCGCTGGAGCTGSAATCGTTGCTGTTGCACT 60
|||||
QY 61 GCTTTGATGCTTCAACGTCGTCGATTCACGTTTACCTTGAATCCAAACCCACCAAGT 120
|||||
Db 61 GCTTTGATGCTTCAACGTCGTCGATTCACGTTTACCTTGAATCCAAACCCACCAAGT 120
|||||
QY 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCCCGTTGTTTCCAATGCC 180
|||||
Db 121 GAAGGTGCTTCTTTTCGGTAACGCTGGTTGCTTCAACGGTTCCCGTTGTTTCCAATGCC 180
|||||
QY 181 ATCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC 240
|||||
Db 181 ATCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCAATGGGTCCATTGTCC 240
|||||
QY 241 ATCCGTTTTCAGCTTACTTTCACCAACCATCATGCTTGGTTGATTCGTTTCTTGTGCTGGA 300
|||||
Db 241 ATCCGTTTTCAGCTTACTTTCACCAACCATCATGCTTGGTTGATTCGTTTCTTGTGCTGGA 300
|||||
QY 301 AGACCAACAAAGGTGAAGGAGCAAGCTAAGGCATCGTGAACCTCATCAAGTCCACTGTG 360
|||||

Db 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCATCTCCGTAACCTCATCAAGTCCACTGTG 360
Qy 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420
Db 361 CCTTTGATCAAGTCCCTTGGCTGAGGAGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420
Qy 421 CACCTTACCGGTGACCGTGGAGAGCAGACATTCGCAAGGACCGTGGAGGTGGGAACCTT 480
Db 421 CACCTTACCGGTGACCGTGGAGAGCAGACATTCGCAAGGACCGTGGAGGTGGGAACCTT 480
Qy 481 CTTCTCTCAACGGTGTTCGTAACCTCAAACTCCTACGCGTGTATGCTGCTGATTCGAT 540
Db 481 CTTCTCTCAACGGTGTTCGTAACCTCAAACTCCTACGCGTGTATGCTGCTGATTCGAT 540
Qy 541 CTTAACTTCTCAGCGCTTTACCAAGGAAATCCTTATCGAAGAGACGGTACACCATC 600
Db 541 CTTAACTTCTCAGCGCTTTACCAAGGAAATCCTTATCGAAGAGACGGTACACCATC 600
Qy 601 AACCCACAAGGTCTCGTACCTCTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 660
Db 601 AACCCACAAGGTCTCGTACCTCTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 660
Qy 661 GTGTCTGCTGTTTATCGGACTTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
Db 661 GTGTCTGCTGTTTATCGGACTTCGAGACTGAAGTCTGCTCTCAAGGGTATCACACC 720
Qy 721 ACCAAGCGTGTTCGTTGTTGATGACAGCTGTGTTGAGCTGGTGCACATCCAAAGTCT 780
Db 721 ACCAAGCGTGTTCGTTGTTGATGACAGCTGTGTTGAGCTGGTGCACATCCAAAGTCT 780
Qy 781 CTTGCTAACTCCCTGTTGATGACATCCATTCGATACCGACGTGGATACCATCTGTG 840
Db 781 CTTGCTAACTCCCTGTTGATGACATCCATTCGATACCGACGTGGATACCATCTGTG 840
Qy 841 ATCGCCAAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Db 841 ATCGCCAAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAGTTCATC 900
Qy 901 GCTACTCTATGAGAGTGGGTCTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 901 GCTACTCTATGAGAGTGGGTCTTCGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Qy 961 GCTGCTCTAACTGAAGCGTCTCACGCTCTCTACACTCAGCTCSTAAGTTCGTTCCA 1020
Db 961 GCTGCTCTAACTGAAGCGTCTCACGCTCTCTACACTCAGCTCSTAAGTTCGTTCCA 1020
Qy 1021 GCTCTCGCTCTCCAGTCTTGAAGACGTTTACTCCAAAGTGGATGGGTTTCGTCCTCAAGC 1080
Db 1021 GCTCTCGCTCTCCAGTCTTGAAGACGTTTACTCCAAAGTGGATGGGTTTCGTCCTCAAGC 1080
Qy 1081 ATCCAGAGATTCCTTCCAGTATGAGTGGTACCCGTATCCAGAGAGTTCATACGCT 1140
Db 1081 ATCCCGGATTCCTTCCAGTATGAGTGGTACCCGTATCCAGAGAGTTCATACGCT 1140
Qy 1141 TTCGTCACGCTACCTCGGTATGACTGGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200
Db 1141 TTCGTCACGCTACCTCGGTATGACTGGTCTCAATGACCGCAACCCCTGTTTCTGAG 1200
Qy 1201 CTCTCTCGAGGTGAGAAGACCTCTATCCACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Db 1201 CTCTCTCGAGGTGAGAAGACCTCTATCAGCATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Qy 1261 ATTGTAAGTCCAAAGCAAACTGGTCTGCATCCTAA 1296
Db 1261 ATTGTAAGTCCAAAGCAAACTGGTCTGCATCCTAA 1296

RESULT 5

US-08-391-339-7
; Sequence 7, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. B44F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391.339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156.968
; FILING DATE:
; APPLICATION NUMBER: US/07/717.370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-391-339-7

Query Match 78.0%; Score 1011.2; DB 1; Length 1296;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
Qy 1 ATGGCTGAGAACCAAGAAGGTTCGCTATCGCTGAGCTGGAATCGTTGCTGTTTGCCT 60
Db 1 ATGGCTGAGAACCAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGCTGTTGCTACT 60
Qy 61 GCTTTGATGCTTCAACGCTGCTGGAATTCAAAGTCACCTTGATTGACCCGAAACCTCTCTGC 120
Db 61 GCTTTGATGCTTCAACGCTGCTGGAATTCAAAGTCACCTTGATTGACCCGAAACCTCTCTGC 120
Qy 121 GAAGTGTCTCTTTTCGGTAACGCTGCTGCTTCAACGGTTCCTCGTGTTCCTCAATGTCC 180
Db 121 GAAGTGTGATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCTGCTATGTCC 180
Qy 181 ATGCCAGGAACCTTACCTAGCGTTCCAAAGTGGCTTCTTGACCCAAATGGCTCCATTGTCC 240
Db 181 ATGCCGGGAACCTTACGAGCGCTGCGAAGTGGCTCTCTTGACCCGATGGGGCGTTGTCA 240
Qy 241 ATCCGCTTTCAGTACTTTTCCAAACCATCATGCTGCTGTTGATTGTTTCTTCTGCTGCTGA 300
Db 241 ATCCGCTTTCAGTACTTTTCCAAACCATCATGCTGCTGTTGATTGTTTCTTCTGCTGCTGA 300
Qy 301 AGACCAAAACAGGTGAAGGAGCAAGCTAAGGCATCTCCGTAACCTCATCAAGTCCACTGTG 360
Db 301 AGACCAAAACAGGTGAAGGAGCAGGAGCAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
Qy 361 CCTTTTGAATCAAGTCTGCTGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGT 420
Db 361 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATGCGAGCCATCTGTATCCGCCATGAAGT 420

Qy 421 CACCTTACCGTGTACCGTGGAGAGACAGACTTCGCCAAGGACCGTGGAGGTGGGAACATT 480
Db 421 CATCTGACCGGTATATCGTGGAGAGACAGACTTCGCCAAGGACCGCGGAGGTGGGAACGTG 480
Qy 481 CGTGGTCTCAACGGTGTTCGTACTCAATCCTCAGCGCTGATGCTATTCGGTGATTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTTCGCGACCGATCCTCTCTGATGCTATTCGGTGATTTTCGAT 540
Qy 541 CCTAACCTTGTCTCAGCGTTCCTTACCAAGGAACTCTTATCGAAGAGAACGGTTCACACCATC 600
Db 541 CCTAACCTTGTCCGATGCTTTTACCAAGGGCATCTTACCAAGGGCATCTTATAGAGAGAACGGTTCACACCAT 600
Qy 601 AACCACCAAGGTCTCGTACTCTCTTCTTCTGCTGCTTCTCATCGCTAACGGTGGAGAGTTC 660
Db 601 AATCCCAAGGGCTCTGACCCCTCTTCTTCTGCGGCTTTTATCGGCAACCGGTGGGCAATT 660
Qy 661 GTGCTCTGCTGTATTCGGAATTCGACACTGAAGGTGCTGCTCTCAAGGGTATCACCACC 720
Db 661 GTATCTCGGGGTGTATCGGCTTTTGAGACTGAAGGTGCTGCTCTCAAGGGCATTTACAAAC 720
Qy 721 ACCAAGCGTGTCTTGTGTTGATGACAGCTGTCTTGTTCAGCTGGTGCACACTCCAAAGTCT 780
Db 721 ACTAACCGGTCTTCTGCTGTGATGACAGCTGTCTTGTTCAGCTGGTGCACACTCTAAATCA 780
Qy 781 CTGCTAACTCCCTTGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCAACATCGTG 840
Db 781 CTTGCTAACTCCGTAGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
Qy 841 ATCCCAACCCAGAGCTGCTCCAGCTATTCCTCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATCCGGAATCCGAAGCGGTCCAGCATTCGAGACCGGATGCTCAGGAAATTCATC 900
Qy 901 GCTACTCTATGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTTCGGTGTCTCACT 960
Db 901 GCGACACTATGGAATGGGTCTTCGTGTTGCTGCTGATGTTGCTGGTCTCACA 960
Qy 961 GCTGCTCCTAACTGGAAGCGTGTACGTTCTCTACACTCACGCTCGTAAAGTTCCTTCCA 1020
Db 961 GCTGCTCCTAACTGGAAGCGTGTACGTTCTCTACACTCACGCTCGTAAAGTTCCTTCCA 1020
Qy 1021 GCTCTCCGCTCGCACTCTGGAAGACGTTACTCCTCAAGTGGATGGCTTTCGGTCCCAAGC 1080
Db 1021 GCGCTCGGGCTCGGAGTCTGGAAGACGATATTCCTCAATGGATGGGTTTTCGTCCTAGC 1080
Qy 1081 ATCCAGATTCCTTCCAGTGATTTGGTCTGCTACCGGTACTTCCAGACGTTATCTACGGT 1140
Db 1081 ATTCTCATCTCTTCCAGTGATTTGGTCTGCTGCAACTCTGACACCGACGTAATCTATGCT 1140
Qy 1141 TTGGTCAACGGTCACTCGGTATGACTGGTGTCCATGACCGCAACCCCTCGTTCTGAG 1200
Db 1141 TTTGGTCAACGGTCACTCGGTATGACTGGTGTCCATGACTGCAACTCTCGTCTCAGAG 1200
Qy 1201 CTCTCCAGGTGAGAAGCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Db 1201 CTCTCCAGGTGAGAAGCTCTATCGACATCTCTCCATTCGCAACCAACCGTTTCGGT 1260
Qy 1261 ATTGGTAAGTCCAGCAAACTGCTCTCCATCTCTAA 1296
Db 1261 ATTGGCAATCCAGCAACCGGTCCGCGCAAGTTAA 1296

RESULT 6

US-08-484-274A-7
; Sequence 7, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/484,274A
; APPLICATION NUMBER: 07 June 1996
; FILING DATE: 435
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: patterson, melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBF130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-484-274A-7

Query Match 78.0%; Score 1011.2; DB 2; Length 1296;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

Qy 1 ATGGCTCAGAACCAAGAGTTCGCTATCGCTCGAGCTGGAATCGTGGTGGTTCGACT 60
Db 1 ATGGCTCAGAACCAAGAGTTCGCTATCGCTCGAGCTGGAATCGTGGTGGTTCGACT 60
Qy 61 GCTTTGATGCTTCAACGTCGTTGAGTTTCAAGGTTACCTTTGATTGATTCGAACCCACCAAGT 120
Db 61 GCTTTGATGCTTCAACGTCGTTGAGTTTCAAGGTTACCTTTGATTGATTCGAACCCACCAAGT 120
Qy 121 GAAGTGTCTTCTTCGGTAACGCTGGTTCCTTCAACGGTTCCTCGTTGGTTCGAATGTC 180
Db 121 GAAGTGTCTTCTTCGGTAACGCTGGTTCCTTCAACGGTTCCTCGTTGGTTCGAATGTC 180
Qy 181 ATGCCAGAACTTGACTAGCGTTTCAAGTGGCTTCTTGACCCCAATGGGTCCATTTGTC 240
Db 181 ATGCCAGAACTTGACTAGCGTCCGAGGCTCCGAGTGGCTCCTTGACCCGATGGGCGCTTGTCA 240
Qy 241 ATCCGTTTCAAGTACTTTTCCAAACCATCATGCTTGGTGGTGGTTCGTTTCTTCTTCTGCTGGA 300
Db 241 ATCCGTTTCAAGTACTTTTCCAAACCATCATGCTTGGTGGTGGTTCGTTTCTTCTTCTGCTGGA 300
Qy 301 AGACCAACAGGTGAGGAGCAAGCTAAGGCACTCGTAACTCACTCACTCACTCACTCACTG 360
Db 301 AGACCAACAGGTGAGGAGCAAGCTAAGGCACTCGTAACTCACTCACTCACTCACTCACTG 360
Qy 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 361 CCTTTGATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGACAGCTTCGCCAAGGACCGTGGAGGTGGGAACATT 480
Db 421 CATCTGACCGGTATATCGTGGAGAGACAGACTTCGCCAAGGACCGCGGAGGTGGGAACGTG 480
Qy 481 CGTGGTCTCAACGGTGTTCGTACTCAATCCTCAGCGCTGATGCTATTCGGTGATTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTTCGCGACCGATCCTCTCTGATGCTATTCGGTGATTTTCGAT 540
Qy 541 CCTAACCTTGTCTCAGCGTTCCTTACCAAGGAACTCTTATCGAAGAGAACGGTTCACACCATC 600
Db 541 CCTAACCTTGTCTCAGCGTTCCTTACCAAGGAACTCTTATAGAGAGAACGGTTCACACCATC 600

Qy 601 AACCCACAGGTCGTCGACTCTCTTCTTTCGTCGTTTCATCGCTAAGCGTGGAGAGTTC 660
Db 601 AATCCGAAGGCGTCGACCCCTCTTCTTTCGCGCTTTTATCGCGAACGGTGGCGCAATTT 660
Qy 661 GTGTCTGCTGCTGTTATTCGGAATTCAGACTCAAGGTCTGCTCTCAAGGGTATCACCAAC 720
Db 661 GTATCTGGGGTGCATCGGTTTGGAGACTGNAUGTCTGCTCTCAAGGGATTTACACACC 720
Qy 721 ACCAAGCGTGTCTTGTGTTGATGTCAGCTGTTGTTGACGCTGTTGTCAGCTGTTGTCACACTCCAAGTCT 780
Db 721 ACTAACGCTGTCTTGGCTGTGATGTCAGCTGTTGTTGACGCTGTTGTCAGCTGTTGTCACACTCTAAATCA 780
Qy 781 CTTGCTTAACCTCCCTTGGTGATGACATCCCATTTGATGATACCCAGACCTGGATACCATCGTG 840
Db 781 CTTGCTTAATTCGCTAGCGATGACATCCCGCTCGATACCCGACCTGGATATCATATCGTC 840
Qy 841 ATCCCAACACAGAGTCTGCCAGCTATTCCAACTACCCGATGCTTCTGGAAGTTTCATC 900
Db 841 ATCCGGAATCCGGAAGCGCTCCAGCATTCGAGACCGATGCTTCAGGAAATTCATC 900
Qy 901 GCTACTCTATGGAGATGGGTCTTCTGTTGCTGGAACCGTTGAGTTGCTGCTGCTCACT 960
Db 901 GCGACACTATGGAATGGGTCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCACA 960
Qy 961 GCTGCTCTTAACCTGGAAGCGTCTGCTCTATACACTCACGCTCGCTAAGTTGCTTCCA 1020
Db 961 GCTGCTCTTAACCTGGAAGCGTCTGCTCTATACACTCACGCTCGCTAAGTTGCTTCCA 1020
Qy 1021 GCTCTGCTCTGCGAGTCTTGAAGACGTTTACTCCAACTGCGGTCTTCCGTCCTCAAGC 1080
Db 1021 GCGCTGCGGCTGCGAGTCTTGAAGACGATATTCCTAAGTGGATGGGTTTTCGCTCTAGC 1080
Qy 1081 ATCCAGATCCCTTCCAGTATGTTGGTGGTCTACCCGCTACTCCAGAGCTTATCTACGCT 1140
Db 1081 ATTCTGATCTCTTCCAGTATGTTGGTGGTCTGCAACTCTACACCGAGCTAATCTATGCT 1140
Qy 1141 TTCGGTCAGGTCACCTCGGTATGACTGCTGCTCAATGACCGCAACCGCTGTTCTGAG 1200
Db 1141 TTTGGTCACGGTCTATCTGCTGATGACAGGTCCTCAATGACTGCAACTCTGCTCTCAGAG 1200
Qy 1201 CTCTCCAGCTGAGAGACCTCTATGACATCTCTCCATCTCCATTCGCAACCAACCGTTCGGT 1260
Db 1201 CTCTCCAGCGGCAAGACCTCTAATGACATTTTCGCCCTTCGCAACCAACCGCTTTGGT 1260
Qy 1261 ATTGGTAAGTCCAAAGCAACTGCTCTGCAATCTTAA 1296
Db 1261 ATTGGCAAAATCCAAAGCAACGGGTCGCGCAAGTTAA 1296

RESULT 7
US-08-391-339-6
; Sequence 6, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/391.339

; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156.968
; FILING DATE:
; APPLICATION NUMBER: US/07/171.370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; US-08-391-339-6

Query Match 74.2%; Score 961.6; DB 1; Length 1296;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGAACCAACGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTGTTGCACT 60
Db 1 ATGGCTGAGAACCAACGAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCAGG 60
Qy 61 GCTTTGATGCTTCAACGCTGTTGATTCAGGTTACCTTGTATGATTCACCAACCCACAGGT 120
Db 61 GCGCTGATGCTTCAAGCTGCGGATTCAGAGTTCACCTTGTATGACCCGGAACCTCTCTGC 120
Qy 121 GAAGGTGCTTCTTTCGGTAAACGCTGGTTCCTTCAACGGTTCCTCGTGTGTTCCATATGCC 180
Db 121 GAAGGTGCTTCTTTCGGTAAACGCTGGTTCCTTCAACGGTTCCTCGTGTGTTCCATATGCC 180
Qy 181 ATGCCAGCAAACTTCACTAGGCTTCCAAAGTGGCTTCTTACCCCAATGGTTCATTTGCC 240
Db 181 ATGCCAGCAAACTTCACTAGGCTTCCAAAGTGGCTTCTTACCCCAATGGTTCATTTGCC 240
Qy 241 ATCCGTTTACGCTACTTTCACCAACCATCATGCTTGTGTTGATTCGTTTCTTGTCTGCTGA 300
Db 241 ATCCGTTTACGCTACTTTCACCAACCATCATGCTTGTGTTGATTCGTTTCTTGTCTGCTGA 300
Qy 301 AGACCAACAAAGTGAAGGAGCAAGCTAAGGCACTCCGTAACTCATCAAGTCCACTGTG 360
Db 301 AGACCAACAAAGTGAAGGAGCAAGCTAAGGCACTCCGTAACTCATCAAGTCCACTGTG 360
Qy 361 CCTTTGATCAAGTCTTTCGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCACCAAGGT 420
Db 361 CCTTTGATCAAGTCTTTCGGCTGAGGAGCTGATGCTAGCCACTTATCCGTCACCAAGGT 420
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTTCGCCAGGACCGTGGAGTTGGGAATTT 480
Db 421 CATCTGACCGTATATCTGTTGAGAGACAGACTTTCGCCAGGACCGTGGAGTTGGGAATTT 480
Qy 481 CGTGTCTCAACGGTGTGCTGATCAAACTCTCAGCGCTGATGCTATTCGTTCCGTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTGCTGATCAAACTCTCAGCGCTGATGCTATTCGTTCCGTTTCGAT 540
Qy 541 CCTAACTTGTCTCAGCGCTTTCACCAAGGAATCTTATCGAAGAACCGGTCCACACCATC 600
Db 541 CGGAATCTGTCGATGCTTTCACCAAGGAATCTTATAGAGAACCGGTCCACACCATC 600
Qy 601 AACCCACAGGTCGTCGACTCTCTTCTTTCGTCGTTTTCATCGCTTAAGCGTGGAGAGTTC 660
Db 601 AATCCGAAGGCGTCGACCCCTCTTCTTTCGCGCTTTTATCGCGAACGGTGGCGCAATTT 660
Qy 661 GTGTCTGCTGCTGTTATTCGGAATTCAGACTCAAGGTCTGCTCTCAAGGGTATCACCAAC 720
Db 661 GTATCTGGGGTGCATCGGTTTGGAGACTGNAUGTCTGCTCTCAAGGGATTTACACACC 720

Db 661 GTATCTCGCGGCTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAACC 720
QY 721 ACCAAGCGTCTTCTGCTTTGATGAGCTGTGTTGTCAGCTGGTGACACTCCAAGTCT 780
Db 721 ACCAAGCGGCTTCTGCGCTTTGATGAGCGGTGTCGAGCGCGGCACACTGAAATCA 780
QY 781 CTTGCTAACTCCCTTGGTGATGACATCCCATTTGATACCGAAGCTGGATACCACTCGTG 840
Db 781 CTTGCTAACTTCCGTAGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
QY 841 ATCGCAACCCAGAACGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATCGCAAACTCCGGAAGCGCTCCACGATTCGAGACGCGTACGGAAGAAATTCATC 900
QY 901 GCTACTCCTATGAGATGGGCTTCTGCTGTGGAACGCTTGAGTTTCGGTGGCTCTCACT 960
Db 901 CGGACACCTATGAAATGGGCTTCCGCTGGCGGTACGGTTGAGTTCCGTTGGGCTCACA 960
QY 961 GCTGCTTAACTGGAAGCGTGCTACGTTCTCTACACTCACGCTCGTAAGTTGCTTCCA 1020
Db 961 GCGGCTCCTAACTGGAAGCGTGCGCATGTCTCTATACGACGCTCGAAAACTTCTTCCA 1020
QY 1021 GCTCTCGCTCCCTCCAGTTGCTGAGAACGTTACTCCAAGTGGATGGTTTCCGTTCCAAGC 1080
Db 1021 GCGCTCGGCGCTCGAGTTCTGGAAGAACGATATTCCAAATGGATGGGTTCCGGCGGAGC 1080
QY 1081 ATCCAGATTCCCTTCCAGTGTGCTGCTACCGCTACTCCAGACGTTATCTACGCT 1140
Db 1081 ATCCGGATTGCTCCCTCGATTGGCGGGCAACCCGGACACCCGACGTAATCTATGCT 1140
QY 1141 TTGCGTCAAGGTCACTCGGTATGATGCTGCTTCAATACCGCAACCCCTCGTTCTGAG 1200
Db 1141 TTCCGGCAGGTCATCTCGCATGACAGGGCGCGCATGACCCCAACGCTGCTCGTCAGAG 1200
QY 1201 CTCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCCACCAACACCGTTTCGCT 1260
Db 1201 CTCTCGCAGGCGAAGACCTCAATCGACATTTCCGCTTCCGCTTCCGCAAAACCGCTTTGGT 1260
QY 1261 ATTGGTAAGTCCAAGCAACTGCTCTGTCATCCTAA 1296
Db 1261 ATTGGCAAAATCCAAGCAACGGGTCCGCAAGTTAA 1296

RESULT 8

US-08-484-274A-6
; Sequence 6, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6

Query Match 74.2%; Score 961.6; DB 2; Length 1296;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 1087; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 1 ATCGCTCAGAACACACAGAAGTTGGTATCGCTCGAGCTGGAATCGTTGGTGTTCGACT 60
Db 1 ATGGCTGAGAACACACAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 60
QY 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTTGATTGATCCAAACCCACACAGT 120
Db 61 GCCTGATGCTTCAGCGCCGCGGATTCAAAAGTCACTTTGATTGACCGGAACCCCTCTGGC 120
QY 121 GAAGTGTCTTCTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCCGTTGTTGCCAATGTC 180
Db 121 GAAGTGTGATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180
QY 181 ATGCCAGGAACCTTGACTAGCTTCCAAAGTGGCTTCTTGACCCCAANTGGTTCATTCCTC 240
Db 181 ATGCCGGGAACCTTGACGAGCGTGCAGAGTGGCTCTTGACCGGATGGGGCGCTTTGTCA 240
QY 241 ATCCGTTTACGCTACTTTCCAAACCATCATCGCTTGGTTGATTGCTTTCTTGTCTGCTGA 300
Db 241 ATCCGTTTACGCTACTTTTCCAAACCATCATCGCTTGGTTGATTGCTTTCTGTAGCCGA 300
QY 301 AGACCAAAACAAAGTGAAGGAGCAAGCTAAGGCATCTCGTAACCTCATCAAGTCCACATGTG 360
Db 301 AGACCAAAACAAAGTGAAGGAGCAAGCTAAGGCATCTCGTAACCTCATCAAGTCCACGGTG 360
QY 361 CTTTGTGATCAAGTCTTGGCTGAGGAGGCTGATCGAGCCATCTGATCCGCTTCTGTTTCT 420
Db 361 CTTCTGATCAAGTCTTGGCGGAGGAGGCTGATCGAGCCATCTGATCCGCTTCTGTTTCT 420
QY 421 CACTTTACCGTGTACCGTGGAGAACGACACTTCGCCAAGGACCGTGGAGGTGGGAACAT 480
Db 421 CATCTGACCGTATATCGTGGAGAACGACACTTCGCCAAGGACCGCGGAGGTGGGAACATG 480
QY 481 CGTCTGTCAACGGTGTCTGCTACTCAATCCTCAGCGCTGATGCAATTCGCTGATTTTCGAT 540
Db 481 CGGCGTCTCAACGGTGTTCGCACGACAGATCCTCAGCGCCGATGCTGTCGGGATTTTCGAT 540
QY 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGGAATCCTTATCGAAGAGAACGCTCACACCATC 600
Db 541 CCGAAGTGTGCGATGCGTTTACCAAGGGAATCCTTATAGAAGAGAACGCTCACACGAT 600
QY 601 AACCCACAAGGTCTCGTGAAGTCTCTTGTCTGCTGTTTCATCGCTAACGGTGGAGAGTTC 660
Db 601 AATCCGCAAGGCTCGTGAAGTCTCTTCTTCTGCGCTTTTATCGCAACGCTGGGGAATTT 660
QY 661 GTGCTGTCTGCTGTTATCGGATTCGAGACTGAAGGTGCTGCTCTCAAGGGTATCACACC 720
Db 661 GTATCTCGCGCTGCTATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTATCAACC 720
QY 721 ACCAAGCGTGTCTTGTGCTGTTGATGACGCTGTCTTCCAGCTGCTGTCAGCTCCAACTCT 780
Db 721 ACCAAGCGGCTTCTGCGGCTTGTGATGACGCGGTTGTCGAGCCGCGCTCACTCGAAATCA 780
QY 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGAAGCTGGATACCACTCGTG 840
Db 781 CTTGCTAACTTCCGTAGCGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 840
QY 841 ATCGCAACCCAGAACGCTGCTCCAGTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 841 ATCGCAAACTCCGGAAGCGCTCCACGATTCGAGACGCGTACGGAAGAAATTCATC 900

Db 841 ATCCGAATCCGGAAGCGCTCCACGCATTCGAGACCGCATGCGTCAGGAAAAATTCATC 900
Qy 901 GCTACTCTATGAGATGGGTCTTCGTGTTGCTCGAACCCTTGAGTTCGCTGGTCTCACT 960
Db 901 GCGACACCTATGGAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTCGCTGGGCTCACA 960
Qy 961 GCTGCTCTTAAGTGAAGCGTGCACGTTCTCTACACTACAGCTCGGTAAGTTGCTTCCA 1020
Db 961 GCGCTCTTAAGTGAAGCGTGGCCATGTGCTCTATAGCACGCTTCGAAACTTCTTCCA 1020
Qy 1021 GCTCTGCTCTCCAGTCTTGAAGAAGCTTACTCCAAAGTGGATGGGTTTCCTCCAAAGC 1080
Db 1021 GCGCTCGCGCTCGAGTCTTGAAGAAGCATATTCCAAATGATGGGTTCCGCGCGAGC 1080
Qy 1081 ATCCACGATTCCTTCAGTAGTATGCTGCTACTACCGTACTCCAGAGGTATCTACGCT 1140
Db 1081 ATCCCGATTCGCTTCGCGTATTTGGCGGGCAACCCGGACACCGAGTAACTATGCT 1140
Qy 1141 TTGGTCAAGGTACCTCGGTATGACTGGTCTCCAATGACCGCAACCCCTCTCTGAG 1200
Db 1141 TTGGCCACGGTCACTTCGGGATGACAGGGCGCGGATGACCGCAACCGTCTCTCAGAG 1200
Qy 1201 CTCTTCGAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGACCAAAACCGTTTCGGT 1260
Db 1201 CTCTTCGAGCGAAGACCTCAATCGACATTTGCGCCCTTCGACCAAAACCGCTTGGT 1260
Qy 1261 ATTGGTANGTCCAGCAAACTGGTCTCGATCCCTAA 1296
Db 1261 ATTGGCAATCCAGCAAAACGGTCCGGCAAGTTAA 1296

RESULT 9

US-08-484-274A-3
: Sequence 3, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1692 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-484-274A-3

Query Match 74.18; Score 960; DB 2; Length 1692;

Best Local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 210; Indels 0; Gaps 0;
Qy 1 ATGCTGAGAACACAGAAAGTTGGTATCGCTGGAGCTGGAATCGTGTGTTGTTGCACT 60
Db 120 ATGCTGAGAACACAAAAAAGTAGGCATCGCTGGAGCGGAATCGTCGGCGTATGCACG 179
Qy 61 GCTTTGATGCTTCAACGCTCGTGGATTCAAGGTTACCTTGATTGATCCAAACCCACCAGGT 120
Db 180 GCGTGTATGCTTTCAGCGCCCGGATTCAAAGTCACTTGTGATTCGACCCGAACCCCTCTCG 239
Qy 121 GAAGGTGCTTCTTCGGTAAAGCTTGGTTCCTCAACGGTTCCTCGCTGTGTTCCAAATGTC 180
Db 240 GAAGGTGCATGCTTGGGAATGCCGGATGCTTCAACGGCTCATCGCTGCTCCTATGTCC 299
Qy 181 ATGCCAGGAAACTTTCAGTACGCTTCCAAAGTGGCTTTCGTGACCCCAATGGGTCCATGTCC 240
Db 300 ATGCCGGGAAACTTGACGAGCGTCCGAAGTGGCTTCTTGACCCGATGGGCGGTGTGCA 359
Qy 241 ATCCGTTTCAGCTACTTTCCAACCATCATGCTTGGTGTGATTGCTTCTTGTGCTGCA 300
Db 360 ATCCGGTTCAGCTATTTTCCAAACCATCATGCCCTGGTTGATTCGCTTCTGTAGCCGGA 419
Qy 301 AGACCAAAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCCACTGTG 360
Db 420 AGACCAAAAGGTGAAGGAGCAGCGAAGCATCCGCAATCTCATCAAGTCCCAAGGTG 479
Qy 361 CTTTGTATCAAGTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 480 CTTGTATCAAGTCAATTTGGCGAGGAGGCTGATGCGAGSCCATCTGATCCGCCATGAAGST 539
Qy 421 CACCTTACCCTGTTACCGTGGAGAGACGACTTCCCAAGGACCGTGGAGGTTGGGAATTT 480
Db 540 CATCTGACCTTATATCGTGGAGAGCAGACTTCGCCAAAGGACCGCGAGGTTGGGAATG 599
Qy 481 CGTCTCTCAACGGTGTTCGTACTCAAAATCCTCAGCGCTGATGCTTCCGTTGATTTCCGAT 540
Db 600 CGGCTCTCAACGGTGTTCGACCGAGATCCTCAGCGCGGATGCGTTGCGGGATTTCCGAT 659
Qy 541 CTTAACTTGTCTACGCGCTTTACCAAGGGAATTCCTTATCGAAGAGAACGGTCCACACATC 600
Db 660 CCGAACTTGTGCGATGCGTTTACCAAGGGCATCTTATAGAAGAGAACGGTCCACAGATT 719
Qy 601 AACCACAAAGTCTCGTCACTCTCTTGTTCGTGCTTTCATCGCTTAACGGTGGAGAGTTC 660
Db 720 AATCCGCAAGGGCTCGTGACCTCTTGTTCGCGGATTTTATCGCGAACGGTGGCGAATTC 779
Qy 661 GTGCTGCTCGTGTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGTTATCACACC 720
Db 780 GTATCTGCGCGTGTATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTAACAACC 839
Qy 721 ACCAAGCGTGTTCCTTGTGCTGATGCTGATGCTGTTGTCAGCTGGTTCACACTTCCAAGTCT 780
Db 840 ACGAAGCGGCTTCTGGCGGTTGATGTCAGCGGTTGTGCGAGCGCGGCGCACACTCGAATCA 899
Qy 781 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGACGCTGGATACACATCGTG 840
Db 900 CTTGCTAACTCCCTTGGTGTGATGACATCCCATTTGATACCGACGCTGGATACACATCGTG 959
Qy 841 ATCGCAACCCAGAGCTGCTCCAGTATTCCAACTACCGATGCTTCTTGGAAAGTTTCATC 900
Db 960 ATCGGAATCCGGAAGCGCTCCAGCATTCGAGACCGATTCGAGACCGGATGCGTCAGGAATTCATC 1019
Qy 901 GCTACTCTATGGAGATGGGCTTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 1020 GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGTACGGTTGAGTTGCTCGCTGGGCTACA 1079
Qy 961 GCTGCTCCTAACTGGAACGGTGTCCACGTTCTCTACACTCAGGCTCGTAAGTTGCTTCCA 1020
Db 1080 GCGGCTCCTAACTGGAAACGTCGCGATGTGCTCTATAGCACGCTTCGGAACACTTCTGCA 1139
Qy 1021 GCTCTGCTCCTGCGAGTTCTCAAGAACGTTACTCCAAAGTGGTTCGCTCAGGCTCAAGC 1080

Db 1140 GCCCTCGCGCCTCGGAGTCTGAAGAACGATATTCAAAATGGATGGGGTTCCGGCCGAGC 1199
QY 1081 ATCCAGATTCCCTTCACGTGATTGGTCGTGCTACCGTACTCCAGACGTTATCTACGCT 1140
Db 1200 ATCCGGATTTCGCTCCCGTGATTGGCCGGGAACCCGGACACCCGACGTAATCTATGCT 1259
QY 1141 TTCCGGTACCGGTACCTTCGCTATGACTGGTGTCCAAATGACCCGAACCCCTTCGTTCTGAG 1200
Db 1260 TTCCGGCATGCTATCTCGCATGACAGGGCGCGGATGACCCGAACGCTCGTCTCAGAG 1319
QY 1201 CTCCTCGCAGGTGAGAGACCTCTATCGACATCTCTCCATTCGCACCAACCCGTTTCGCT 1260
Db 1320 CTCCTCGCAGGGGAAAAGACCTCAATCGACATTTTCGCCCTTCGCACCAAAACCCGTTTGGT 1379
QY 1261 ATTGGTAAGTCCCAAGCAAGTGTCTCTGTCATCCTAA 1296
Db 1380 ATTGGCAATCCCAAGCAAGGCTCCGGCAAGTTAA 1415

RESULT 10

US-08-391-339-4
: Sequence 4, Application US/08391339
: Patent No. 5463175
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dennis R. Hoerner, Jr.,
: ADDRESSEE: Monsanto Co. B4F
: STREET: 700 Chesterfield Village Parkway
: CITY: St. Louis
: STATE: Missouri
: COUNTRY: USA
: ZIP: 63198
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/391,339
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,968
: FILING DATE:
: APPLICATION NUMBER: US/07/717,370
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoerner, Dennis R., Jr.
: REGISTRATION NUMBER: 30,914
: REFERENCE/DOCKET NUMBER: 38-21(10533)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314)537-6099
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1293 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1293
US-08-391-339-4

Query Match 71.7%; Score 928.8; DB 1; Length 1293;
Best Local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

QY 1 ATGCTGTGAGAACACACAAAGAGTTGGTATTCGCTGGAGCTGCAATTCGTTGGTGTTCGACT 60
Db 1 ATGCTGTGAGAACACACAAAGTAGGCATCGCTGGAGCCGGAATTCGTCGGGTATGCACG 60
QY 61 GCTTTGATGCTTCAACGCTCGTGATTCAAAGGTTACCTTGATTCATCAAAACCCACAGGT 120
Db 61 GCCTGTGATGCTTCAGCGCCCGGATTCAAAAGTCACTTCGTTGATTCACCGGAACCCCTTCCTGGC 120
QY 121 GAAGGTGCTTCTTTTCGGTAAACGCTGGTTCGTTCAACGGTTCCCTCCGTTGTTCCAAATGCTC 180
Db 121 GAAGGTGCTATGTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCTTATGTCC 180
QY 181 ATCCAGGAAACTTGACTACGCTTCCAAAGTGGCTTCTTGACCCAAATGGGTTCCTATGTCC 240
Db 181 ATCCGGGAAACTTGACGAGCGTGCAGAGTGGCTCTTTCGACCCGATGGG - CGGTTGTCA 239
QY 241 ATCCGTTTCAGCTACTTTCCAACCATCATGCTTGGTTGATTCGTTCTTCTTGTCTGCTGGA 300
Db 240 ATCCGTTTCAGCTA -TTTCCAAACCATCATGCC -TGGTTGATTCGCTTCTTGTTCAGCCGA 297
QY 301 AGACCAAAACAAAGTGAAGGAGCAAGCTAAGGCACCTCCGTAACCTCATCAAGTCCACATGTG 360
Db 298 AGACCAAAACAAAGTGAAGGAGCAGGCAAGAGCACTCCGCAATCTCATCAAGTCCACGGTG 357
QY 361 CCTTGATCAAGTCTTGGCTGAGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT 420
Db 358 CCTTGATCAAGTCTTGGCGGAGAGGCTGATGCGAGGCCATCTGATCCGCCCATGAAGGT 417
QY 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTCGGAACTT 480
Db 418 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCCCGGAGGTTCGGAACTG 477
QY 481 CGTCGCTCAACGCTGTTCGTACTCAAACTCTCAGCGCTGATGCATTCGCTGATTCGAT 540
Db 478 CGCGGTCTCAACGCTGTTCGCACGCGAGATCCTCAGCCCGCATGCGTTGCGGGATTCGAT 537
QY 541 CTTAACTTGTCTCACGCCCTTTACCAAGGGAATCCTTATCGAAGAGAACGCTCACACCATC 600
Db 538 CCGAACTTGTGCGCATGCGTTTACCAAGGCGCTTCTTATAGAAGAACGCTCACACGATT 597
QY 601 AACCCACAGGCTCTCGTACTCTCTTGTTCGTCGTTTCATCCTACGCTGAGAGATTC 660
Db 598 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGCGCTTTTATCGCGAACGCTGCGGAATTC 657
QY 661 GTGCTGTGCTGTATTCGGATTTCGAGACTGAAGGCTGCTCTCTCAAGGGTATTCACACCC 720
Db 658 GTATCTGGCGGTGCTATCGCTTTGAGACTGAAGGTAGGCGCTTAAGGCGATTCANACC 717
QY 721 ACCAACGGTGTCTTGTGTTGATGAGCTGTTGTTGCAAGCTGGTGCACACTCCAAATGCT 780
Db 718 ACGAAGCGGCTTCTGCGCGTTGATGACGCGGTTGTGCGAGCGGCGCACACTCGMAATCA 777
QY 781 CTTGTCTAACTCCCTTGGTGATGACATCCCATTCGATACCGAACGCTGGATACCATCGTG 840
Db 778 CTTGTCTAAATTCGCTAGCGGATGACATCCCGCTCGATACCGAACGCTGGATATCATATCGTC 837
QY 841 ATCGCAAAACCCAGAGCTGCTCCACGATATTCCAACTACCGATACCGATGCTTCTGAAAAGTTCATC 900
Db 838 ATCGCAATCCCGAAGCCGCTCCACGATTCGCCAGCAGCGATCGGTCAGGAAATTCATC 897
QY 901 GCTACTCTCTATGAGATGGGTCTTTCGTTGCTGGAACCGTTCGAGTTCGCTGCTCACT 960
Db 898 GCGACACCTATGAAATGGGGCTTCGCGTGGCGGGTACGGTTCAGTTCGCTGGGCTCACA 957
QY 961 GCTGCTCTAACTGGAAGCGTGTCTACGTTCTCTACACTCACGCTCGTAGTTGCTTCCA 1020
Db 958 GCGGCTCTCTAACTGGAAGCGTGGCGCATGTCTATACGCAACGCTCGAAATTCCTTCCA 1017
QY 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTTACTCCAAGTGGATGGTTTCCTGCTCAAGC 1080
Db 1018 GCGCTCGCGCTGCGAGTCTGAAGAACGATATTCCAATGGATGGGTTCGCGCCGAGC 1077
QY 1081 ATCCCAAGATTCCTCCAGTGATGTTGGTGTGCTACCGCTACTCCAGACGTTATCTACGCT 1140

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Db 1078 ATCCGGATTGCTCCCGGTTGGCGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 1137
Qy 1141 TTCGGTCACGCTACCTCGGTATGACTGGTCTCCAATGACCGCAACCTCGTGTCTTGAG 1200
Db 1138 TTCGGCCATGGTCATCTCGGCATGACAGGGCGCGGATGACCGCAACGCTCGTCTCAGAG 1197
Qy 1201 CTCTCCGAGGTGAGAGACCTCTATGACATCTCTCATTCGACCAACACCGTTTCGGT 1260
Db 1198 CTCTCCGAGCGGAAAGACCTCAATGACATTTGCGCCTTCGCAACCAACCGCTTTGGT 1257
Qy 1261 ATTGCTAAGTCCAGCAACACTGTCCTGCACTCTAA 1296
Db 1258 ATTGCAATCCAGCAACACGGTCCGCGCAAGTTAA 1293

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RESULT 11

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US-08-484-274A-4
: Sequence 4, Application US/08484274A
: Patent No. 5776760
: GENERAL INFORMATION:
: APPLICANT: Kishore, Ganesh M.
: APPLICANT: Barry, Gerard F.
: TITLE OF INVENTION: Glyphosate Tolerant Plants
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,274A
: FILING DATE: 07 June 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Patterson, Melinda L.
: REGISTRATION NUMBER: 33,062
: REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (713)789-2679
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1293 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1293
: US-08-484-274A-4

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Query Match 71.7%; Score 928.8; DB 2; Length 1293;
Best local Similarity 83.8%; Pred. No. 0;
Matches 1086; Conservative 0; Mismatches 207; Indels 3; Gaps 3;

Qy 1 ATGGCTGAGAACCAAGAAGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTCGACT 60
Db 1 ATGTCTGAGAACCAAAAAAGTAGGATCGCTGGACCGGAATCGTCGGCGTATGCACG 60

Qy 61 GCTTTCATGCTTCAACGTCGCTGGATTCAAGGTTACCTTGTATTGATCCAAACCCACCAAGGT 120
Db 61 GCGCTGATGCTTACGCGCGCGGATTCAAGTCACCTTGATTGACCCGAAACCTCTCTGGC 120

Qy 121 GAAGTGCTTCTTTTCGGTAAACGCTGGTGGTTTCAACGGTTCCCTCCGTTGTTCCAATGTCC 180

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Db 121 GAAGTGCTCATCGTTTGGGAATGCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180
Qy 181 ATGCCAGAAACTATGACTAGCTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTTGCC 240
Db 181 ATGCCGGAAACTATGACGAGCGTCCGAAGTGGCTCCTTTGACCCGATGGG-CCGTTGTCA 239
Qy 241 ATCCGTTTTCAGCTACTTTTCCAAACCATCATGCCTTGGTGTGATTCGTTTCTGCTTTCCTGGA 300
Db 240 ATCCGGTTTCAGCTA-TTTTCCAAACCATCATGCC-TGGTTGATTCGCTTCTCTGTAGCCGA 297
Qy 301 AGACCAACAAGGTGAAGGAGCAAGCTAAGGCACCTCCGTAACTTCATCAAGTCCACATGTG 360
Db 298 AGACCAACAAGGTGAAGGAGCAGCGCAAAACACTTCGCGCAATCTCATCAAGTCCACGCTG 357
Qy 361 CCTTTGATCAAGTCTCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCTCCGTCACGAAGGT 420
Db 358 CCTCTGATCAAGTCAATTTGGCGGAGGAGGCTGATCCGAGCCATCTGATCCGCCATGAAGGT 417
Qy 421 CACCTTACCGTGTACCGTGGAGAGCAGACTTCGCCAAGGACCGTGGAGGTTTGGAACTT 480
Db 418 CATCTGACCGTATATCTGTGGAGAGCAGACTTCGCCAAGGACCGCGGAGGTTTGGAACTG 477
Qy 481 CCTCGTCTCAACGCTGTTCTGACTCAAAATCCTTCAGCGCTGATGCAATTCGCTGATTTGAT 540
Db 478 CGCGCTCTCAACGCTGTTTCGCACGCAGATCCTCAGCGCCGATGGGTTTCGGGGATTTTCGAT 537
Qy 541 CCTAACTTGTCTCAGCGCTTTTACCAAGGAATCCTTATCGAAGAGAGCGGTCAACACATC 600
Db 538 CCGAACTTGTCCGATGCGGTTTACCAAGGCCATTCCTTATAGAAGAGAGCGGTCAACAGAT 597
Qy 601 AACCACAAGGTCGTGACTCTCTTGTGTGTCGTCTTTCATCGCTAAACGGTGGAGAGTTC 660
Db 598 AATCCGCAAGGGCTCGTGACCCCTCTTGTTCGGCGTTTTATCGCGAAGCGGTGGCGAATTC 657
Qy 561 GTGCTCTGCTCGTGTATATCGGATTCGAGACTGAAGTCTGCTCTCAAGGGTATCACCAC 720
Db 658 GTATCTCGCGTGTGTCATCGGCTTTGAGACTGAAGTGAAGGCGCTTAAAGGCAATTACAACC 717
Qy 721 ACCAAGCGTGTCTTGTGTTGATGTCAGCTGTTTGCAGCTGGTGACACTCCCAAGTCT 780
Db 718 ACGAACCGCGTTCGCGCGTGTGATGCGAGCGGTTGTCGACGCCGCGGCACACTCGAAATCA 777
Qy 781 CTTCCTAACTCCCTTGGTGTGATGACATCCCATTTGGATACCGAAGCTGGATACCACATCGT 840
Db 778 CTTCCTAACTCGTAGCGGATGACATCCCGCTCGATACCGAAGCTGGATATCATATCGTC 837
Qy 841 ATCCGCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTCTGGAAAGTTTCATC 900
Db 838 ATCCGCAATCCGGAAGCGCTCCACGCAATTCGCGACGCCGATGCGTTCAGSAAAAATTCATC 897
Qy 901 GCTACTCTATGGAGATGGGTCTTCTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960
Db 898 GCGACACTATGGAATGGGCTTCGCGTGGCGGTACGGTTGAGTTGCGCTGGCGTCCACA 957
Qy 961 GCTGCTCTTAACGGAAGCGTGTCTCAGCTTCTCTACACTCAGCTCGCTAAGTTCCTTTCCA 1020
Db 958 GCGCTCTCTTAACGGAAGCGTGTCTCAGCTTCTCTATACGCAAGCTTCGGAATACTTCTTCCA 1017
Qy 1021 GCTCTCGCTCTGCCAGTTCTGAAGAAAGCTTACTTCCAAAGTGGATGGGTTTCCGTCCCAAGC 1080
Db 1018 GCGCTCGCGCTGCGAGTTCTGAAGAAACGATATTTCCAAATGGATGGGTTTCCGCGCCGAGC 1077
Qy 1081 ATCCAGATTCCTTCCAGTGAATTTGGTGGTCTACCGCTACTCCAGAGCTTATCTAGCT 1140
Db 1078 ATCCCGGATTCGCTTCCCGGTGATTTGGCGGGCAACCCGACCCCGAGCTAATCTATGCT 1137
Qy 1141 TTCGGTCACGCTCACCTCGGTATGACTGGTGTCTCCAATGACCGCAACCCCTCGTTTCTGAG 1200
Db 1138 TTCGGCCATGCTCATCTCGGCATGACAGGGGCGCGGATGACCGCAACGCTCGCTCAGAG 1197
Qy 1201 CTCTCCGAGGTGAGAGAGACCTCTATGCAATCTCTTCCATTCGCAACCAACCGTTTCGGT 1260

```


RESULT 13
US-08-391-339-27
; Sequence 27, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co., B4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-27

Query Match 4.5%; Score 58.8; DB 1; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 30 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 89
|||||
Db 1 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 60
Qy 90 GG 91
|
Db 61 AG 62

RESULT 14
US-08-484-274A-27
; Sequence 27, Application US/08484274A
; Patent No. 5776760
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-27

Query Match 4.5%; Score 58.8; DB 2; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 30 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 89
|||||
Db 1 CGCTGGAGCTGGAATCGTTGGTGTTCGACATGCTTTGATGCTTCAACGTCGTGGATTCAA 60
Qy 90 GG 91
|
Db 61 AG 62

RESULT 15
US-08-391-339-30
; Sequence 30, Application US/08391339
; Patent No. 5463175
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Glyphosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr.,
; ADDRESSEE: Monsanto Co., B4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,339
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/156,968
; FILING DATE:
; APPLICATION NUMBER: US/07/17,370
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner, Dennis R., Jr.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10533)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-391-339-30

Query Match 4.5%; Score 58.4; DB 1; Length 69;
Best Local Similarity 91.2%; Pred. No. 2.3e-10;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 715 ACCACCACCAACGGTGTCTTGGTGTGATGCAGCTGTTGTCAGCTGGTGCACACTCC 774
Db 2 ACAACCACTAACGGTGTCTTGGTGTGATGCAGCTGTTGTCAGCTGGTGCACACTCT 61

QY 775 AGTCTCT 782
Db 62 AAATCACT 69
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Search completed: January 1, 2001, 03:18:40
Job time: 29344 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 1, 2001, 01:12:53 ; Search time 3327.86 Seconds
(without alignments)
2407.829 Million cell updates/sec

Title: US-08-484-274-8
Perfect score: 1296
Sequence: 1 ATGGGTGAGACCAACAGAA.....AAACTGGTCTGCATCCTAA 1296

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues 14379728
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
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8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
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102: em_gss6.*
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104: em_gss8.*
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110: em_gss12.*
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112: gb_gss13.*
113: gb_gss14.*
114: gb_gss15.*
115: gb_gss16.*
116: gb_gss17.*


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Db 417 GTTGTTCCTGCTGCTGCTGTTGTCCT 391
RESULT 4
CNS04RW2
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
005C20 of library H from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL304427.1 GI:8192034
VERSION AL304427.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 805)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 805)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 805)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..805
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="005C20"
/clone_lib="H"
/note="Genoscope sequence ID : COBH005BB10XE1-end :
PUC-ori"
BASE COUNT 87 a 194 c 293 g 226 t 5 others
ORIGIN

Query Match 3.4%; Score 44.4; DB 123; Length 805;
Best Local Similarity 45.6%; Pred. No. 0.032;
Matches 156; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 643 GCTAACGGTGGAGTTCGGTGTCTGCTCGGTATATCGGATTCGAGACTGAAGGTGCTGCT 702
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 399 GCTACTGGTGTGCAGCTGGTGTGCTGCTACTGGTGGTGGTGGTGGTGGTGGTGGTGGT 458
QY 703 CTCAAGGGTATACACCAACGAGTGGTTCCTGCTGTTGATGCAGCTGTTGTCAGCT 762
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 459 GCAGCTGGTGTGCTACTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 518
QY 763 GGTGCACACTCCAAAGTCTCTTGTCTAACTCCCTTGGTGATGACATCCCATTTGGATACCGAA 822
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 519 GGTGCTGGTGTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 578
QY 823 CGTGGATACACATCGTGTGTCGCAAGCTGCTCCAGCATATCCAACTACCGAT 882
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 579 GGTGCTGCTGCTGCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
```

```
QY 883 GCTTCTCGAAAGTTCATCGCTACTCCTCTATGGAGATGGGTCCTTCTGTTGCTGCGAACCGTT 942
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 639 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
QY 943 GAGTTCGCTGCTCTCACTGCTGCTCCTCACTAACTGGAAGCGTGCCT 984
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 699 GCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
RESULT 5
FR0006944
LOCUS
DEFINITION F.rubripes GSS sequence, clone 133B16aC7, genomic survey sequence.
ACCESSION FR0006944
VERSION 290754.1 GI:1867968
KEYWORDS GSS: genome survey sequence.
SOURCE Fugu rubripes.
ORGANISM Fugu rubripes.
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
1 (bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,
Williams,G. and Brenner,S.
AUTHORS Direct Submission
TITLE Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
JOURNAL Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT Vector: pBluescript II KS
KEYWORDS V.type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
source
1..619
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16aC7"
BASE COUNT 75 a 150 c 116 g 175 t 103 others
ORIGIN

Query Match 3.3%; Score 42.6; DB 124; Length 619;
Best Local Similarity 45.0%; Pred. No. 0.1;
Matches 144; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 688 ACTGAAGTGTGCTCTCAAGGGTATCACCACCAACCGTGTTCCTTGGTGTGATGCA 747
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 72 ACTGCNACTACTGCTACTGCTGCTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCT 131
QY 748 GCTGTTGTTGTCAGCTGGTGCACACTCCCAAGTCTCTTCTTAACCTCCCTTGGTGATGACATC 807
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
QY 808 CCATTGGATACCAACCGTGGATACACCATGCTGATGCCAACCCAGAGTGTCTCCACGT 867
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 192 GCTACTACTACTGCTGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
QY 868 ATTCCCAACTACCGATGCTTCTGGAAAGTTCAATGCTACTCTCTATGGAGATGGGTCTTCGT 927
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 ACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
QY 928 GTTGTGGAACCGTTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 GCTACTGCTACTGCTGCTGCTACTANTGNTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 371
QY 988 GTTCTCTACACTCACGCTCG 1007
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Db 372 GATCNAATTCCTNCANCNG 391
RESULT 6
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FR0013713
LOCUS FR0013713 619 bp DNA GSS 18-SEP-1997
DEFINITION F.rubripes GSS sequence, clone 133B16dB11, genomic survey sequence.
ACCESSION AL004959
VERSION AL004959.1 GI:2450529
KEYWORDS GSS: genome survey sequence.
SOURCE Fugu rubripes.
ORGANISM Fugu rubripes.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

TITLE Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
AUTHORS Williams,G. and Brenner,S.
JOURNAL Direct Submission

COMMENT Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES
source Location/Qualifiers
1..619
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16dB11"
BASE COUNT 83 a 163 c 139 g 180 t 54 others
ORIGIN

Query Match 3.1%; Score 40.6; DB 124; Length 619;
Best Local Similarity 43.3%; Pred. No. 0.39;
Matches 139; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

Qy 722 CAACGGTGTTCCTGCTGCTGATGACGCTGTTGTCAGCTGGTGACACATCCCAAGTCTC 781
Db 26 CTACTGTTNATGACGNCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 85
Qy 782 TTGCTAACTCCCTGGTGCATGACATCCCATTTGGATACCGAAGTGGATACCATCTGTA 841
Db 86 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 145
Qy 842 TCGCAACCCAGAAAGCTGCTCCACGCTATTCCAACTACCGATGCTTCTGGAAGTTTCATCG 901
Db 146 CTGCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
Qy 902 CTACTCTATGGAGATGGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
Db 206 CTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
Qy 962 CTGCTCTTAAGTGGGAAGCTGCTACGCTTCTACACTCAGCTCGTAACTGCTTCCAG 1021
Db 266 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
Qy 1022 CTCTGCTCTCTGCCAGTTCGT 1042
Db 326 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346

RESULT 7
CNS04QUZ 1003 bp DNA GSS 24-MAY-2000
LOCUS CNS0034Y/c
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
130A16 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL303092
VERSION AL303092.1 GI:8184772
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 1003)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1003)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1003)
AUTHORS Genoscope.
TITLE Direct Submission

JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source Location/Qualifiers
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_lib="130A16"
/clone="130A16"
/note="Genoscope sequence ID : C0BGL30BA08Lp1-end : T7"

BASE COUNT 167 a 296 c 282 g 234 t 4 others
ORIGIN

Query Match 3.1%; Score 40.4; DB 123; Length 1003;
Best Local Similarity 47.3%; Pred. No. 0.53;
Matches 122; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 712 ATCCACCACCAACGGGTTCCTGCTGTTGATGACGCTGTTGTCAGCTGCTGTCACAC 771
Db 726 ACCAACAGTAGGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
Qy 772 TCCAAAGTCTCTTGTAACTCCCTTGGTGATGACATCCCATTTGGATACCGACGTGATAC 831
Db 786 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
Qy 832 CACATCGTATCGCCCAACCCAGAAAGCTGCTCCACGCTATTCCAACTACCGATCTTCTGA 891
Db 846 GCTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
Qy 892 AAGTTCATCGCTACCTACCTATGGAGATGGGTCTTCTGTTGCTGGAAACCGTTGAGTTCG 951
Db 906 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 965
Qy 952 GGTCTCACTGCTGCTCCT 969
Db 966 GCTGCTGCTGCTGCTGCT 983

RESULT 8
CNS0034Y/c 1101 bp DNA GSS 03-JUN-1999
LOCUS CNS0034Y
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR07E07 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL063860
VERSION AL063860.1 GI:4941616
KEYWORDS GSS.
SOURCE fruit fly.

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
GENOSCOPE.
TITLE Direct Submission
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/dev_stage="0 to 24 hours mixed stage embryonic"
/sex="male and female"
/lab_host="XLI Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2."

BASE COUNT 276 a 306 c 227 g 232 t 60 others
ORIGIN

Query Match 3.1%; Score 40.4; DB 121; Length 1101;
Best Local Similarity 45.5%; Pred. No. 0.55;
Matches 143; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 708 GGGTATCACCAACACCGTGTCTTGTGTTGATGCAGCTGTTGTCAGCTGCTGC 767
|||||
Db 631 GGCTGGAACTCGCACTGCTGTGCTGGAGCTGCTGATGGTGTGCTGCTGATGG 572
QY 768 ACATCCAAAGTCTTGTCTAACTCCCTTGGTGATGACATCCCAATTTGGATCCGCAACCTGG 827
|||||
Db 571 AACGGCAATCTCTGCTGATCTGATGTCATGCTGTTGGCAGACAGTAGCGGTTTCATGTTGCTC 512
QY 828 ATACCACATGCTGATGCCCAACCCAGAGCTGCTCCAGCTATTCCAACTACCGATGCTTC 887
|||||
Db 511 GTAGCTGGCTGATAAGGATACGCCCGCAACGTTCTGCAATTTCCGGCAGCAGCTGGCTGCGGC 452
QY 888 TGGAAATTCATCCCTACTCTATGGAGATGGGTCTTCTGTTGCTGGAACCGTTGAGTT 947
|||||
Db 451 TGGAACTGCTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
QY 948 CGCTGGTCTCACTGCTGCTCCTAACTGGAACCGTGTCTACGTTCTCTACACTCAGCTCG 1007
|||||
Db 391 TGGTGATGCTGCTGATTCAACTGGCCGGCGCTCGGCATCATATGTCCTATCATCG 332
QY 1008 TAAGTGTCTCCAG 1021
|||||
Db 331 CCAATGGTGCCTG 318

RESULT 9
AA940845/c
LOCUS AA940845 752 bp mRNA EST 25-NOV-1998
DEFINITION LD23113.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD23113 5prime similar to M23221: fs(1)h
F8gn0004656 PID:g157453 SWISS-PROT:P13709, mRNA sequence.
ACCESSION AA940845
VERSION AA940845.1 GI:3100758

KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 752)
AUTHORS Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein
BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 231 row: B column: 1
High quality sequence stop: 639.
Location/Qualifiers
1..752
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XLI Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2."

BASE COUNT 234 a 231 c 177 g 108 t 2 others
ORIGIN

Query Match 3.1%; Score 40; DB 7; Length 752;
Best Local Similarity 51.1%; Pred. No. 0.64;
Matches 91; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 641 TCGCTAACGGTGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 700
|||||
Db 486 TTGCTGCTGTTGGAGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 427
QY 701 CTCTCAAGGTATCACCAACCAACCGTGTCTTGTGTTGATGCAGCTGTTGTTGCTGAG 760
|||||
Db 426 CTGGTTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
QY 761 CTGGTGCACACTCCAACTCTTGTGCTAACTCCCTTGTGCTGATGACATCCCATTTGATGATAC 818
|||||
Db 366 CTGGTGCCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309

RESULT 10
CNS03ILL 906 bp DNA GSS 13-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
141F22 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL199074
ACCESSION AL199074.1 GI:7837225
VERSION GSS; genome survey sequence.
KEYWORDS Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 906)
AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the

Query Match	3.0%;	Score 38.8;	DB 10;	Length 612;
Best Local Similarity	51.1%;	Pred. No. 1.3;		

Tue Jan 2 15:21:47 2001

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